RAYSTATION 7

User Manual

RayStation

Trace back information:
Workspace Main version a347
Checked in 2017-12-08
Skribenta version 4.6.316

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Declaration of conformity

CE 0413

Complies with 93/42/EEC Medical Device Directive as amended by M1 to M5. A copy of the corresponding Declaration of Conformity is available on request.

Safety notices

This user documentation contains WARNINGS concerning the safe use of the product. These must be followed.

WARNING!

The general warning sign informs you of a risk for bodily harm. In most cases the risk is related to mistreatment of the patient.

Note: *The note informs of a risk for loss of data or other impairment of the work.*

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RaySearch Laboratories

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1 INTRODUCTION

About RayStation 7

RayStation 7 integrates all RaySearch's advanced treatment planning solutions into a flexible treatment planning system. It combines unique features such as Multi-Criteria Optimization tools with full support for 4D adaptive radiation therapy. It also includes functionality such as Plan Explorer as well as algorithms for SMLC, DMLC, VMAT, TomoHelical and IMPT optimization and highly accurate dose engines for photon therapy, electron therapy, proton therapy and carbon ion therapy.

In this chapter

This chapter contains the following sections:

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1.5	Other associated documentation	p. 23

About this manual

This manual describes the functionality of the RayStation 7 application and gives step by step instructions on how to perform the most common operations. The following information is included in this manual:

- **Chapter Introduction** gives an introduction to the RayStation system and the corresponding documentation.
- **Chapter Product description** describes the RayStation 7 product.
- **Chapter The Graphical User Interface** describes the graphical user interface.
- **Chapter Patient Data Management** describes the planning activity Patient Data Management.
- **Chapter Patient Modeling** describes the planning activity Patient Modeling and its program modules Image Registration, Structure Definition and Deformable Registration.
- **Chapter Plan Design** describes the planning activity Plan Design and its program modules Virtual Simulation, Plan Setup, 3D-CRT Beam Design, Electron Beam Design and Proton Beam Design.
- **Chapter Plan Optimization** describes the planning activity Plan Optimization and its program modules Plan Optimization and Multi Criteria Optimization.
- **Chapter Plan Evaluation** describes the planning activity Plan Evaluation and its program modules Plan Evaluation and Biological Evaluation.
- **Chapter QA Preparation** describes the planning activity QA Preparation.
- **Chapter Automated Planning** describes the planning activity Automated Planning and its program modules Automated Breast Planning, Fallback Planning, Fallback Protocol Management and Plan Explorer.
- **Chapter Treatment Adaptation** describes the planning activity Treatment Adaptation and its program modules Dose Tracking and Adaptive Replanning.
- The **Appendices** include the following information:
  - *Appendix A* describes the definitions in the graphical user interface and in the RayStation documentation.
  - *Appendix 4.4* describes the DICOM export procedure.
  - *Appendix B* describes the various shortcuts that can be used within RayStation.
  - *Appendix C* describes scripting in RayStation.
  - *Appendix D* describes system administration.
  - *Appendix E* describes the RayBiology application.
  - *Appendix F* describes the RayStation Report Designer.
  - *Appendix G* describes the line dose export procedure.

1.1 PRODUCT INFORMATION

Intended use

RayStation 7 is a software system designed for treatment planning and analysis of radiation therapy. The treatment plans provide treatment unit set-up parameters and estimates of dose distributions expected during the proposed treatment, and may be used to administer treatments after review and approval by the intended user.

The system functionality can be configured based on user needs.

Intended user

The intended users of RayStation 7 shall be clinically qualified radiation therapy staff trained in using the system.

WARNING!

Restricted sale in the U.S. Federal (U.S.) and State laws restrict the sale of this product to a physician or on a physician's order. (7305)

Contraindications

None known.

1.2 PATIENT WORKFLOW

The RayStation system plays a key role in radiation therapy clinics and is involved in almost all of the steps in the patient workflow.

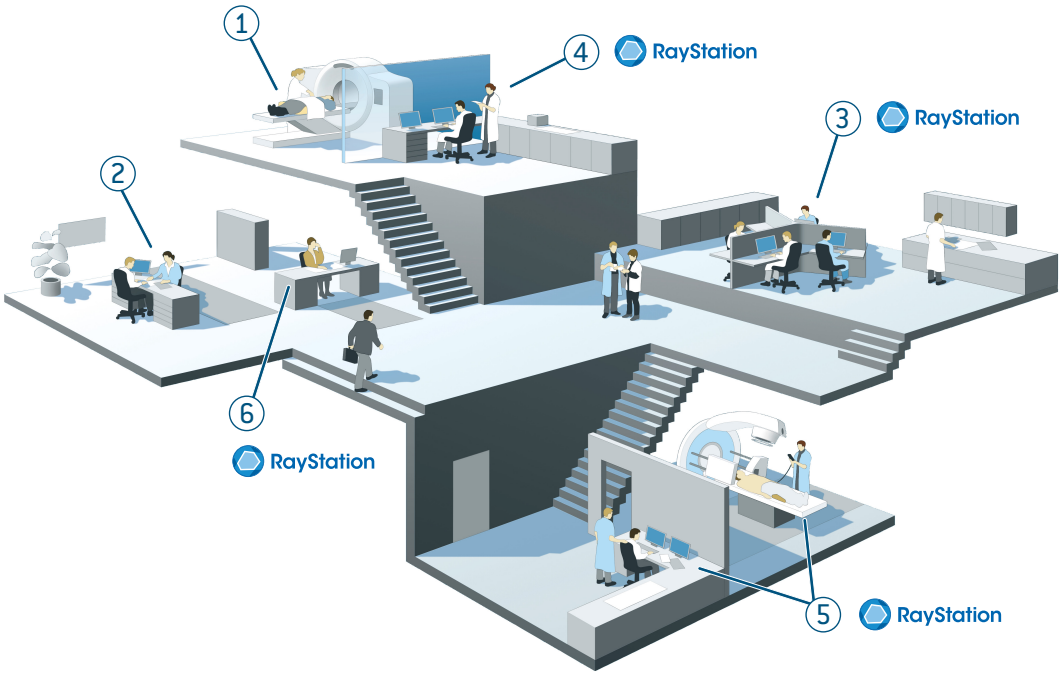


Figure 1. This figure illustrates a schematic overview of the patient workflow that includes the following steps: 1) Diagnosis 2) Prescription 3) Treatment planning 4) Simulation 5) Treatment 6) Follow-up.

1.3 RAYSTATION SYSTEM APPLICATIONS

The RayStation system consists of the following applications:

RayStation – the main application where all the activities associated with treatment planning can be performed.
The RayStation application is described in this manual.

RayPhysics – the beam commissioning application where activities such as beam commissioning, CT commissioning and beam 3D modeling activities can be performed.
The RayPhysics application is described in *RSL-D-RS-7.0-RPHY, RayStation 7 RayPhysics Manual*.

RayBiology – the manager where models for radiobiological evaluation and optimization, and relative biological effectiveness (RBE) can be administrated.
The RayBiology application is described in *Appendix E RayBiology*.

Clinic Settings – the clinic settings administration tool.
The Clinic Settings application is described in *section D.2 The Clinic Settings application on page 920*.

RayStation Storage Tool – the database administration tool.
The RayStation Storage Tool application is described in *section D.3 The RayStation Storage Tool application on page 940*.

1.4 RAYSTATION SYSTEM DOCUMENTATION

The RayStation 7 system documentation consists of:

Document	Description
RSL-D-RS-7.0-RPHY, RayStation 7 RayPhysics Manual	This manual describes the RayPhysics application.
RSL-D-RS-7.0-REF, RayStation 7 Reference Manual	This manual contains algorithm descriptions and physical reference information.
RSL-D-RS-7.0-OPT, A guide to optimization in RayStation 7	This manual contains detailed information about optimization in RayStation 7.
RSL-D-RS-7.0-IFU, RayStation 7 Instructions For Use	This manual contains regulatory information and safety information concerning the RayStation 7 system.
RSL-D-RS-7.0-USM, RayStation 7 User Manual	This manual describes the functionality of the RayStation 7 system and gives step by step instructions on how to perform the most common operations.
RSL-D-RS-7.0-RN, RayStation 7 Release Notes	This document provides a summary of new features, known issues and changes since the previous version of RayStation.

Note: *In the case of a service pack, only the affected manuals will be updated. For a complete list of the manuals that have been updated in the service pack, refer to the Release Notes document for that specific service pack.*

1.5 OTHER ASSOCIATED DOCUMENTATION

- *RSL-D-RS-7.0-SEAT, RayStation 7 System Environment Acceptance Test Protocol*
- *RSL-D-RS-7.0-SG, RayStation 7 Scripting Guideline*
- *RSL-D-RS-7.0-BCDS, RayStation 7 Beam Commissioning Data Specification*
- *RSL-D-RS-7.0-TPL, RayStation 7 Third Party Licenses*
- *RSL-D-RS-7.0-DCS, RayStation 7 DICOM Conformance Statement*
- *RSL-D-RS-7.0-SEG, RayStation 7 System Environment Guidelines*

2 PRODUCT DESCRIPTION

This chapter gives an introduction to the functions and features of the RayStation application.

In this chapter

This chapter contains the following sections:

2.1	RayStation overview	p. 26
2.2	Planning activities and modules	p. 28
2.3	Advanced features	p. 42
2.4	Hardware compatibility	p. 46

2.1 RAYSTATION OVERVIEW

In the RayStation application, all activities associated with treatment planning can be performed.

RayStation consists of a set of planning activities and each planning activity contains at least one program module. A module corresponds to a coherent group of functionality for the selected planning activity. The module includes at least one workspace with patient views and toolbars where various operations and evaluations can be performed.

In addition to the ordinary planning activities, RayStation also supports scripting. Scripting in RayStation provides automation, connectivity and flexibility. For more information about scripting, see *Appendix C Scripting* and *RSL-D-RS-7.0-SG, RayStation 7 Scripting Guideline*.

Some modules described in this manual are not included in the standard configuration of RayStation 7 and may require additional licences. The required licenses are summarized in the following table.

The following table lists the planning activities and the corresponding modules:

Planning activity	Program module within the planning activity
Automated Planning	• **Automated Breast Planning** (Required license: rayAutoBreast) • **Fallback Planning** (Required license: rayFallback) • **Fallback Protocol Management** (Required license: rayFallback) • **Plan Explorer** (Required license: RayExplorer)
Patient Data Management	• **Patient Information** (Included in standard configuration)
Patient Modeling	• **Image Registration** (Required license: rayAnatomy) • **Structure Definition** (Required license: rayAnatomy) • **Deformable Registration** (Required license: rayDeformable)
Plan Design	• **Virtual Simulation** (Required license: raySimulation) • **Plan Setup** (Included in standard configuration) • **3D-CRT Beam Design** (Required license: rayConformal) • **Electron Beam Design** (Required license: rayElectronPlanning) • **Proton Beam Design** (Required licenses: rayUniformScanning (Uniform Scanning) or rayPassiveScattering (Double Scattering) or rayWobbling (Wobbling))

Planning activity	Program module within the planning activity
Plan Optimization	• **Plan Optimization** (Required license: rayOptimizer) • **Multi Criteria Optimization** (Required license: rayNavigator)
Plan Evaluation	• **Plan Evaluation** (Required license: rayEvaluation) • **Biological Evaluation** (Required license: rayBiology)
QA Preparation	• **QA Preparation** (Included in standard configuration)
Treatment Adaptation	• **Dose Tracking** (Required license: rayTracker) • **Adaptive Replanning** (Required license: rayAdaptive)

2.2 PLANNING ACTIVITIES AND MODULES

This section gives an introduction to the RayStation planning activities and the corresponding program modules. It also describes when to use the different modules in the treatment planning process.

In this section

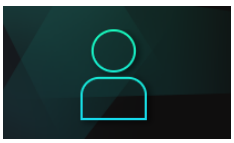
This section contains the following sub-sections:

2.2.1	Patient Data Management	p. 29
2.2.2	Patient Modeling	p. 30
2.2.3	Plan Design	p. 32
2.2.4	Plan Optimization	p. 34
2.2.5	Plan Evaluation	p. 37
2.2.6	QA Preparation	p. 38
2.2.7	Automated Planning	p. 39
2.2.8	Treatment Adaptation	p. 41

2.2.1 Patient Data Management

The Patient Information module

The Patient Information module, presents an overview of the current patient, case and plan. The module provides functions for opening, editing, saving, importing, exporting and deleting patient/case data. This is where image set data is managed, for example selection of CT to density conversion tables.



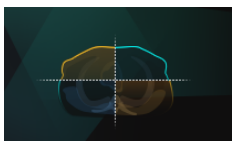
The Patient Information module is described in detail in *chapter 4 Patient Data Management*.

2.2.2 Patient Modeling

The Patient Modeling activity in RayStation contains tools for creating a rich and accurate representation of the patient anatomy used in the treatment planning process.

The Image Registration module

In the Image Registration module, rigid registration of multi-modality imaging CT, CBCT, PET or MR is fully supported and integrated. It can be used for showing fused images as reference while contouring, and for mapping regions or points of interest between image sets.



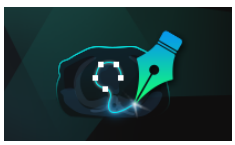
Required license: rayAnatomy.

The Image Registration module is described in detail in *section 5.2 The Image Registration module on page 173*.

The Structure Definition module

Advanced manual and semi-automatic contouring

The Structure Definition module includes a comprehensive tool set for manual contouring such as polygon, freehand, 2D rollerball, smart brush and local deformations (push-and-pull). It also supports Regions of Interest (ROIs) with voxel-based triangulation, 4D visualization and boolean algebra for combining ROIs. Templates can be saved with or without the geometries included and the templates can then be reused for future patients.



Model-Based Segmentation (MBS)

MBS is a semi-automatic tool for delineation of ROIs based on biomechanical and statistical information about organs. Volumetric images are segmented semi-automatically, utilizing a combination of grey-scale gradients and models with knowledge of how organs may change shape. It is possible to delineate multiple ROIs simultaneously which increases throughput, accuracy and reproducibility.

Atlas-Based Segmentation, a versatile auto-segmentation tool

Existing data from the clinic database is used to create templates with multiple image sets - atlases. The atlases are used to segment new image data by finding the best matching atlases through rigid image registration. Deformable registration is then applied to deform the ROI and POI geometries onto the new image set.

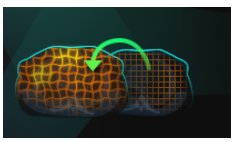
The geometries contained in each atlas can be manually contoured or generated with MBS. If MBS ROIs are available in the template, they may be automatically adapted after atlas-based initialization is completed. Derived ROIs created from a template will automatically be updated after initialization and MBS adaptation.

Required license: rayAnatomy.

The Structure Definition module is described in detail in *section 5.3 The Structure Definition module on page 186*.

The Deformable Registration module

When images of the patient in treatment position, from CT, PET/ CT, cone-beam CT or MR, are acquired during the treatment course, the Deformable Registration module makes it possible to establish a deformable registration between the new geometry and the planning geometry.



Required license: rayDeformable.

The Deformable Registration module is described in detail in *section 5.4 The Deformable Registration module on page 252*.

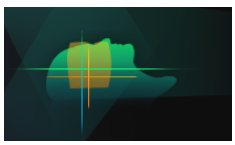
2.2.3 Plan Design

The Plan Design activity in RayStation contains tools for designing the patient plan used in the treatment planning process.

In the Beam Design modules, beam orientations, apertures and various beam modifiers are designed by the user in order to manually create the optimal plan.

The Virtual Simulation module

The Virtual Simulation module provides a streamlined and straightforward workspace to perform fast plan design of virtual simulation plans as well as functionality to use laser export for patient marking on planned isocenter position.

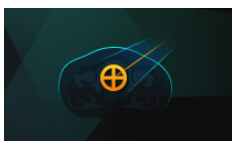


Required license: raySimulation.

The Virtual Simulation module is described in detail in *section 6.2 The Virtual Simulation module on page 386*.

The Plan Setup module

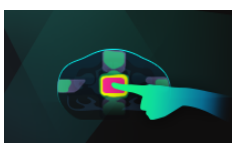
The Plan Setup module is where the basis for the treatment plan is specified such as treatment modality, treatment technique, treatment orientation, number of beams and isocenter positioning.



The Plan Setup module is described in detail in *section 6.1 The Plan Setup module on page 295*.

The 3D-CRT Beam Design module

The 3D-CRT Beam Design module in RayStation provides conventional 3D-CRT, forward treatment planning, with manual and automatic tools to create conformal treatment using treat and protect, beam weighting, wedges etc. 3D-CRT plans can be automatically optimized with respect to any combination of segment shapes, segment monitor units, collimator, gantry and couch angles. This makes the creation of high quality 3D-CRT plans faster and more consistent.

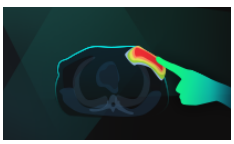


Required license: rayConformal.

The 3D-CRT Beam Design module is described in detail in *section 6.3 The 3D-CRT Beam Design module on page 421*.

The Electron Beam Design module

In the Electron Beam Design module, it is possible to mix electrons and photons in a single treatment plan using multiple coupled or independent beam sets. The Graphical User Interface offers a range of tools and a 3D visualization of the treatment setup. In the 3D view, the physical perimeter of the selected applicator, in the patient geometry, can be inspected to assist the planner in collision avoidance. The Electron Beam Design module supports automatic generation of the cutout shape by the same treat and protect tools used in the 3D-CRT Beam Design module. The cutout can also be created and edited by a manual brush tool.

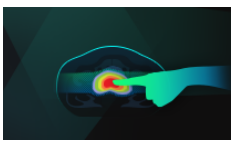


Required license: rayElectronPlanning.

The Electron Beam Design module is described in detail in *section 6.4 The Electron Beam Design module on page 460*.

The Proton Beam Design module

The Proton Beam Design module provides modern tools for efficient planning of Uniform Scanning, Double Scattering and Wobbling to help the user create clinical treatment plans and subsequent milling machine instructions including the automated creation of compensators and aperture with manual editing possibilities.



Required licenses: rayUniformScanning, rayPassiveScattering or rayWobbling.

The Proton Beam Design module is described in detail in *section 6.5 The Proton Beam Design module on page 478*.

2.2.4 Plan Optimization

The Plan Optimization module - photon planning

The Plan Optimization module can be used to generate optimized SMLC, DMLC, VMAT, Conformal Arc, 3D-CRT, and TomoHelical photon treatment plans through optimization with respect to user-defined treatment objectives and constraints.

Required license: rayOptimizer.

3D-CRT/Conformal Arc

The Plan Optimization module provides tools to design and optimize 3D-CRT plans. It is also possible to further optimize plans of 3D-CRT and Conformal Arc type that were initially created in the 3D-CRT Beam Design module.

Required license: rayConformal.

SMLC/DMLC

The Plan Optimization module provides tools to design and optimize SMLC treatment plans. Through direct optimization of step-and-shoot segments, SMLC/DMLC plans of high quality and with a minimum number of segments are created. This increases the overall treatment quality by speeding up both the planning and delivery process. Conversion for Sliding Window (i.e., DMLC) is also supported.

Required license: rayIntensity.

VMAT

RayStation offers design and optimization of single or multiple-arc plans. VMAT is planned through an optimization procedure (inverse planning) where objectives and constraints for the desired dose are defined, and the system produces the plan that best matches these criteria within the limitations of the treatment machine. That means the optimized plan is directly deliverable and no quality-degrading post processing is required.

Required license: rayArc.

TomoHelical

The optimization procedure for TomoHelical plans is similar to the one used for e.g., SMLC or VMAT. Objectives and constraints are defined and the optimized plan is directly deliverable.

Required license: rayTomo

The Plan Optimization module for photon planning is described in detail in *section 7.1 The Plan Optimization module - photons on page 518*.

The Plan Optimization module - proton planning

RayStation provides tools for designing and optimizing actively scanned pencil beam proton treatment plans like IMPT, single field uniform dose and distal edge tracking.

Required license: rayPencilScanning or rayLineScanning.

The Plan Optimization module for proton planning is described in detail in *section 7.2 The Plan Optimization module - protons on page 565*.

The Plan Optimization module - carbon ion planning

RayStation provides tools to generate optimized carbon ion plans for Pencil Beam Scanning in the Plan Optimization module through optimization with respect to user-defined treatment objectives and constraints.

Required license: rayCarbonPlanning.

The Plan Optimization module for carbon ion planning is described in detail in *section 7.3 The Plan Optimization module - carbon ions on page 610*.

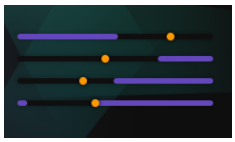
The Multi Criteria Optimization module

A constant difficulty encountered in radiation therapy treatment planning is the patient-specific trade-off between appropriate tumor coverage and avoiding excessive radiation to healthy structures.

Such tradeoffs are conventionally resolved by manually altering an optimization problem formulation and re-optimizing the treatment plan multiple times. Trial and error of this form is time consuming and even if a treatment plan deemed satisfactory is found, it is not clear if better treatment options exist for the current patient.

Instead, RayStation's Multi-Criteria Optimization tool (MCO) generates a set of relevant treatment plans that are Pareto optimal with respect to the user-specified set of tradeoffs, objectives and constrains. These Pareto optimal plans are feasible with respect to all constraints where no objective can be improved without impairing another one.

Based on these plans, the planner or physician can navigate sliders in real-time to balance between conflicting clinical goals.



Required license: rayNavigator.

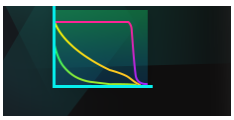
The Multi Criteria Optimization module is described in detail in *section 7.4 The Multi Criteria Optimization module on page 653*.

2.2.5 Plan Evaluation

The Plan Evaluation module

The Plan Evaluation module contains a comprehensive toolbox for evaluation and comparison of treatment plans and plan approval. From a number of pre-defined layouts, dose distribution, dose statistics, clinical goals and dose volume histograms of up to three different plans can be simultaneously compared.

Dose can directly be computed on additional image sets and summed up using the deformable registration provided in the Deformable Registration module. For evaluation of robustness dose can also be computed for a density perturbation or isocenter shift.



Required license: rayEvaluation.

The Plan Evaluation module is described in *section 8.1 The Plan Evaluation module on page 718*.

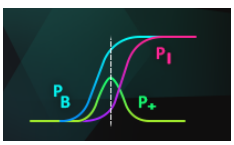
The Biological Evaluation module

RayStation provides tools for both biological optimization and evaluation.

The biological optimization tools can be used to optimize directly on the biological indices in combination with physical dose-based optimization functions. Optimization problems which more closely describe the clinical intentions, e.g, minimizing normal tissue complication probabilities subject to a guaranteed homogenous target dose within a specified standard deviation, can be defined.

The biological evaluation tools includes Tumor Control Probability (TCP) and Normal Tissue Complication Probability (NTCP) models which can be combined with tissue repair and tumor growth models. Some biological tools are integrated in the Plan Evaluation module, the physical properties of the existing plan can then be investigated if unexpected differences in the biological response are observed between different plans.

The Biological Evaluation module is dedicated to the exploration of the biological effects of altering the fractionation schedule of a single treatment plan.



Required license: rayBiology.

Biological evaluation in the Plan Evaluation module is described in detail in *section 8.1.14 Biological evaluation on page 743*.

The Biological Evaluation module is described in detail in *section 8.2 The Biological Evaluation module on page 758*.

2.2.6 QA Preparation

The QA Preparation module

The module for Quality Assurance preparation (QA Preparation) allows the user to easily transfer the clinical plan to a phantom and recalculate dose, either beam by beam or for the entire plan. The output from the module is the dose distribution in DICOM format or a 2D dose plane, a QA report and optionally a new treatment plan with collapsed gantry angles.

The QA Preparation module is described in detail in *chapter 9 QA Preparation*.

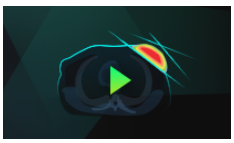
2.2.7 Automated Planning

The Automated Breast Planning module

The Automated Breast Planning module is the first step towards automated standard procedures in RayStation.

The Automated Breast Planning module provides tools for automated generation of tangential breast IMRT plans using heuristic optimization and includes features such as:

- Automatic detection of radio-opaque markers defining the breast
- Automatic contouring of all the relevant target and risk organs
- Automatic setup of beams, including heuristic optimization of gantry and collimator angles
- Automatic creation of objective functions, optimization and segmentation settings and clinical goals



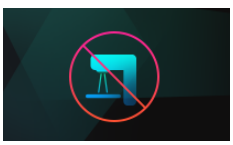
Required license: rayAutoBreast.

The Automated Breast Planning module is described in detail in *section 10.2 The Automated Breast Planning module on page 829*.

The Fallback Planning module and the Fallback Protocol Management module

Fallback planning in RayStation is a tool for creating additional plans to be used in a contingency situation, enabling a patient to be treated on another machine, possibly with a different modality and/or treatment technique, in case the original machine is unavailable.

Fallback planning is performed in both the Fallback Planning module and the Fallback Protocol Management module. A suggested workflow of the entire fallback planning process is described in *section 10.3 The Fallback Planning workflow on page 843*.



Fallback planning can be used to convert plans, including proton plans and TomoTherapy plans, to photon plans with various treatment techniques such as 3D-CRT, SMLC and/or VMAT. A dose mimicking function is used to replicate the DVHs of a given plan, but with a different treatment machine or treatment modality. Before approval, the fallback plans can be compared and evaluated using a number of visual tools such as DVH curves, dose statistics, dose difference and clinical goals.

If the original treatment machine becomes available again, it is also possible to convert back to the original plan.

The Fallback Planning module can drastically reduce planning time in emergency situations when a machine is down, allowing the patients' treatment to continue.

Required license: rayFallback.

The Fallback Planning module is described in detail in *section 10.4 The Fallback Planning module on page 849*.

The Fallback Protocol Management module is described in detail in *section 10.5 The Fallback Protocol Management module on page 856*.

The Plan Explorer module

The Plan Explorer module provides tools to automatically generate multiple plans and quickly select the most suitable plan(s) based on clinical goals and hardware properties.

The Plan Explorer module fully supports photon plans with treatment techniques SMLC, DMLC and VMAT. Plans of other treatment modalities and treatment techniques can be copied to Plan Explorer for plan comparison.

The module includes features such as:

- automatic optimization with the objective to fulfill clinical goals
- high-speed calculations using a High Performance Computing (HPC) cluster
- plan filtering with respect to fulfillment of clinical goals
- plan filtering with respect to treatment machines and treatment setup parameters
- fast plan comparison using clinical goals radar charts
- detailed side-by-side comparison of plans

Required license: RayExplorer.

The Plan Explorer module is described in detail in *section 10.1 The Plan Explorer module on page 803*.

2.2.8 Treatment Adaptation

RayStation was designed from the very beginning with a strong focus on handling the dynamic aspects of radiation therapy. By explicitly representing the time dimension throughout the domain model, RayStation provides a framework for planning and managing adaptive radiation therapy.

The Dose Tracking module

When images of the patient in treatment position, from CT, PET/ CT, Cone-Beam CT (CBCT) or MR, are acquired during the treatment course, the Deformable Registration module makes it possible to establish a deformable registration between the new geometry and the planning geometry.

In the Dose Tracking module, the deformable registration can be used to recalculate, deform and accumulate doses from different fractions in a common geometry, thereby computing the dose delivered to the patient anatomy.

Required licenses: rayTracker.

The Dose Tracking module is described in detail in *section 11.2 Dose Tracking on page 868*.

The Adaptive Replanning module

If there are deviations from the planned dose distribution, found in the Dose Tracking module, that require action, the Adaptive Replanning module provides a wide range of adaptive offline or online replanning tools that take into account the accumulated dose and observed deviations of the patient geometry.

Plans can then be re-optimized and adjusted to compensate for dose coverage problems or to adapt to adjusted clinical goals. The replanning options range from simple adaptations such as adjustments of beam weights to complete replanning that involves re-optimization of the intensity modulation.

RayStation's adaptive replanning tools, combined with powerful deformation algorithms, can improve the planning process.

Required licenses: rayAdaptive.

The Adaptive Replanning module is described in detail in *section 11.2 Dose Tracking on page 868*.

2.3 ADVANCED FEATURES

RayStation contains advanced features for automation and streamlining of the treatment planning process; automatic generation of treatment plans via plan generation protocol and automation of common processes through scripting.

In this section

This section contains the following sub-sections:

2.3.1	Templates	p. 43
2.3.2	Plan generating protocols	p. 44
2.3.3	Scripting	p. 45

2.3.1 Templates

A template is a predetermined definition on how to automatically create a set of items added to a treatment plan. It is also used in plan generating protocols. Examples of items created by templates includes structures, beams, optimization functions and clinical goals. By utilizing templates it is possible to reduce the time spent on setting up treatment plans.

Approval of templates

In RayStation it is possible to approve templates. It is only the users of the Administration group (admin users) that may approve templates and delete approved templates. For structure templates an admin user may also unapprove templates. An approved template is indicated by a padlock icon next to the template name.

If a non-approved template is used, either when applying a template or being added to a protocol, a warning will be displayed. However, it is still possible to continue by acknowledging the warning. These warnings can also be deactivated in Clinic Settings. For more information, see *section D.2.2 The Preferences tab on page 922*.

2.3.2 Plan generating protocols

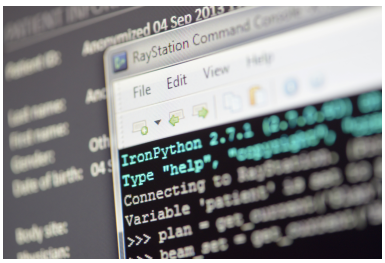
RayStation supports several tools such as templates and plan generation protocols to automate parts of the planning process. A protocol is a list of plan generation steps which can be applied automatically. Examples of plan generation steps include atlas based segmentation, plan creation, add dose prescription, set dose grid resolution, add beams, add optimization functions, add beam optimization settings, start optimization and dose computation. When a protocol is running it will automatically modify an existing treatment plan or create a new treatment plan using the included steps, which significantly reduces the planning time.

Plan generation protocols are described in detail in *section 6.1.2 Plan generation protocols on page 300*.

2.3.3 Scripting

Scripting in RayStation provides automation, connectivity and flexibility beyond the standard user interface.

The available script languages, IronPython 2.7 and CPython 2.7, are complete programming languages. They let the user access all capabilities of the operating system and other applications, for example to write files, start processes, communicate with other computers, and control other scriptable applications such as Microsoft Office or .NET.



Automation

Through scripting, the clinic specific procedures can be automated. For example, a script can check for properties in a plan such as small segments, disconnected target volumes, hot spots, undesirable gantry and couch angles, and based on this information display a warning message or create a report.

Connectivity

Scripting provides a way to customize the interaction between RayStation and other systems for scenarios where DICOM is not sufficient.

Flexibility

Scripting can be used to create capabilities which are not specifically available in the standard interface. For example, automatic marker detection, export of images of non-standard dose planes and images of all control points can be utilized as desired. Scripting puts power in the hands of the clinicians to use RayStation in a way that best serves the needs of their department.

Scripting on multiple patients - a potential research tool

Through its ability to execute over multiple patients, scripting is an ideal tool for retrospective data analysis and for evaluating new treatment techniques. For example, a script can go through a cohort of patients and systematically alter some parameter and record the effect or just extract data such as dose statistics.

Related information

Scripting in RayStation is described in *Appendix C Scripting*.

For more detailed information about scripting, refer to *RSL-D-RS-7.0-SG, RayStation 7 Scripting Guideline*.

2.4 HARDWARE COMPATIBILITY

RayStation is compatible with all linear accelerators commercially available.

RayStation's data model is fully compatible with the DICOM standard, allowing the system to import and export any DICOM RT object. This includes multiple CT, MR and PET image series, 4D-CT, structure sets, doses and RT Plan and RT Ion treatment plans. In addition, RayStation communicates with other data sources such as IHE RO, DICOM senders and receivers or DICOM archives, using either file transfer, DICOM storage service classes or DICOM query/retrieve.

3 THE GRAPHICAL USER INTERFACE

This chapter presents an overview of the Graphical User Interface (GUI) of the RayStation 7 system. It describes the various buttons and navigators, common symbols, common views, common graphs and tables, visualization settings and the context menu. Operations such as undo/redo and backup and restore are also described in this chapter.

In this chapter

This chapter contains the following sections:

3.1	The Graphical User Interface overview	p. 48
3.2	Typographical conventions	p. 49
3.3	Buttons and navigators	p. 50
3.4	The tool panel tabs - ROI list, POI list, Visualization, etc.	p. 53
3.5	Common symbols	p. 68
3.6	Common views	p. 71
3.7	Common graphs, tables and tools	p. 77
3.8	Level/window and color tables	p. 93
3.9	The context menu	p. 102
3.10	Undo and redo procedures	p. 105
3.11	Cancel procedure	p. 106

Precautions

WARNING!

Running multiple instances of RayStation 7. Take extra care when running multiple instances of RayStation 7. Always make sure that you are working on the correct patient. (24593)

3.1 THE GRAPHICAL USER INTERFACE OVERVIEW

The RayStation 7 application is divided into different parts, called planning activities. Each planning activity holds at least one program module with functionality related to the planning activity. Each module includes at least one workspace with patient views and toolbars.

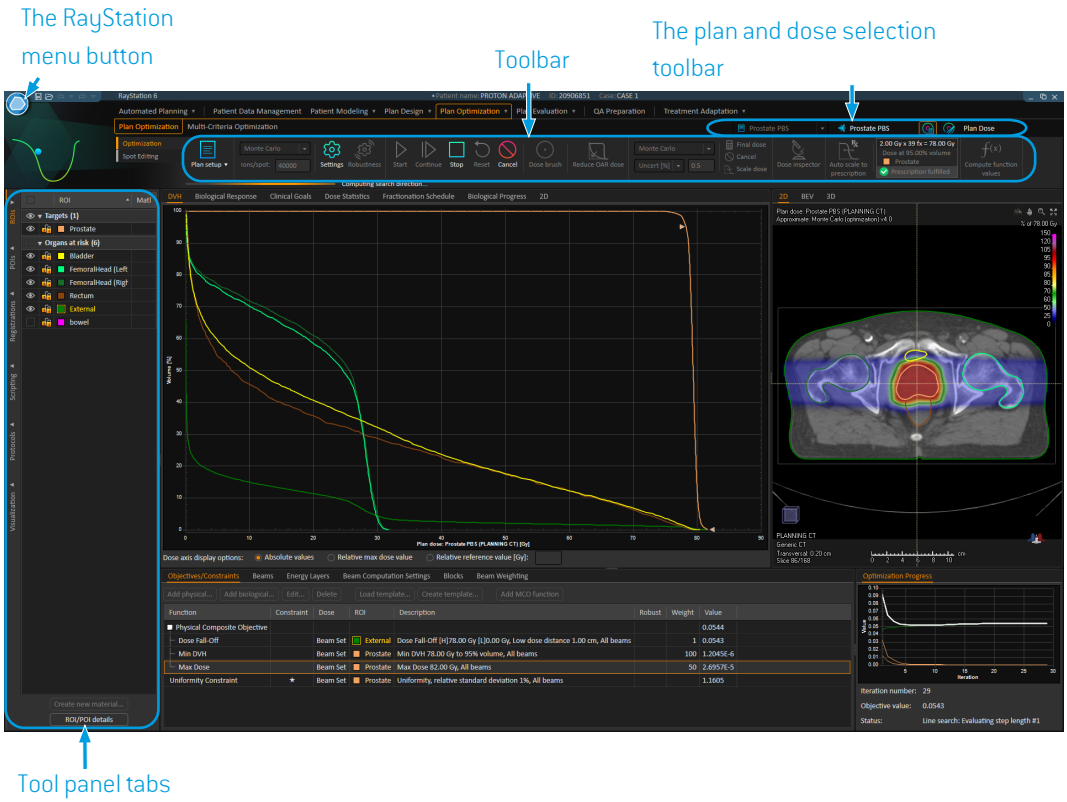


Figure 2. The RayStation user interface overview. This example shows the planning activity Plan Optimization with the active module Plan Optimization.

3.2 TYPOGRAPHICAL CONVENTIONS

Names (e.g., beam names) entered by the user are unique if they differ by upper case/lower case letters or space characters. Be aware of that beam names that technically are unique, may seem identical.

Beam meterset unit

The default beam meterset unit in RayStation is Monitor Units (MU). For ion treatment machines it is possible to select the primary dosimetry unit to Number of Particles (NP) instead of MU. Plans created with an ion machine with the primary dosimetry unit set to NP will present beam meterset values as NP in RayStation. This is also the case for DICOM export/import (see Ion DICOM Conformance Statement).

Note: *In this manual MU is used for beam meterset in most descriptions and screenshots.*

Jaw naming convention in this manual

The examples in this manual uses jaw labeling convention according to the IEC 61217 standard.

In **IEC 61217**, Y2 is close to the gantry and Y1 is away from the gantry, X1 is to the left and X2 to the right for an observer facing the gantry with gantry and collimator angle zero in the IEC 61217 coordinate system.

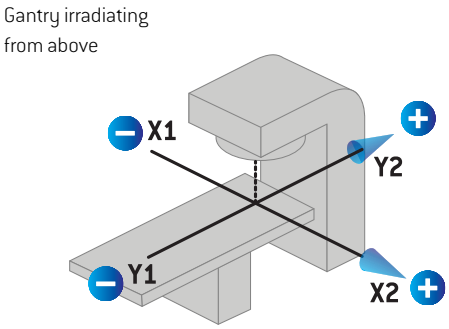


Figure 3. The jaw and MLC labels (IEC 61217).

For more information about coordinate systems, refer to the *RSL-D-RS-7.0-IFU, RayStation 7 Instructions For Use*.

Display formats

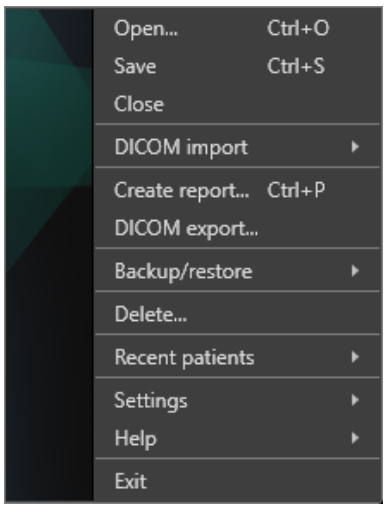
In RayStation date and time is displayed in format "DD MMM YYYY, hh:mm:ss (hr:min:sec)", e.g., "14 Jan 1975, 08:20:42 (hr:min:sec)".

3.3 BUTTONS AND NAVIGATORS

This section presents the various buttons and navigators presented in the RayStation 7 graphical user interface.

The RayStation menu

The RayStation menu provides access to global functions such as opening, saving and deleting patient data, GPU settings, RayStation Help (integrated help) and functions for importing and exporting DICOM data. The RayStation menu is opened by clicking the RayStation icon in the upper left corner.



RayStation Help

The *RSL-D-RS-7.0-USM, RayStation 7 User Manual* can be opened in html format from the RayStation menu. To open the the RayStation Help, select **Help: RayStation Help** from the RayStation menu or type F1.

The RayStation Help must be configured in Clinic Settings. For more information, see *section D.2 The Clinic Settings application on page 920*.

The title bar toolbar

The title bar toolbar is located next to the blue icon in the upper left corner. The title bar toolbar holds buttons for opening and saving patient data and for undo and redo.

The planning activity tabs

The planning activity tabs are located at the top of the workspace. They are placed in ascending order, from left to right, in which the activities are typically performed. The planning activities are:

- Automated Planning

- Patient Data Management
- Patient Modeling
- Plan Design
- Plan Optimization
- Plan Evaluation
- QA Preparation
- Treatment Adaptation

The user can toggle between different activities by clicking the tabs. Each planning activity contains at least one module where various operations related to the planning activity can be performed.

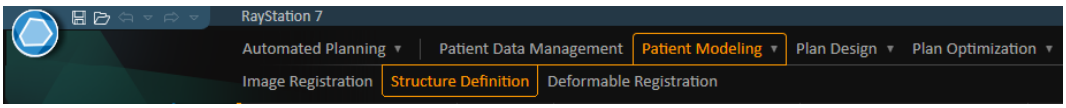


Figure 4. The planning activity tabs, where Patient Modeling is currently active.

The module tabs

A module corresponds to a coherent group of functionality for the selected planning activity. The module includes at least one workspace with patient views and toolbars where various operations and evaluations can be performed. The user can toggle between different modules for the selected activity by clicking the module tabs or by clicking the desired module in the module drop-down menus next to the activity tabs.

The plan and dose selection toolbar

The plan and dose selection toolbar is located in the top right corner. It contains the **Plan** drop-down list which contains all the plans created for the current patient, the **Beam Set** drop-down list, which contains all the beam sets for the current plan and the dose presentation buttons.

Figure 5. The plan and dose selection toolbar.

Note: *In the Structure Definition module the active image set can be set to an image set which is not the planning image set. To be able to show dose, the active image set needs to be the same as in the selected plan.*

Select to display **Plan dose**, **Beam set dose** or **Beam dose** for the current beam set and plan.

The **Plan dose** button.

The **Beam Set dose** button.

The **Beam dose** button.

The **Delivered dose** button.

The **Background dose** button.

The **Beam Set + Background dose** button.

3.4 THE TOOL PANEL TABS - ROI LIST, POI LIST, VISUALIZATION, ETC.

To the left in the RayStation 7 workspace is the tool panel which contains both general and module specific tool tabs. The tool panel can be hidden by clicking the header of the active tab.

There are six general tool tabs, i.e., tool tabs that remain throughout the different planning activities and modules. These are:

- the **ROI list** tab
- the **POI list** tab
- the **Registration** tab
- the **Scripting** tab (described in detail in *Appendix C Scripting*)
- the **Protocols** tab (described in detail in *section 6.1.2 Plan generation protocols on page 300*)
- the **Visualization** tab

In this section

This section contains the following sub-sections:

3.4.1	The ROI list	p. 54
3.4.2	The POI list	p. 57
3.4.3	ROI/POI details	p. 59
3.4.4	The Registrations tab	p. 61
3.4.5	The Visualization tab	p. 62

3.4.1 The ROI list

The ROI list (**ROIs**) shows the ROIs of the current patient, grouped by Organ type (Target, Organ at risk, Other or Unknown). For each ROI, settings can be changed directly in the ROI list. Visibility can be toggled on or off by checking/unchecking the visibility checkbox for an individual ROI, for a group of ROIs, or for all ROIs. Select several ROIs in the list by pressing the SHIFT or CTRL key while selecting the desired ROIs in the list. Right-click in the ROI list and select to **Show ROI(s)**, **Hide ROI(s)** or **Delete ROI(s)**.

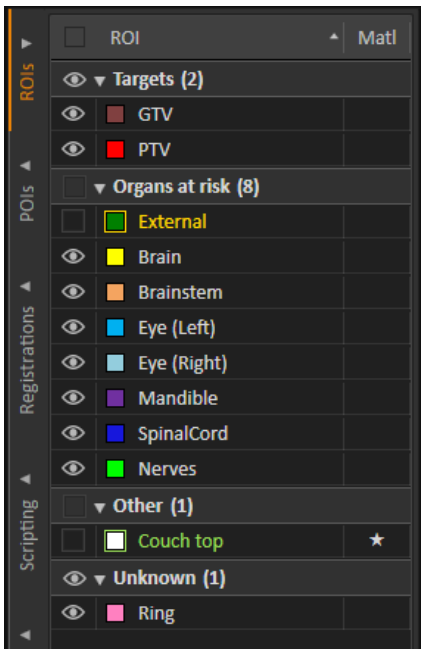


Figure 6. The ROI list.

Double-click on an ROI in the list or right-click an ROI and select **Properties** to open the **ROI Properties** dialog. The **ROI properties** dialog displays properties for the selected ROI. Each property is editable as long as the ROI is not approved. There is also a list of geometries displaying approval status, derived ROI status, representation, volume, and min/max/average intensity for each image set.

Note: *Ensure that the correct Organ type is set. Otherwise, it may be impossible to select the desired optimization function or treat/protect ROI. Moreover, the ROI may not be possible to include in the deliverable plan generation in MCO.*

Note: *If the user has a carbon planning license and has selected an RBE cell type for an ROI, the RBE cell type will be shown next to the ROI in the ROI list.*

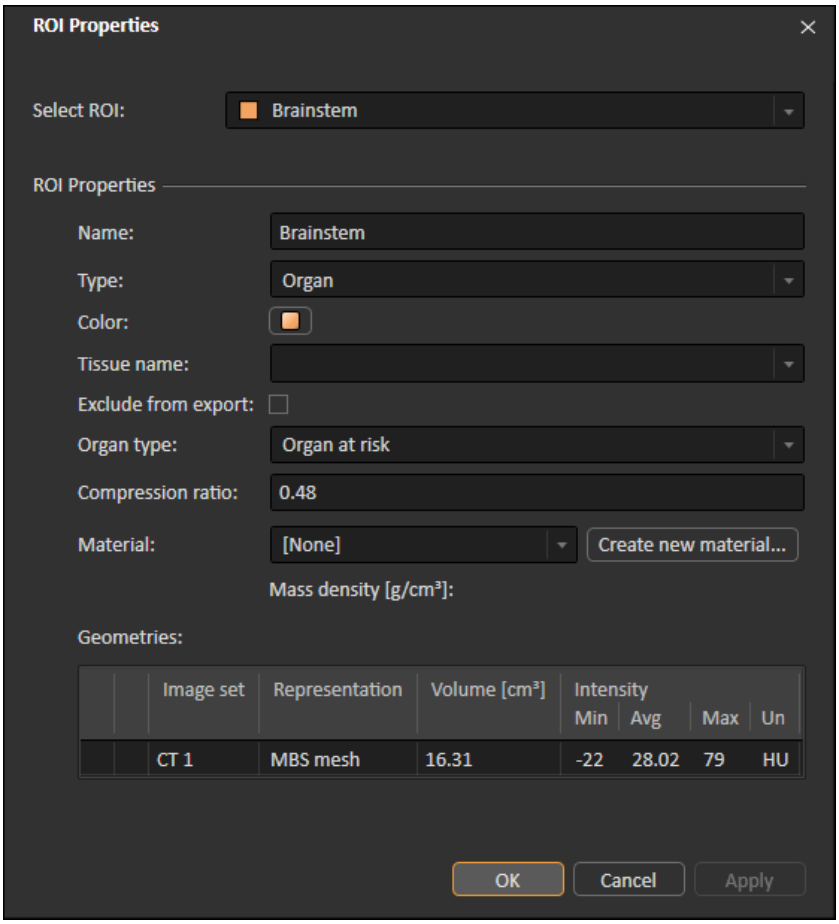


Figure 7. The **ROI Properties** dialog.

WARNING!

Material override for multiple structure sets. If material override is defined for an ROI which does not have any geometry defined in the used image set, there will be no warning when computing dose. (7608)

Note: *If the user has a carbon planning license, it is possible to select a cell type for the ROI. For the carbon ion RBE dose computation, a cell type (which is present in the plan RBE model) must be defined for the External ROI. No other ROIs can have a cell type defined when computing RBE dose.*

Note: *If the ROI is approved it is not possible to modify the tissue.*

Note: *If there are any TCP or NTCP functions defined on the same ROI in any plan in the patient and a new tissue type is selected, a warning will be displayed stating that all other TCP and NTCP functions must be deleted.*

Note: *If Exclude from export is selected in the ROI Properties dialog, the ROI and all its contours will be excluded from the DICOM export. It is not possible to exclude ROIs of type Bolus or ROIs with material override.*

3.4.2 The POI list

The POI list (**POIs**) lists the POIs of the current patient.

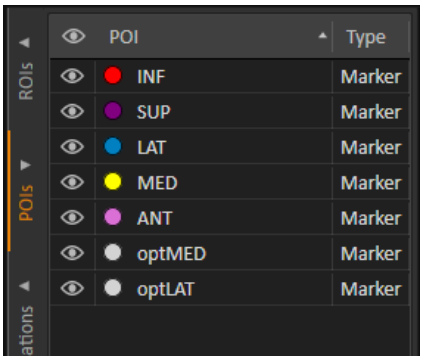


Figure 8. The POI list.

Double-click on a POI in the list or right-click on a POI and select **Properties** to open the **POI Properties** dialog. The **POI Properties** dialog displays properties for the selected POI. Each property is editable as long as the POI is not approved. There is also a list of geometries displaying approval status and point position for each image set.

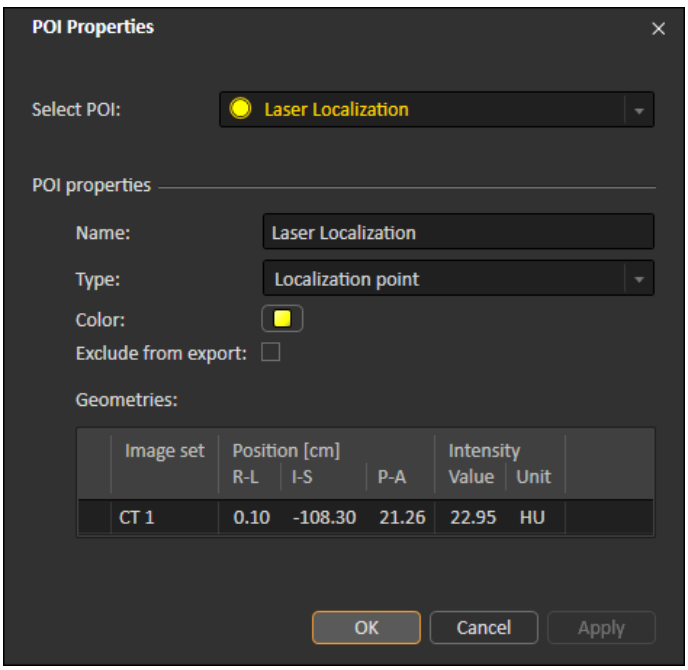
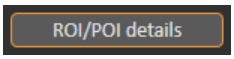


Figure 9. The **POI Properties** dialog.

Note: *If Exclude from export is selected in the POI Properties dialog, the POI will be excluded from the DICOM export.*

3.4.3 ROI/POI details

The **ROI/POI Details** button in either the ROI list or in the POI list, opens the ROI/POI Details dialog.



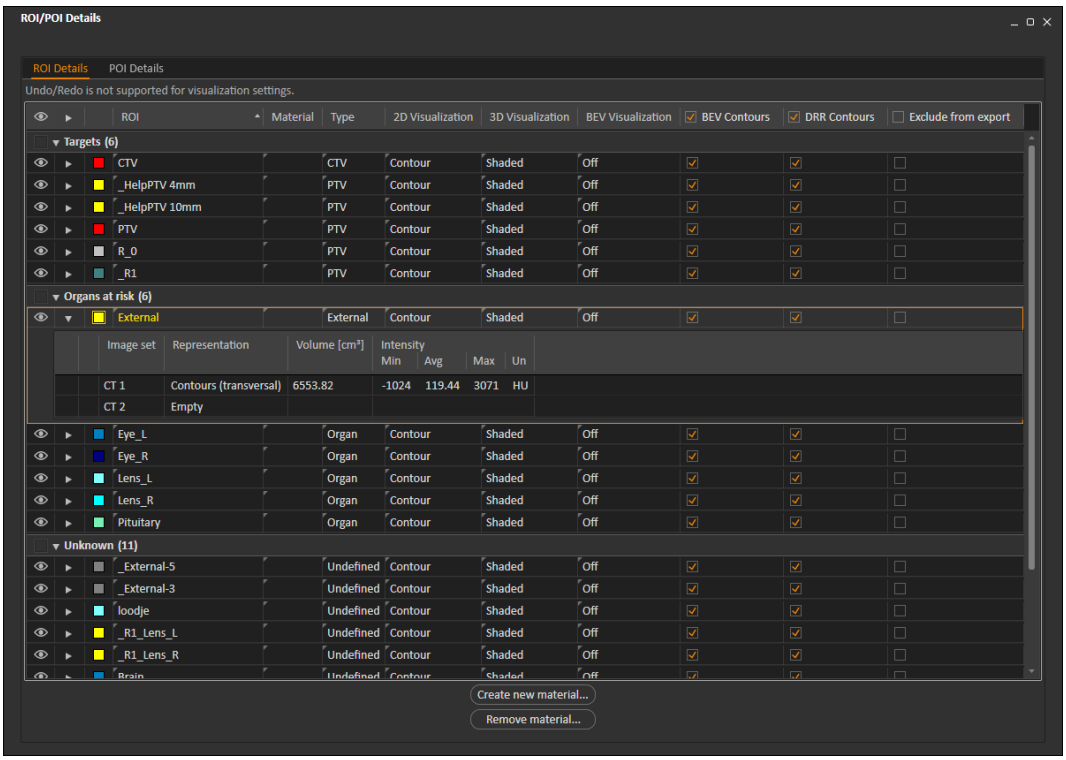


Figure 10. The ROI/POI Details dialog.

The ROI/POI Details dialog provides an overview of the existing ROIs and POIs and their geometries on various image sets. On geometry level, information such as ROI representation type, absolute volume, and min/max/average intensity is presented.

In the **ROI Details** tab, it is possible to set ROI visualization options, as well as specifying ROI type. It is also possible to change ROI material, define new materials and to exclude the ROI from export. Each row can be expanded in order to show details about the geometries in each image set such as approval status, derived ROI status, representation, volume, and min/max/average intensity. Create a new material by clicking the **Create new material...** button. The new material will be selectable in the **Material** column for each ROI.

Note: *It is only possible to compute electron dose with the materials that are already present in the material list from installation. The electron dose calculation does not support materials that have been created by the user.*

Note: *If the user has a carbon planning license and has selected an RBE cell type for a ROI, the RBE cell type will be shown in the ROI/POI Details dialog.*

The visualization columns in the **ROI Details** tab (**2D Visualization**, **3D Visualization** and **BEV Visualization**) define the ROI visualization types for the different patient views. Projected ROI outline in the BEV is toggled on and off from the **BEV Contours** column. The **DRR Contours** column is used to define which ROIs to display in DRR views - both in the RayStation user interface and in the generated reports.

In the **POI Details** tab, it is possible to specify POI type. Each row can be expanded in order to show details about the geometries in each image set such as approval status and point position.

All fields with a triangle in the upper left corner are editable. If a setting is changed for an ROI or POI, it can be applied to all other items in the list by right-clicking the desired setting field and selecting **Copy to all** or **Copy to selection** if multiple items have been selected.

3.4.4 The Registrations tab

The **Registrations** tab lists all image registrations for the current patient.

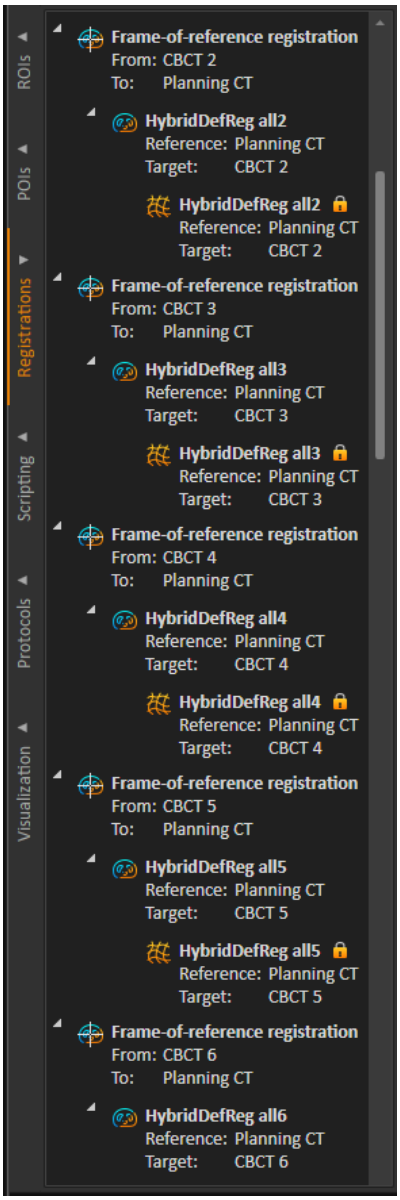


Figure 11. The **Registrations** tab.

3.4.5 The Visualization tab

In the **Visualization** tab, the user can specify a number of visualization settings. The settings are divided into the following sections: **Fusion**, **Dose**, **Beam**, **Patient**, **Image view transformation**, **PET**, and **Defaults**. For VMAT, Conformal Arc and Static Arc plans, an animation can also be displayed. Depending on the active patient and plan, some of the fields may be disabled or hidden. Default visualization settings can also be defined for the clinic and for individual users.

The settings in the **Visualizations** tab are global, i.e., any changes made in this tab will be reflected in all applicable views. The visualization settings in a view's Context menu are local, i.e., any changes made in the Context menu will be reflected in that view only.

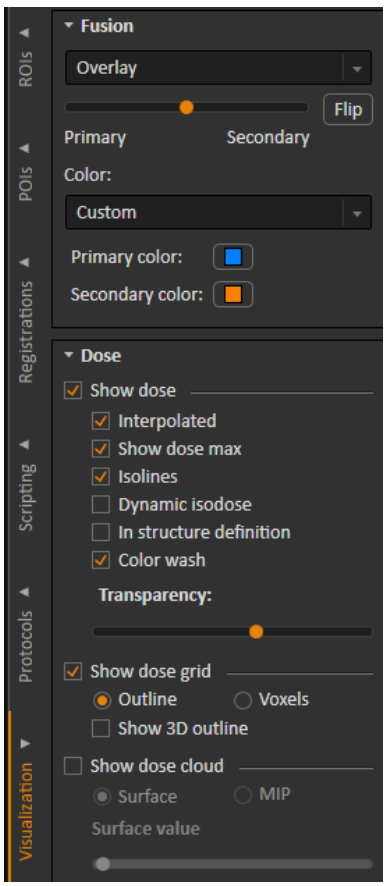


Figure 12. The **Visualization** tab.

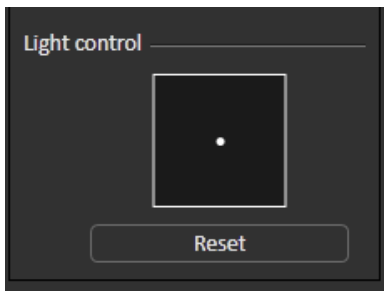
Visualization settings

The following visualization settings are available:

Visualization settings	Description
Fusion specific visualization settings	
Fusion	Specify settings for image fusion. See *section 5.2.5 Image fusion on page 184*.
Dose specific visualization settings	
Show dose	Toggle visualization of dose on and off using the **Show dose** checkbox. • **Interpolated** - Select to show the interpolated dose. • **Show dose max** - Select to show the dose max position as a plus symbol in 2D and 3D views. • **Isolines** - Select to show the dose isolines. • **Dynamic isodose** - Select to show the dynamic isoline through the cursor position in 2D views. • **In Structure Definition** - Select to show dose for all views in the Structure Definition module. • **Color wash** - Select to show the color wash with a transparency slider.
Show dose grid	Toggle visualization of the dose grid on and off using the **Show dose grid** checkbox. • Select either **Outline** or **Voxels** to only show the outline or every voxel • **Show 3D outline** - show the grid in 3D
Show dose cloud	Toggle visualization of a 3D dose cloud on and off using the **Show dose cloud** checkbox. • Set the surface value using the **Surface value** slider or using the edit field. • Select either **Surface** or **MIP** (Maximum Intensity Projection). If **Surface** is selected, the surface opacity can be modified.
Brighter DVH	Toggle visualization of Brighter DVHs to visualize the DVHs using thicker lines and lighter background.
Beam animation	
Play and **Rewind**	For VMAT, Conformal Arc, Static Arc, TomoTherapy and DMLC plans it is possible to start an animation of the treatment delivery. It is also possible to change the **Speed** of the animation.

Visualization settings	Description
Beam specific visualization settings	
Show beams	Toggle visualization of beams on and off using the **Show beams** checkbox. • Select to show the beam **Contour** or the **Center line** or both. • **Reticule in 3D** - Shows a cross where centerline of beam intersects the outermost ROI (often the external ROI). • **Show all beam sets** - Select to show beams from all beam sets in patient views. • **Show isocenter names** - Select to display the isocenter names in the views. • **In Structure Definition** - Select to show beams for all views in the Structure Definition module.
Show jaws	Toggle visualization of jaws on and off using the **Show jaws** checkbox. Select **Transparent** to display the jaws transparent.
Show leaves	Toggle visualization of leaves on and off using the **Show leaves** checkbox. Select **Transparent** to display the leaves transparent.
Aperture shapes	Toggle visualization of the aperture shapes that can be drawn in the Virtual Simulation module.
Compensator	Toggle the visualization of the compensator on and off.
Block	Toggle visualization of blocks on and off.
Scan spots	Toggle the visualization of the scan spots in beams on and off. Only applicable for proton PBS, Line Scanning and carbon ion PBS.
Scan spots direction line	Toggle visualization of the spot order and scanning direction in beams on and off. Only applicable for proton PBS, Line Scanning and carbon ion PBS.
Bragg peaks	Toggle visualization of bragg peak locations in 2D and 3D views. Note that if there are many bragg peaks this might degrade RayStation performance. Only applicable for proton PBS, proton Line Scanning and carbon ion PBS computed or optimized with a Pencil Beam dose engine.
Range Shifter	Toggle visualization of Range Shifter on and off.
Bore and FOV	Toggle the visualization of the FOV and Bore on and off.
Range Shifter	Toggle the visualization of the range shifter on and off.
Snout	Toggle the visualization of the snout on and off.

Visualization settings	Description
Show fluence	Toggle the visualization of fluence on and off using two independent settings; one for the **3D** view and one for the **BEV**.
Show in BEV	Toggle the visualization in the BEV on and off using following settings: • **DRR** - Select to show DRR • **Slice indicator** - Select to show the intersection with the transversal slice as intersection on the isocenter plane • **Slice indicator (external)** - Select to show the intersection with the transversal slice and the external contour as intersection on the isocenter plane • **Show crosshair** – Select to show crosshair When a patient plane is displayed in the BEV the indicated intersection will be between the transversal slice and the current patient plane.
Color	Beam colors in the patient views can be one of the following options: • **Standard**: Blue beams with the selected beam in orange. • **Beam**: Beam colors selected from a default template of nine colors. Selected beam highlighted. • **Isocenter**: The beam color is the same as the color of the isocenter of that beam. Selected beam highlighted.
Show Light Field	Toggle visualization of Light fields on and off using the **Show Light Field** checkbox. The Light field visualization settings are used to visualize the beam's projection on the surface of the selected ROI(s). It can be easier to see the Light fields on the External ROI if the Transparent external ROI option is switched off (from the context menu in the 3D view or Room View). If **Show all beam sets** is enabled, the light field for those are colored differently from the current beam set. • Select the **Beam exit** option to show a Light field at beam exit. • Select the **Highlight intersection** option to emphasize the intersection(s) of the Light fields. To see light fields of all beam sets, make sure that the **Show all beam sets** option in the Beam visualization settings is selected. • **Show in BEV**: Select to show light field in BEV. In order to show light field in BEV, make sure that the **External as mesh in BEV** is selected.
Transparent External ROI	Select to show the External ROI as transparent in the 3D views.

Visualization settings	Description
External as mesh in BEV	Overrides the ROI setting and shows the external ROI as a mesh in BEV. This can be used to see structures on the ROI or when showing the light field in BEV.
Patient specific visualization settings	
Image data	The following options for visualization of image data are available: • **Show as Head First**: Only applicable in the Patient Modeling modules. Always display the patient as lying Head First. • **Show in 3D** - Toggle visualization of the image data plane in the 3D view on and off. • **Interpolated** - Toggle interpolation of image data on and off. • **Volume Rendering Jitter** - Toggle the Volume Rendering Jitter on and off for a smoother Volume Rendering. This setting uses randomly casted rays for Volume Rendering which helps to smooth out the rendered image slice contours. • Modify the transparency of image data using the **Transparent** slider. • Modify the **ROI line width** using the corresponding slider.
Light control	The user can change where the light source is located when rendering the ROIs. Click and drag the white dot to move the location of the light source. 
Image view transformation settings	
Manual rotation	Select the **Manual rotation** option to specify the rigid transformation rotation angles [deg] for the **Roll**, **Pitch** and **Yaw** directions. Click the **Reset** button to reset the rotation. To set the pivot point to the slice intersections: 1. Change the slice intersection to the desired position (click the middle mouse button in a patient view). 2. Click the **Set pivot point** button.

Visualization settings	Description
PET specific visualization settings	
Show SUV	Toggle to show the SUV (Standardized Uptake Value) for PET images.
Color table	Toggle visualization of Color table for PET images.

Default visualization settings

Default visualization settings can be defined for the clinic and for individual users. User defaults are stored per Microsoft Windows user. For users without defined user defaults, the clinic defaults will be used.

User and clinic defaults can be loaded on demand by clicking the **Apply user defaults** button or the **Apply clinic defaults** button at the bottom of the **Visualization** tab.

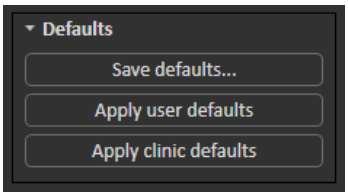


Figure 13. Default visualization settings (at the bottom of the **Visualization** tab).

To save default visualization settings:

1. Click the **Save defaults...** button at the bottom of the **Visualization** tab to open the **Save Visualization Defaults** window.
2. Select the preferred settings in the **Save Visualization Defaults** window.

   Note: *Some settings are not allowed to be saved even if they may be modified for visualization. These are hidden when the save dialog is opened.*
3. Select if the visualization settings should apply as user defaults (**Save settings as user defaults**) or as defaults for the clinic (**Save settings as clinic defaults**).

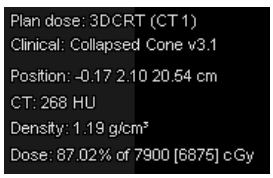
3.5 COMMON SYMBOLS

The corners and borders of each view presents information and various tools.

Upper left corner

The upper left corner contains:

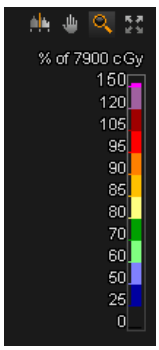
- Dose type and plan name
- Position of the mouse cursor
- HU (Hounsfield unit) value or material density at the cursor position
- Density, at the mouse cursor position
- Dose, at the mouse cursor position


Plan dose: 3DCRT (CT 1)
Clinical: Collapsed Cone v3.1
Position: -0.17 2.10 20.54 cm
CT: 268 HU
Density: 1.19 g/cm³
Dose: 87.02% of 7900 [6875] cGy

Upper right corner

The upper right corner of the view contains:

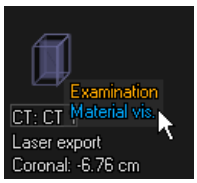
- buttons for Level/Window settings, Pan, Zoom and Maximize view.
- the color table. Click on the color table legend to open the Color table settings window. Click on the numerical values to toggle highlighting of the dose isoline or temporarily hide the level completely.



Lower left corner

The lower left corner of each patient view contains:

- Slice orientation cube – Indicates the position of the current slice in the total image volume.
- Image set identification. It is possible to select to display the patient image (Examination) or densities based on CT to density conversion and material overrides (Material vis.) by clicking the image set identification name. The densities based on CT to density conversion and material overrides can only be selected after dose computation and are only valid for the selected plan. The selection will affect all views in the current module.



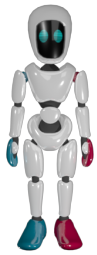
- Name of selected CT to density table
- The direction of the view as well as the position. For original slices it also displays slice number/total number of slices.

Ruler

At the bottom of the view is a ruler indicating the scale.

RayMan

RayMan is located in the lower right corner of all views displaying patient image data, to indicate the patient orientation. It is possible to change the view direction (transversal, coronal or sagittal) by clicking the RayMan icon. This can be done in all views except the BEV and DRR views.



Pie Chart

The Pie Chart is found in the Beam's Eye View (BEV) and in the DRR views. It represents beams and segments. The inner pie slices represents the beams and the outer part represents the segments in each beam. The size of the beam and the segment slices are scaled based on monitor units (MU).

Show dose max position

The maximum dose position is displayed as a red plus symbol in the 2D patient views and as a sphere in 3D and BEV, and is labelled **Max Dose** followed by the absolute dose value. The dose reported is the maximum dose for the currently selected dose type (i.e., for plan dose, beam set dose, beam dose etc. respectively). The display of the dose maximum position can be toggled on and off using the **Show dose max** option in the Visualization settings.

3.6 COMMON VIEWS

This section describes the most common views that are presented in the various modules.

Double-clicking the mouse button in a patient view enlarges the current window to the entire workspace. Double-click again to restore the workspace. Hold the SHIFT key down while double-clicking to get Full Screen display.

The two dimensional patient view (2D)

A 2D patient view shows the image set data, either the original image slices or reconstructed planes (e.g. sagittal or coronal), with ROI geometries, beams and dose. Use the mouse wheel to scroll through the slices, or press n for next slice and p for previous slice.

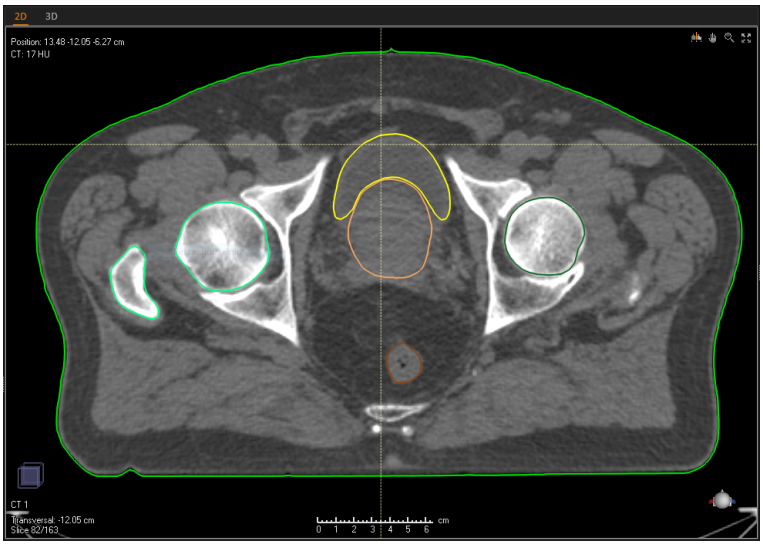


Figure 14. The 2D view of a prostate case. Transversal plane with bladder, prostate, rectum and femoral head ROIs.

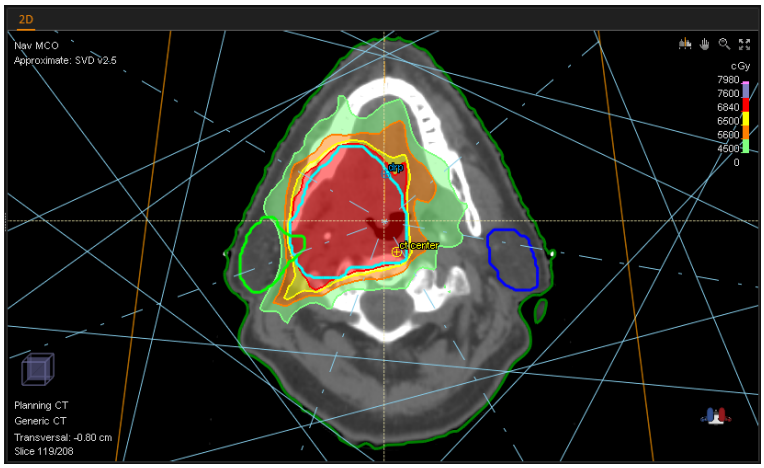


Figure 15. Example of a 2D patient and dose view.

The three dimensional patient view (3D)

The 3D view shows a 3D model of the patient anatomy and by choice ROIs, beams and dose.

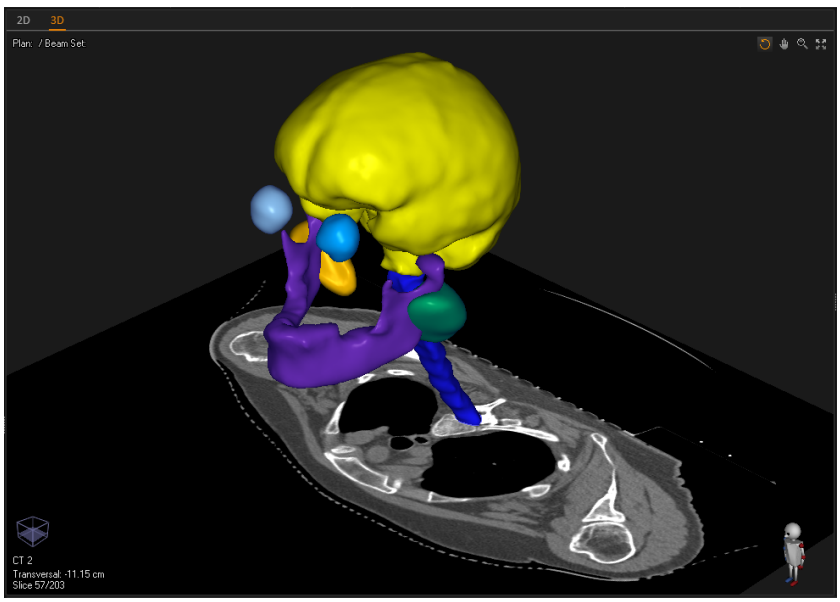


Figure 16. Example of a head and neck 3D patient view.

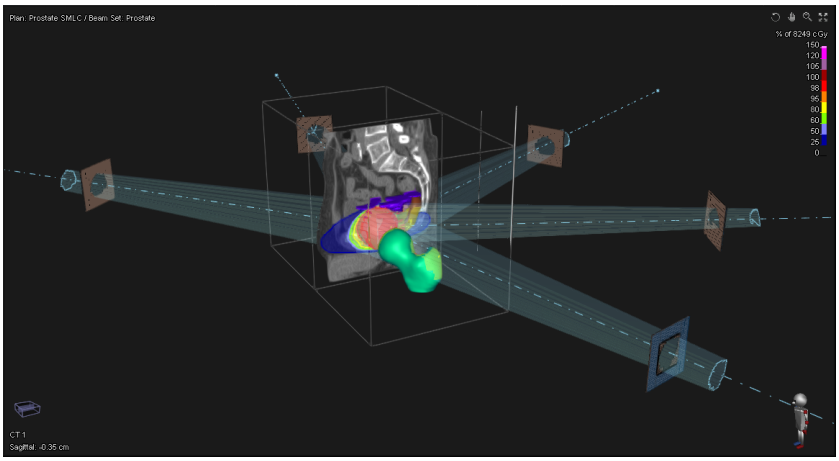


Figure 17. Example of a 3D patient and plan view in prostate case, using a dose cloud with maximum intensity projection.

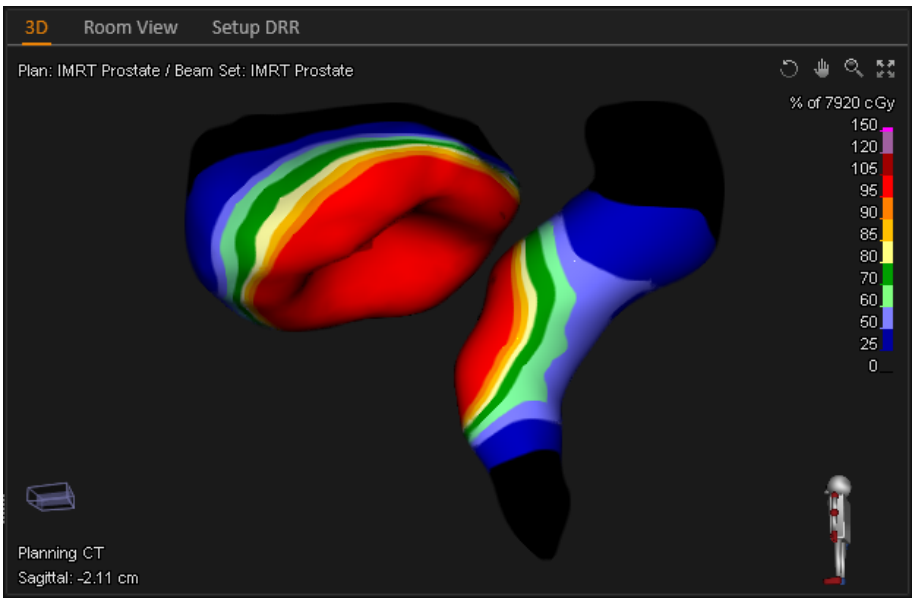


Figure 18. Example of a 3D patient view, showing the dose distribution on the ROI surfaces.

Beam's Eye View (BEV)

The Beam's Eye View shows the patient from the perspective of the beam source. The view shows ROIs and POIs. The view also visualizes important plan parameters, such as collimator jaws, MLC leaves and fluence for photon plans or spot positions and weights for proton PBS.

Note: *The coordinates of the Beam's Eye View are always IEC coordinates, even if the machine uses another coordinate representation.*

In the upper left corner is a pie chart. The inner pie chart represents the MU per beam and an outer ring represents the MU per segment. The selected beam and segment is highlighted in the pie chart.

In the BEV it is possible to navigate among the beams by holding the mouse cursor over the inner pie chart – use the mouse wheel to scroll through the beams. By holding the cursor over the outer ring and using the mouse wheel segment shapes can be browsed through. By scrolling up as far as possible, over the segment ring, a display of the total beam opening is given, i.e., the beam's maximum leaf opening for each leaf. An additional way to navigate among beams and segments is to use arrow up key/arrow down key to switch beam and arrow left/arrow right to move between segments for the current beam. It is possible to change the selected beam in the BEV by clicking the beam name in the lower left corner of the view.

By default the intersection with the current transversal slice, on the isocenter plane, is displayed as a dashed line. The intersection with the external contour on the current transversal slice can also be displayed in the BEV. For visualization settings, see *section 3.4.5 The Visualization tab on page 62*.

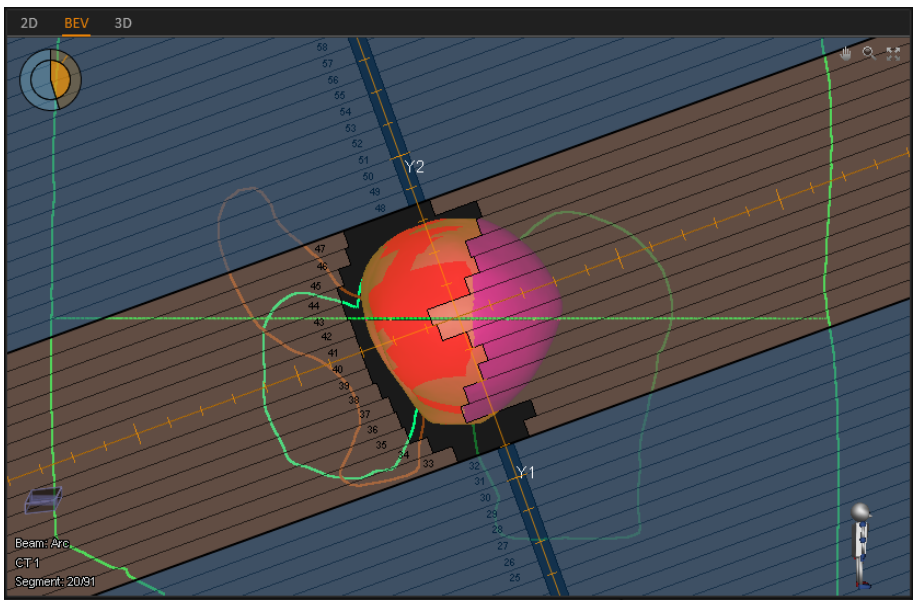


Figure 19. Example of the Beam's Eye View where jaws (blue), leaves and target are visualized.

The BEV can display a DRR. For a description of DRR settings, see *section 6.1.8 The DRR views and settings on page 330*.

The Dose difference view

The Dose difference view displays the difference between two doses, i.e., dose 1 minus dose 2. Only dose within the area of the first image set will be displayed. If dose 2 is present outside this area it will not be displayed.

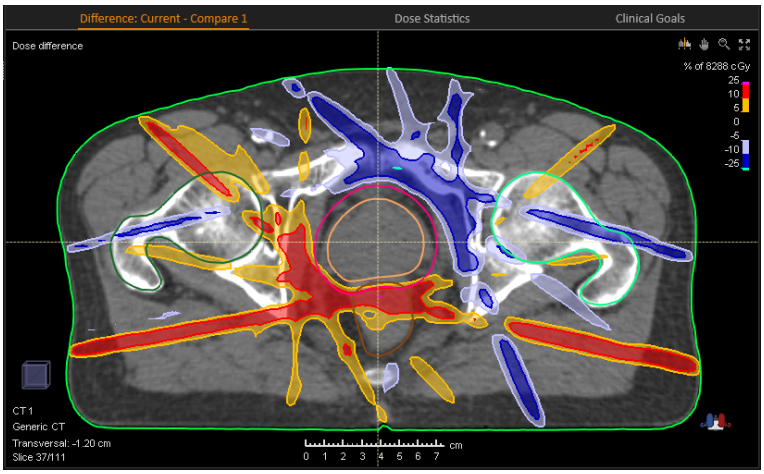
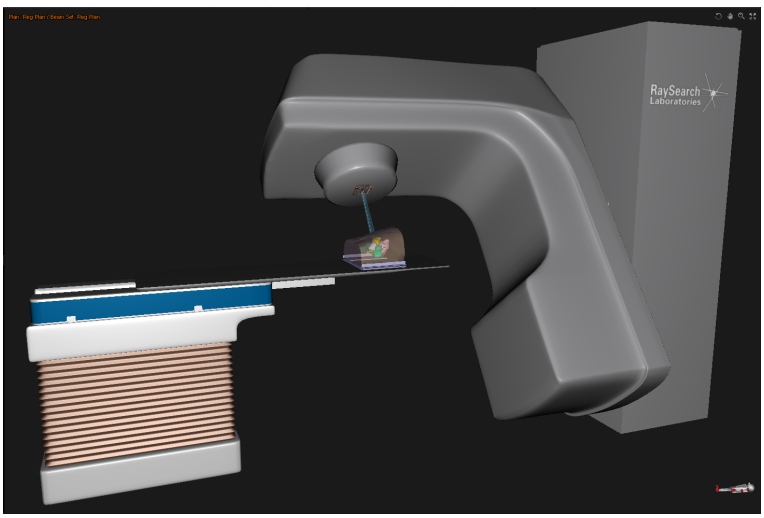


Figure 20. The Dose difference view visualizes Dose 1 minus Dose 2.

Room view

The Room View gives a schematic view of the gantry, couch and patient for the current beam.



WARNING!

Collision avoidance: Always verify gantry and couch angles (gantry and ring angles for the Vero machine). The patient/machine setup must be manually verified for all beams to avoid collisions causing patient injury or equipment damage. The Room view shall not be used to verify that no collisions will occur with current patient/machine set up. For TomoHelical treatment, see also warning 254787. (6294)

Leaf Open Times

For TomoHelical plans there is a **Leaf Open Times** view that displays a histogram for the leaf open time of all leaves and of all projections. The height of each block shows the number of leaves that have a leaf open time in the corresponding time interval.

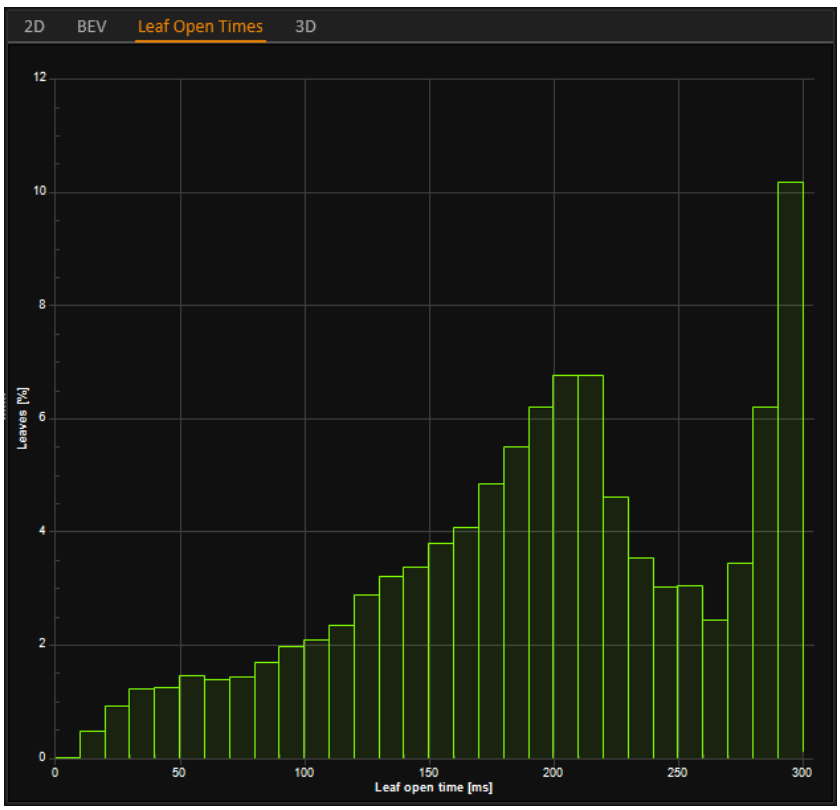


Figure 21. The **Leaf Open Times** view.

3.7 COMMON GRAPHS, TABLES AND TOOLS

This section describes the most common graphs, tables and tools.

In this section

This section contains the following sub-sections:

3.7.1	Dose Volume Histogram (DVH)	p. 78
3.7.2	Dose statistics table	p. 79
3.7.3	Clinical goals	p. 81
3.7.4	Line dose	p. 88
3.7.5	Dynamic isodose tool	p. 90
3.7.6	Dose inspector	p. 91

3.7.1 Dose Volume Histogram (DVH)

The DVH view presents the cumulative dose volume histograms for the selected dose of the selected ROIs in the ROI List.

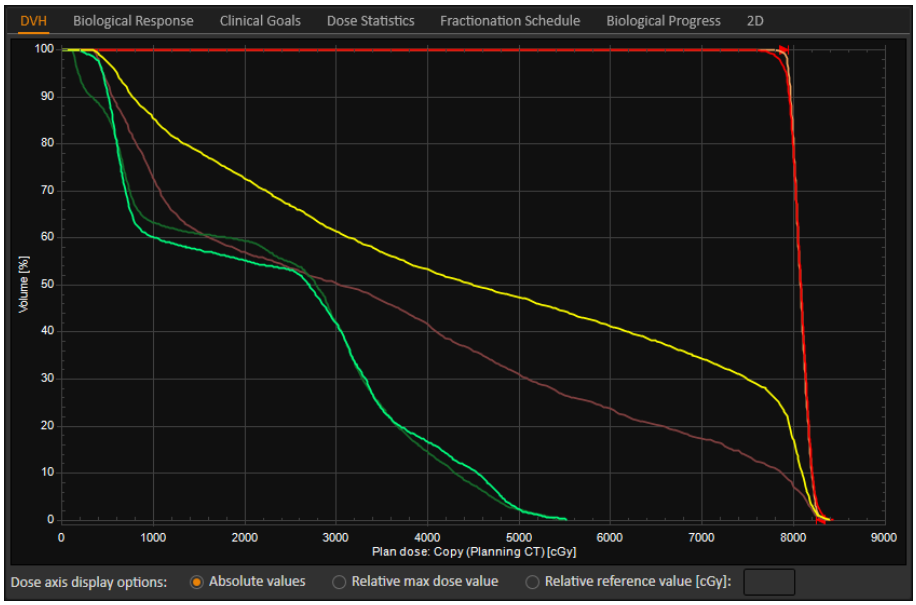


Figure 22. The Dose Volume Histogram.

Use mouse over on a DVH curve to see legend information about that DVH curve. The DVH curve legend will show: ROI: [dose Gy, volume %].

The mouse can be used to click and drag a rectangle to get a specific area zoomed in. Right-click in the DVH view to see the context menu, which offers options to zoom out the DVH.

At the bottom are display option buttons which allows the user to choose between absolute and relative dose scale and possibility to manually set the reference value for the relative scale.

In some modules, e.g. Plan Evaluation, the DVH can show dose data from more than one plan at a time. Above the curve area each dose is presented with a unique line style and a check box for visibility selection, making it possible to select which doses to show in the DVH.

WARNING!

Ensure that the dose grid covers all intended ROIs. Only the part of an ROI covered by the dose grid is included in the DVH and in the dose statistics computation. (6265, 6288)

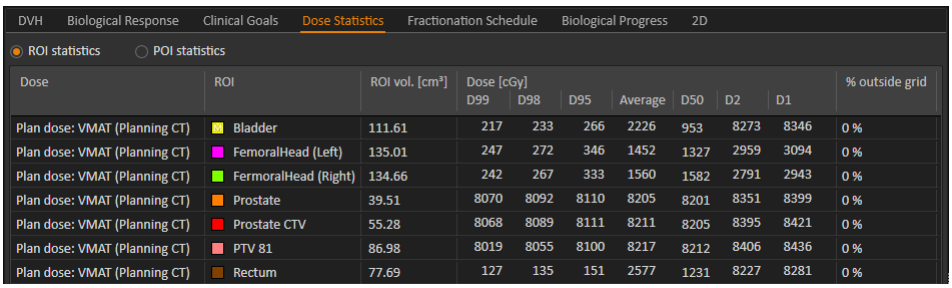
3.7.2 Dose statistics table

The dose statistics table lists dose information for the selected dose and for each ROI or POI. In the Plan Evaluation module the view lists ROI dose statistics for each plan selected for comparison. The Dose statistics computation is described in *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual*.

Note: *There are differences in how volumes and doses are handled when computing dose statistics compared to how they are visualized. The underlying reason for these differences lies in the interpolations effects which are created when representing the smooth nature of anatomy and dose in the jagged representation of Cartesian grids. The dose statistics computations are based on the dose grid representation of the ROIs while the visualization uses a grid with higher resolution and relies on tri-linear interpolation. This may lead to discrepancies between dose statistics and the visualized contours and iso-dose lines.The impact of these differences is most pronounced when considering statistics such as the minimum or maximum dose to a structure. For more information on how dose statistics is computed, refer to RSL-D-RS-7.0-REF, RayStation 7 Reference Manual.*

ROI statistics

Toggle the **ROI statistics** option button in order to display ROI statistics.



Dose	ROI	ROI vol. [cm³]	Dose [cGy]							% outside grid
			D99	D98	D95	Average	D50	D2	D1	
Plan dose: VMAT (Planning CT)	Bladder	111.61	217	233	266	2226	953	8273	8346	0 %
Plan dose: VMAT (Planning CT)	FemoralHead (Left)	135.01	247	272	346	1452	1327	2959	3094	0 %
Plan dose: VMAT (Planning CT)	FermoralHead (Right)	134.66	242	267	333	1560	1582	2791	2943	0 %
Plan dose: VMAT (Planning CT)	Prostate	39.51	8070	8092	8110	8205	8201	8351	8399	0 %
Plan dose: VMAT (Planning CT)	Prostate CTV	55.28	8068	8089	8111	8211	8205	8395	8421	0 %
Plan dose: VMAT (Planning CT)	PTV 81	86.98	8019	8055	8100	8217	8212	8406	8436	0 %
Plan dose: VMAT (Planning CT)	Rectum	77.69	127	135	151	2577	1231	8227	8281	0 %

Figure 23. The Dose Statistics tab showing the ROI statistics table.

WARNING!

Ensure that the dose grid covers all intended ROIs. Only the part of an ROI covered by the dose grid is included in the DVH and in the dose statistics computation. (6265, 6288)

POI statistics

Toggle the **POI statistics** option button in order to display POI statistics.

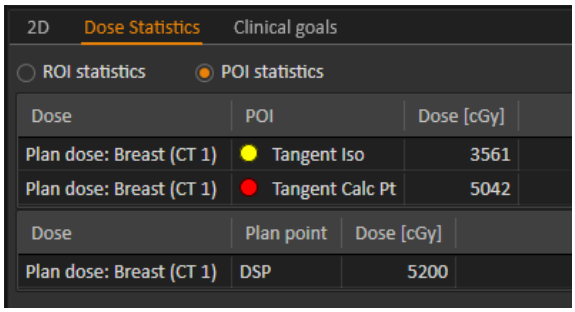


Figure 24. The Dose Statistics tab showing the POI statistics table.

The plan points, Dose Specification Points (DSP), and their corresponding doses are displayed below the POI statistics table in the **Dose Statistics** tab. Only points from the currently selected beam set are shown. In the QA Preparation module, points are shown from the QA beam set.

3.7.3 Clinical goals

The user can define clinical goals, i.e. evaluation criteria for specific ROIs or POIs. The clinical goals can be either physical or biological. The result (pass/fail) is easy-to-read in a single column. The clinical goals are different from the optimization goals and will not affect the optimization. The clinical goals are accessible in the following modules: Plan Optimization, Multi Criteria Optimization, Plan Evaluation, Dose Tracking and Adaptive Replanning.

Order of priority in the Clinical Goals tab

It is possible to specify the order of priority in the **Clinical Goals** tab. If desired, the user can specify a **Priority** value from 1 and higher to each clinical goal. 1 represents the highest priority. If no priority value is entered, the clinical goal will have the lowest priority when sorting the list.

Define physical clinical goals

To add a physical clinical goal:

1. Click the **Clinical goals** tab.
2. Click the **Add physical...** button. This opens the **Add Clinical Goal** dialog.

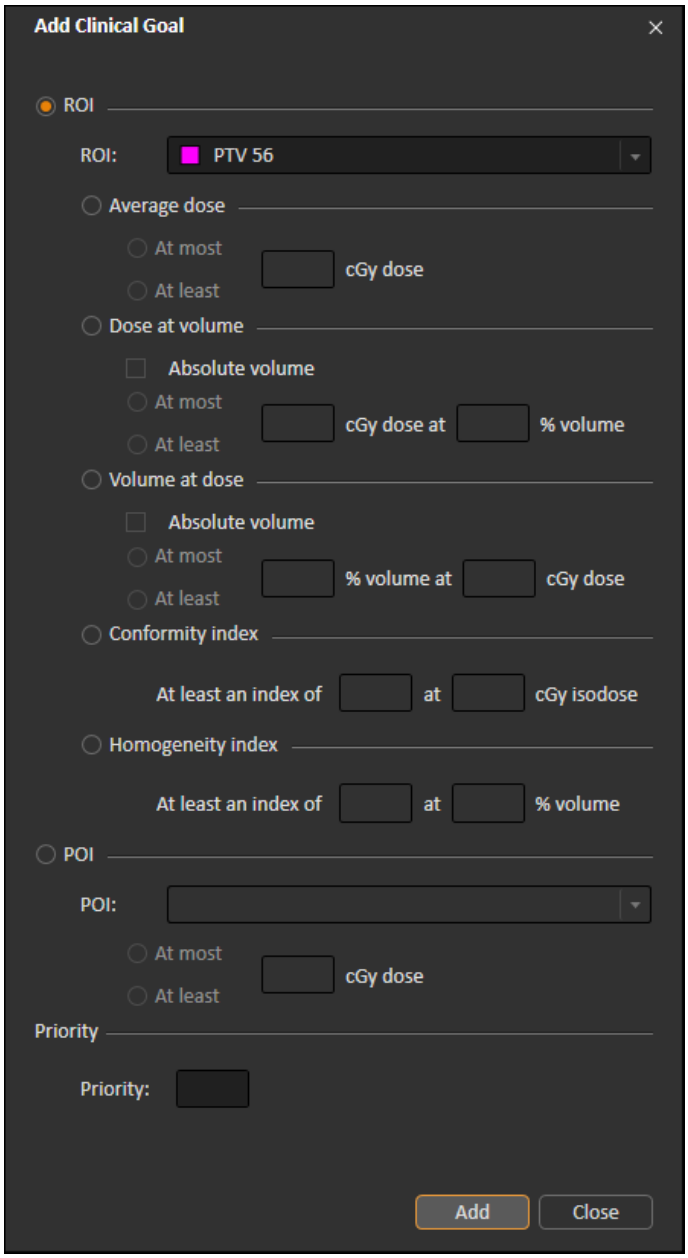


Figure 25. The **Add Clinical Goal** dialog.

3. Select the desired **ROI** or **POI** from one of the drop-down lists.
4. Select goal type for the chosen ROI or POI.

The ROI alternatives are **Average dose**, **Dose at volume**, **Volume at dose**, **Conformity index** and **Homogeneity index**.

- **Average dose**: specify the dose level that the ROI should receive, **At most** or **At least**.
- **Dose at volume** or **Volume at dose**: specify in what percentage of the ROI the dose level should be At most or At least. The goal can be set to operate on the **Absolute volume**.
- **Conformity index**: specify an index value between 0 and 1 that is acceptable for the given isodose level. The index is defined as the ratio between the ROI volume covered by the isodose and the total isodose volume.
- **Homogeneity index**: specify an index value between 0 and 1 that is acceptable at the volume percentage for the given ROI. The index is defined as D(x) / D(100-x) where D(x) is dose at x % volume.

For POIs, select the dose level that the POI should receive, **At most** or **At least**.

Note: *There is no limit for the absolute volume that can be specified by the user, other than that it has to be larger than zero when creating clinical goals. If setting a 'Dose at volume' goal to a volume larger than the dose grid ROI or a 'Volume at dose' goal to a value that generates a volume that is larger than the ROI, no result will be displayed.*

5. If desired, specify a **Priority** value from 1 and higher to specify the order of priority for this clinical goal in the **Clinical Goals** tab.
6. Click **Add** to add the clinical goal to the list.
7. Repeat step 2-5 to add additional clinical goals.
8. Click **Close**.

Define biological clinical goals

For information on how to add biological clinical goals, see *section 7.5 Biological optimization on page 689*.

Edit clinical goals

To edit a clinical goal:

1. Select the clinical goal in the list by clicking on it.
2. Click the **Edit...** button or double-click on the value/setting. This opens the **Edit Clinical Goal** dialog.

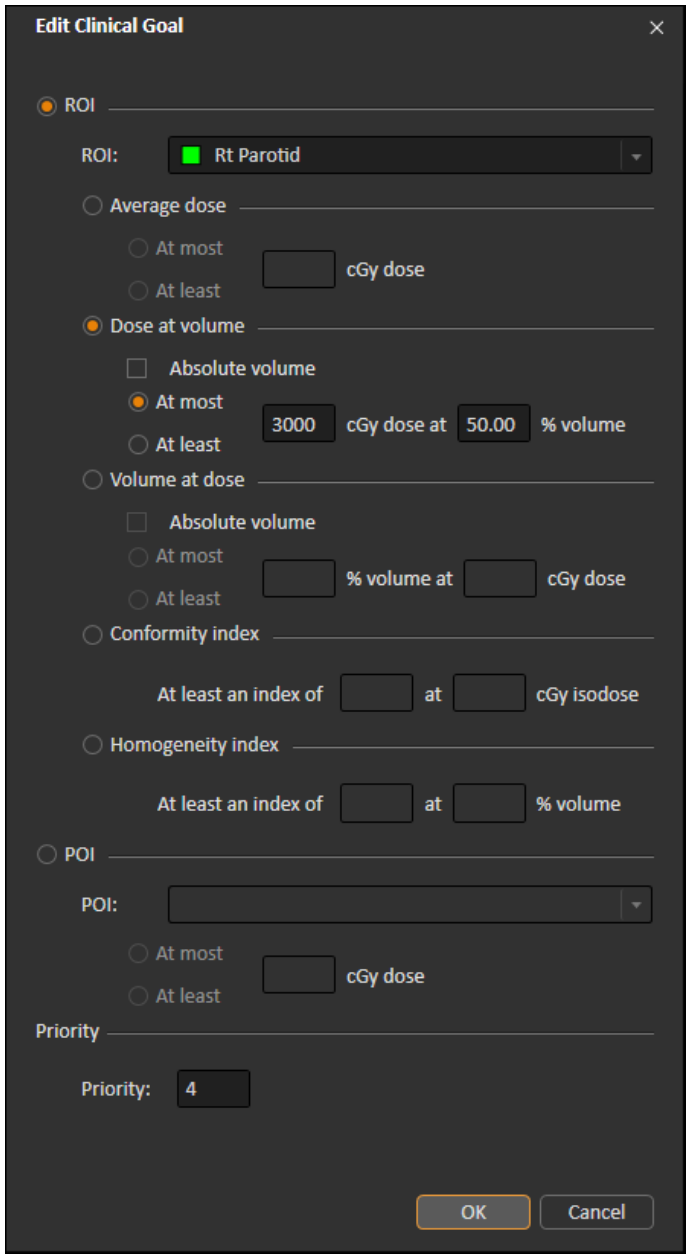


Figure 26. The **Edit Clinical Goal** dialog.

3. Edit the goal definition and click **OK**.

Evaluate clinical goals

The **Clinical goals** tab lists the current status of the defined goals for one or several dose distributions. A green or red lamp indicates whether or not the goal is fulfilled. The current value of the goal is also displayed.

Use the **Edit...**, **Copy** and **Delete** buttons to edit, copy or delete clinical goals in the list.

For carbon ions: Clinical goals can only be evaluated for RBE dose. For more information about carbon ion planning, see *section 7.3 The Plan Optimization module - carbon ions on page 610*.

It is possible to specify the order of priority in the **Clinical Goals** tab if at least one of the clinical goals has a priority.

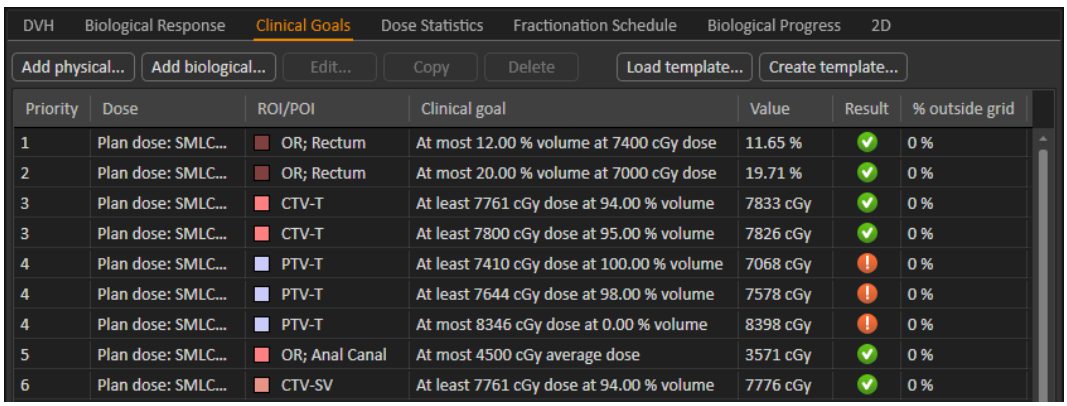

DVH
Biological Response
Clinical Goals
Dose Statistics
Fractionation Schedule
Biological Progress
2D
Add physical...
Add biological...
Edit...
Copy
Delete
Load template...
Create template...
Priority | Dose | ROI/POI | Clinical goal | Value | Result | % outside grid
1 | Plan dose: SMLC... | OR; Rectum | At most 12.00 % volume at 7400 cGy dose | 11.65 % | 0 %
2 | Plan dose: SMLC... | OR; Rectum | At most 20.00 % volume at 7000 cGy dose | 19.71 % | 0 %
3 | Plan dose: SMLC... | CTV-T | At least 7761 cGy dose at 94.00 % volume | 7833 cGy | 0 %
3 | Plan dose: SMLC... | CTV-T | At least 7800 cGy dose at 95.00 % volume | 7826 cGy | 0 %
4 | Plan dose: SMLC... | PTV-T | At least 7410 cGy dose at 100.00 % volume | 7068 cGy | 0 %
4 | Plan dose: SMLC... | PTV-T | At least 7644 cGy dose at 98.00 % volume | 7578 cGy | 0 %
4 | Plan dose: SMLC... | PTV-T | At most 8346 cGy dose at 0.00 % volume | 8398 cGy | 0 %
5 | Plan dose: SMLC... | OR; Anal Canal | At most 4500 cGy average dose | 3571 cGy | 0 %
6 | Plan dose: SMLC... | CTV-SV | At least 7761 cGy dose at 94.00 % volume | 7776 cGy | 0 %

Figure 27. The **Clinical Goals** tab.

Tolerances for dose-volume clinical goals

Clinical goals for DVH goals can be formulated either in terms of dose at volume, or in terms of volume at dose. Fulfillment is decided with a small allowed deviation, respectively in dose (0.5 cGy) or in volume (0.005%). Due to this and rounding of displayed figures the GUI can exhibit a minor inconsistency. Say that a DVH point, such as D100(%) = 5700 Gy is described by the two clinical goals:

- dose at volume 100% $\geq$ 5700 cGy
- volume at dose 5700 cGy $\geq$ 100%

If the DVH curve is such that the curve drops from 100% at a dose level below 5700-0.5 = 5699.5 cGy and passes 5700cGy at a volume larger than 99.995% the dose at volume goal will fail, and the volume at dose will pass. The opposite situation could also occur. Due to rounding of the respective figures presented in the GUI, the clinical goals fulfillment will in the case appear inconsistent. These inconsistencies are always due to very small numerical effects.

Add clinical goals from template

A set of clinical goals can be stored as a template. The clinical goal list template can be re-used for evaluation of new plans.

To add goals from a clinical goals list template:

1. Click the **Load template…** button. This opens the **Load clinical goal list template** dialog.

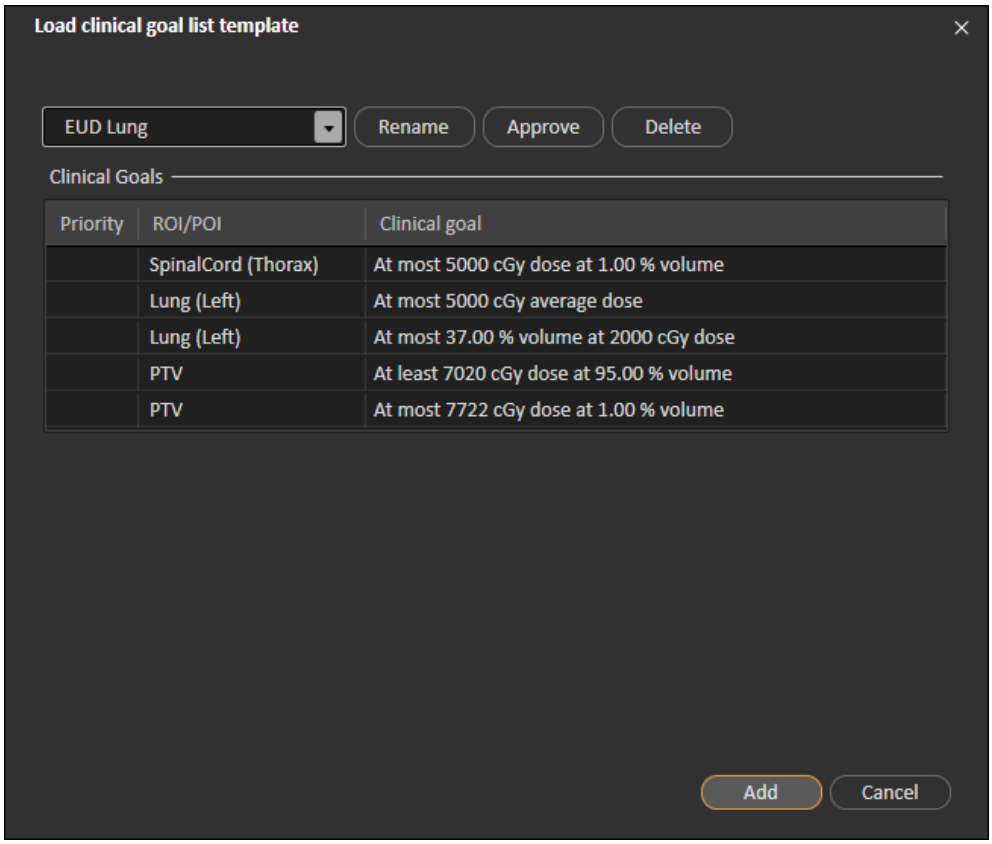


Figure 28. The **Load clinical goal list template** dialog.

2. Select a template in the drop-down list. The goals for the selected template are listed in the **Clinical Goals** tab.
   - To rename the selected template, click **Rename** and enter a new name for the template.
   - To approve the selected template, click **Approve**. If a template is approved, a padlock will be displayed next to the template name in the list. Only admin users can approve a template.
   - To delete the selected template, click **Delete**.

3. Click **Add** to add the template goals to the plan.

   If a non-approved template is added, a warning will be displayed. These warnings can be disabled in Clinic Settings (*section D.2.2 The Preferences tab on page 922*).

Create clinical goal list template

A clinical goal list template is created from a plan's existing set of goals.

To store the goals of the current plan as a template:

1. Click the **Create template...** button.

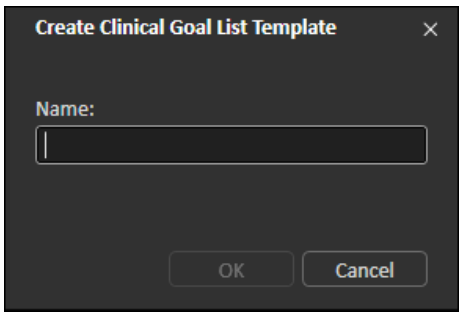


Figure 29. The Create clinical goal list template dialog.

2. Enter a name for the new template. (The template can later be renamed or deleted from the Load template ... dialog).
3. Click **OK**.

3.7.4 Line dose

The line dose tool is used to inspect dose gradients at locations of special interest.

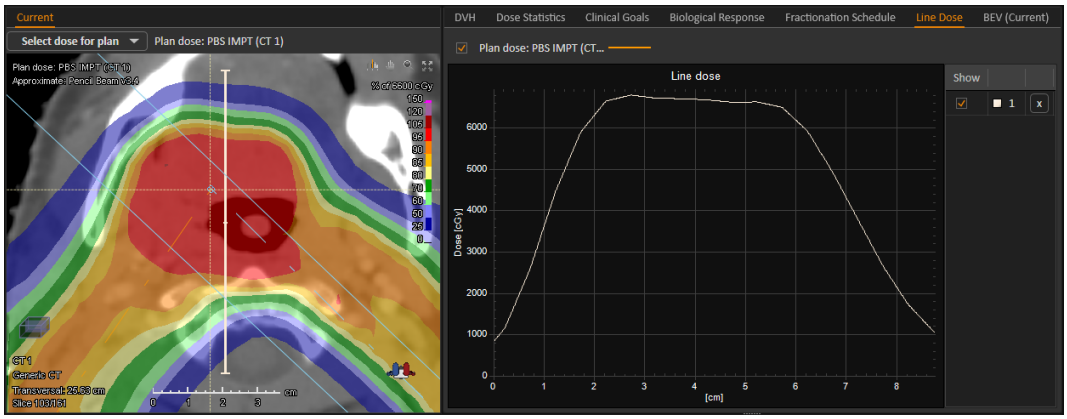


Figure 30. The line dose histogram to the right shows how the dose differs across a dose line as defined in the dose distribution to the left.

Dose lines can be added from a view in the Plan Evaluation module, in a 2D view in the QA preparation module or in a 2D view in the Beam 3D Modeling module in RayPhysics.

To add a dose line:

1. Right-click in a view and select **Add/edit dose line** from the context menu.
2. Click where the dose line should start, move the mouse and release the mouse button where the line shall end. This creates a dose line. The line will appear in the view, and the corresponding values will be shown in the **Line dose** tab. Several dose lines can be added.

To move the dose line, the end points and the middle points is selectable and moveable using the mouse pointer. When a dose line is added the line is editable by default. To edit a dose line later on, select **Add/edit dose line** from the context menu.

To delete a dose line, click the cross marked button in the legend of the line dose tab.

Note: *Holding down the ALT key will move the dose line in increments of 90 degrees. Releasing the ALT key will move the dose line back to the mouse pointer.*

Note: *For rotated images, a dose line drawn in the Dose 1 view will not be displayed in the Dose 2 view. The dose values will however be displayed in the line dose graph.*

Export dose lines

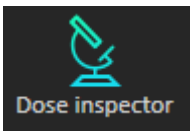
It is also possible to export dose lines to a csv file using the **Export line doses** button. All lines visualized in the line dose histogram will be exported to the same file. The file format is specified in *Appendix G Line dose export*.

3.7.5 Dynamic isodose tool

The dynamic isodose tool makes it possible to see an arbitrary isodose line. The tool is toggled on and off from the Visualization settings. The isoline is displayed as soon as the mouse button is pressed somewhere in a 2D patient view, and the line moves with the mouse cursor. Note that the tool also can be used for plan comparison, e.g., when using workspace layouts for comparison in Plan Evaluation and Dose Tracking.

3.7.6 Dose inspector

The dose inspector can be used to visualize hot spots and cold spots for a selected ROI or in all visible ROIs (all ROIs in RayStation that have the eye-icon checked). Click the **Dose inspector** button to open the Dose inspector dialog.



The Dose inspector dialog is accessible from the Plan Design, Plan Optimization, Multi-Criteria Optimization and Plan Evaluation modules. Once activated, the Dose inspector dialog will stay open while switching between modules. The dose inspector dialog is closed by closing the dialog or by clicking the **Dose inspector** button.

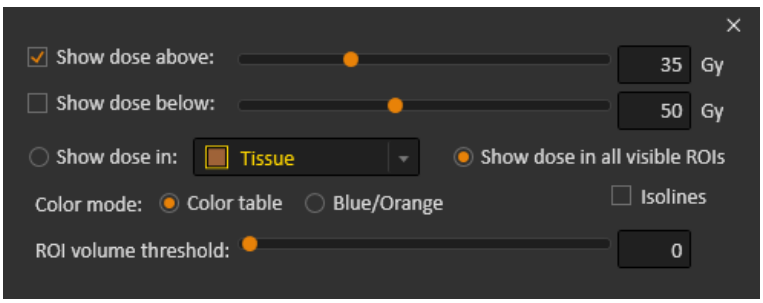


Figure 31. The Dose inspector dialog.

The Dose inspector defaults to show dose above the input value (hot spots) in all visible ROIs using the color table colors.

Setting	Description
Show dose above/below	To show dose above the input value (hot spot): Check the **Show dose above** checkbox and adjust the slider to the desired dose level or enter a dose value manually. To show dose below the input value (cold spot): Check the **Show dose below** checkbox and adjust the slider to the desired dose level or enter a dose value manually.
Show dose in	To visualize hot/cold spots within a certain ROI, select **Show dose in** radio button and select an ROI from the drop-down list. To visualize hot/cold spots within all visible ROIs (all ROIs in RayStation that have the eye-icon checked), select **Show dose in all visible ROIs** radio button.

Setting	Description
Color mode	The option **Color table** will display the dose above and below the entered value(s) as color wash. The option **Blue/Orange** will display dose below the entered value in blue and dose above the entered value in orange.
Isolines	Check the **Isolines** checkbox to show an isodose line above/below the dose level that is chosen for display.
ROI volume threshold	The threshold determines the voxels of the ROIs that will be filtered out of the dose visualization, e.g., a threshold value of 0.75 will remove all voxels with relative voxel volume that is below 75% from the visualization while the Dose inspector is active. The value 0 will include all voxels for the selected ROI. This can be used to visualize the voxel representation of an ROI on the dose grid if both **Show dose above** and **Show dose below** is unchecked and the option **Blue/Orange** is selected.

3.8 LEVEL/WINDOW AND COLOR TABLES

This section describes Level/window settings and color tables.

In this section

This section contains the following sub-sections:

3.8.1	Level/window	p. 94
3.8.2	Color tables	p. 96

3.8.1 Level/window

The Level and Window tool is used to change the contrast of the image data and can be reached from the Context menu or by clicking the **Level/Window** button in the upper right corner of a patient 2D view.

Level/window tool: Click the mouse button and move the mouse up and down to change Level. Move the mouse left and right to change Window.

Level/window region: The mouse can be used to click and drag to select a rectangular region of the image. The level/window settings are automatically calculated to match the pixel data in the selected region.

For most organs and CT data sets, the Default Level and Window settings are suitable. For CT and CBCT, there are some presets available from the 2D patient view context menu.

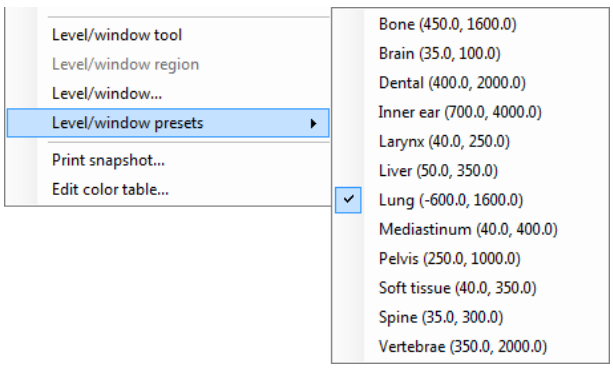


Figure 32. The 2D patient view context menu - Level/window presets.

For 4DCT datasets, the level/window settings are automatically adjusted for all phases when using the level/window tools.

Adjust level/window

To adjust the level and window settings:

1. Right-click in an image and select **Level/Window…**. This opens the Adjust Level & Window dialog.

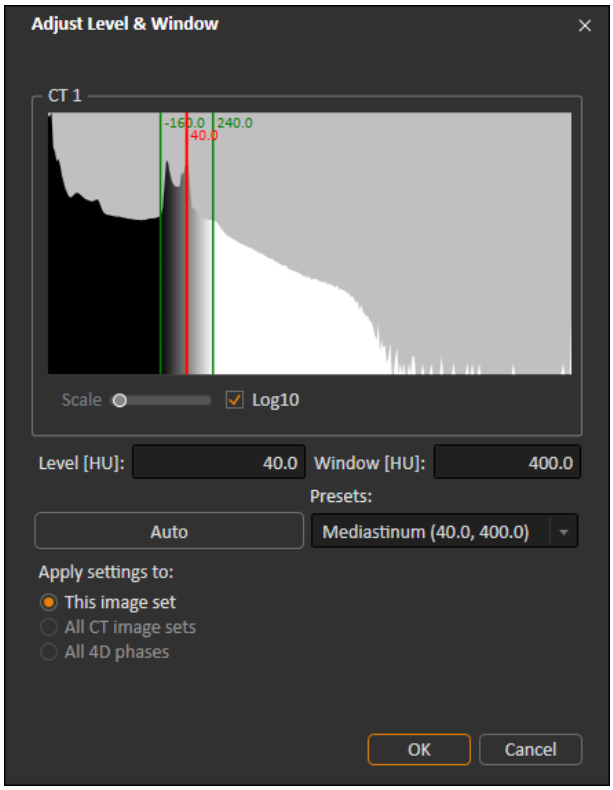


Figure 33. With the Level and Window tool the shading level and shading interval can be adjusted manually, automatically or by various presets suitable for different datasets.

2. Click on the red line and move the mouse to change the overall shading level.
3. Click on one of the green lines and move the mouse to increase or decrease the shading interval (window).
4. If applicable, select if the setting shall apply to this image set only, all image sets of same modality, or all image sets within 4D dataset.

3.8.2 Color tables

There are several color tables in RayStation 7; for Compensator, Fluence, Dose difference, Dose, RBE, Displacement field and PET. The general behavior is common for all color tables, and the visualization options are the same.

The display is based on either absolute or relative values – relative is either relative the max value or relative a user defined reference value.

The dialog also supports manual editing of values directly in the table, add and removal of new levels, selection of interpolated or discrete values, and restoral of default settings.

The Dose color table is reached through the context menu in a 2D patient view. The Fluence color table is reached through the context menu in the Beam's Eye View (BEV). The Adjust color table dialog can also be opened by clicking on the color table legend in the upper right corner of a view.

The dose color table

The dose color table offers three different definitions of 100%; a user defined reference value, current dose maximum and current prescription. When current dose max or current prescription is used as reference the dose color table used will depend on the content of each view. I.e. if two plans are compared in Plan Evaluation, the dose color table used may differ between the plans since it will be based on either the dose max or the prescription of each plan. Using the user defined reference value means that the dose color table will be identical for all views for the current patient.

When Current prescription is selected as reference the value is further computed to ensure a usable color table. If beam dose display is selected the prescription value is divided with the number of beams. In the QA Preparation module the prescription value is divided with the number of fractions. When working with multiple independent beam sets, the plan prescription is defined as the sum of the two beam sets' prescriptions. When working with dependent beam sets the plan prescription is defined as the (plan) prescription defined with the dependent beam set, and the beam set prescription for the dependent beam set is defined as the plan prescription minus the prescription of the other beam set.

Note: *If a prescription needed to compute the Current prescription reference value is missing, the max dose value will be used as reference.*

Note: *When a prescription percentage is used, note that the color table reference dose value will be either Prescription dose value/Prescription percentage or Prescription dose. This is set by checking or unchecking the Use normalized dose prescription for color table checkbox in the Preferences tab in the Clinic Settings application. For more information, see section D.2 The Clinic Settings application on page 920.*

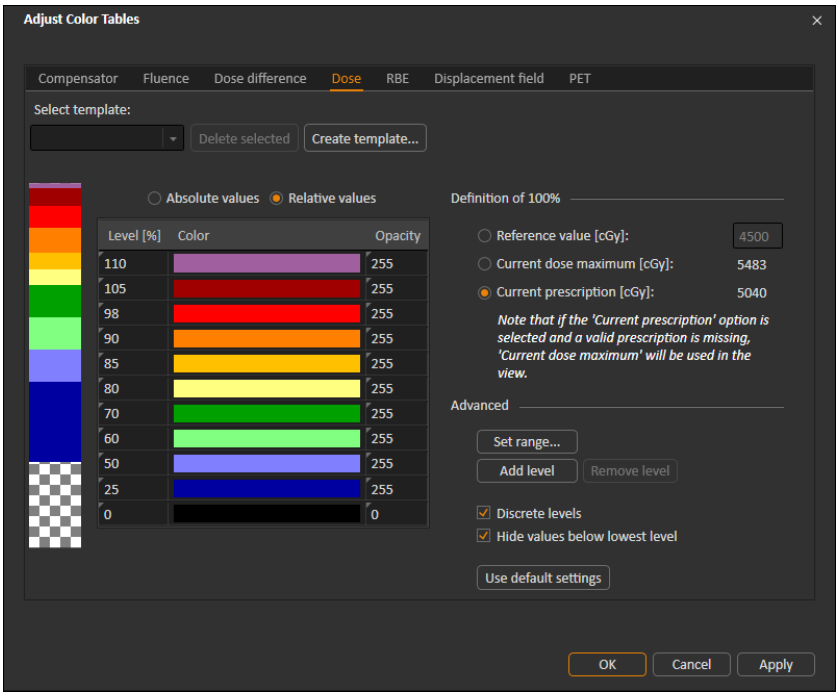


Figure 34. The adjust dose color table.

Individual isodose levels can be highlighted by clicking the corresponding value in the dose color table legend. As a result, the value in dose color table legend will turn orange and the isodose line will double its width.

It is also possible to temporarily switch off individual isodose levels by clicking the corresponding value two times in the dose color table legend. Click once more to display the isodose level again.

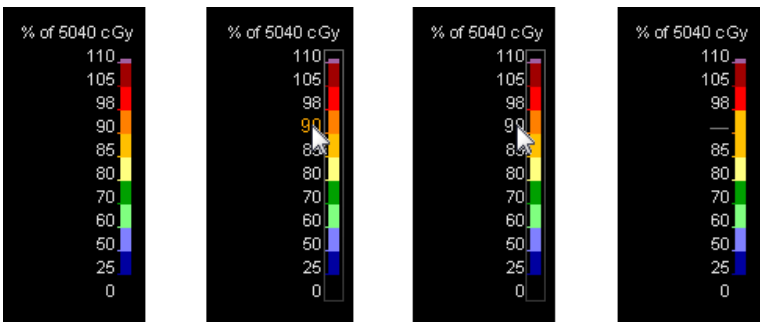


Figure 35. Highlight or hide individual isodose levels by clicking the corresponding value in the dose color table legend.

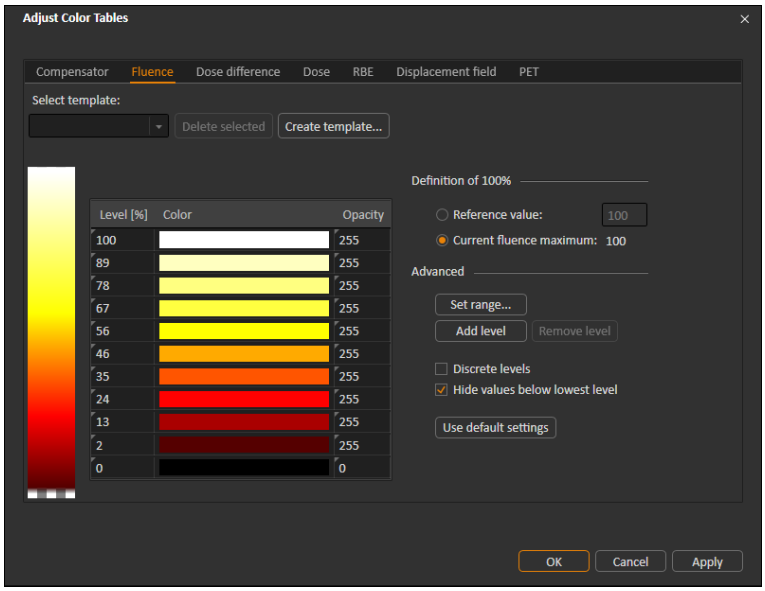


Figure 36. The adjust fluence color table.

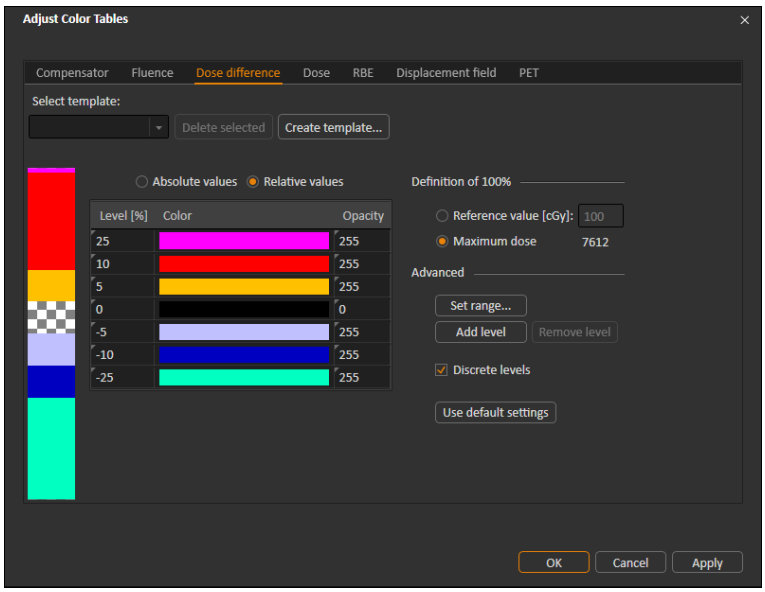


Figure 37. The adjust dose difference color table.

The RBE color table

The RBE color table is used for displaying RBE factors when evaluating carbon ion plans. The RBE color table cannot be defined as relative values.

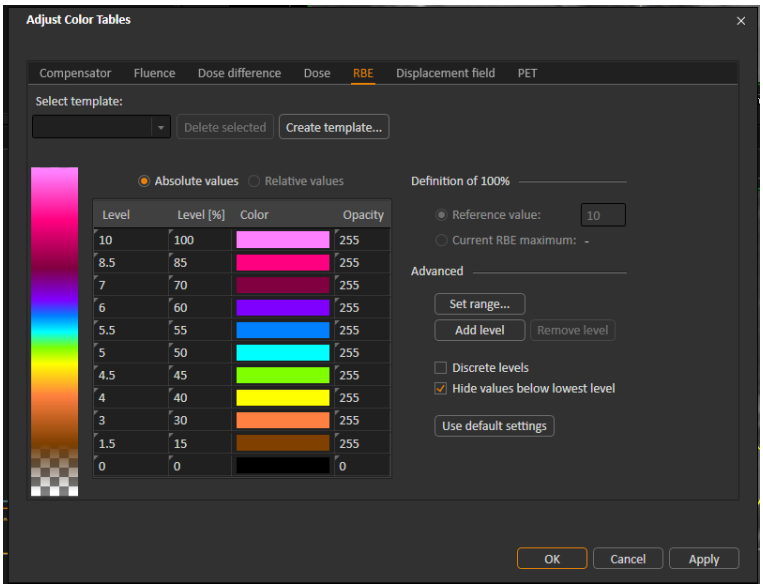


Figure 38. The RBE color table.

The displacement field color table

The displacement field color table is used for the displacement field in a deformable registration.

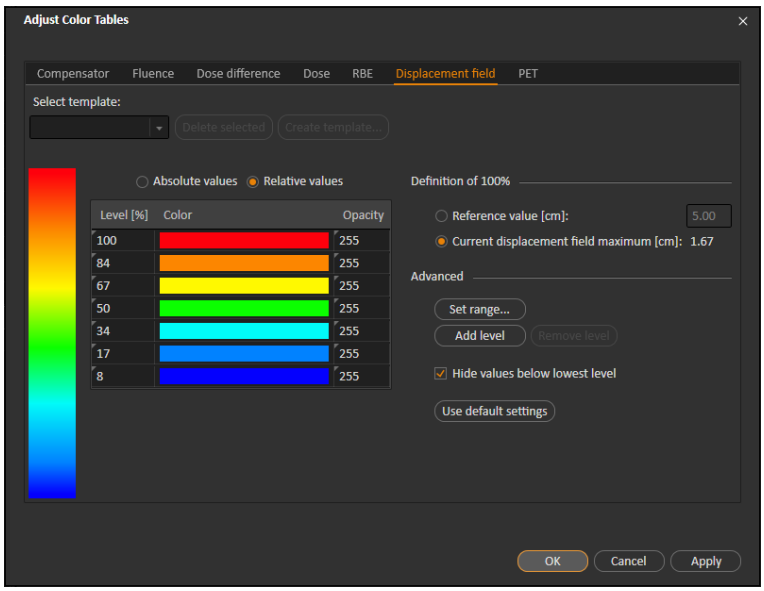


Figure 39. The displacement field color table.

The adjust PET color table

The PET color table editor is reached from the context menu or from the fusion panels in the Structure Definition module or the Image Registration module. There are a number of presets available. If desired, these can be modified and saved as templates. The default for PET is a relative color table where the current level/window settings define the 100% level (L + W/2). It is also possible to let the maximum value in the image set define the 100% level.

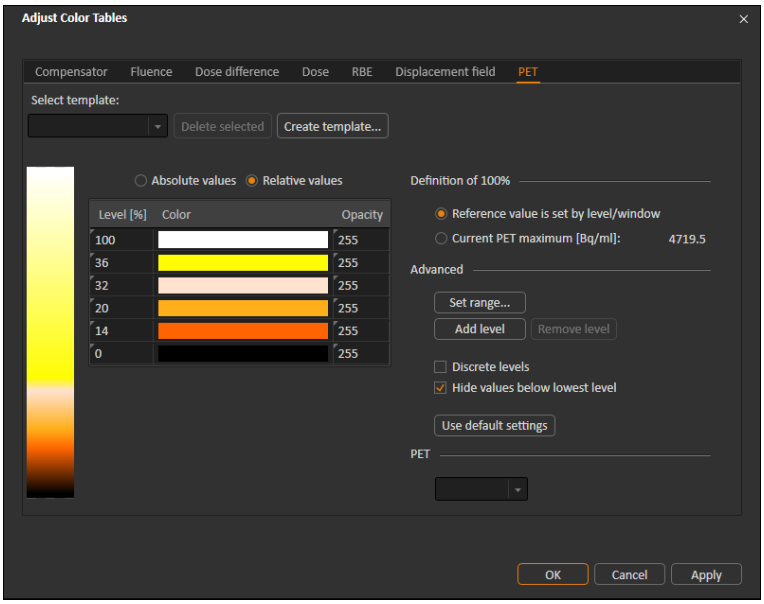


Figure 40. The adjust PET color table.

3.9 THE CONTEXT MENU

Each view holds a context menu which is accessed by right-clicking in the view. Several of the view functions of the context menu are common for all views (pan, zoom, and measure etc.) while others vary with the view type.

For a description of the most common menu options, see *View manipulation tools on page 102*.

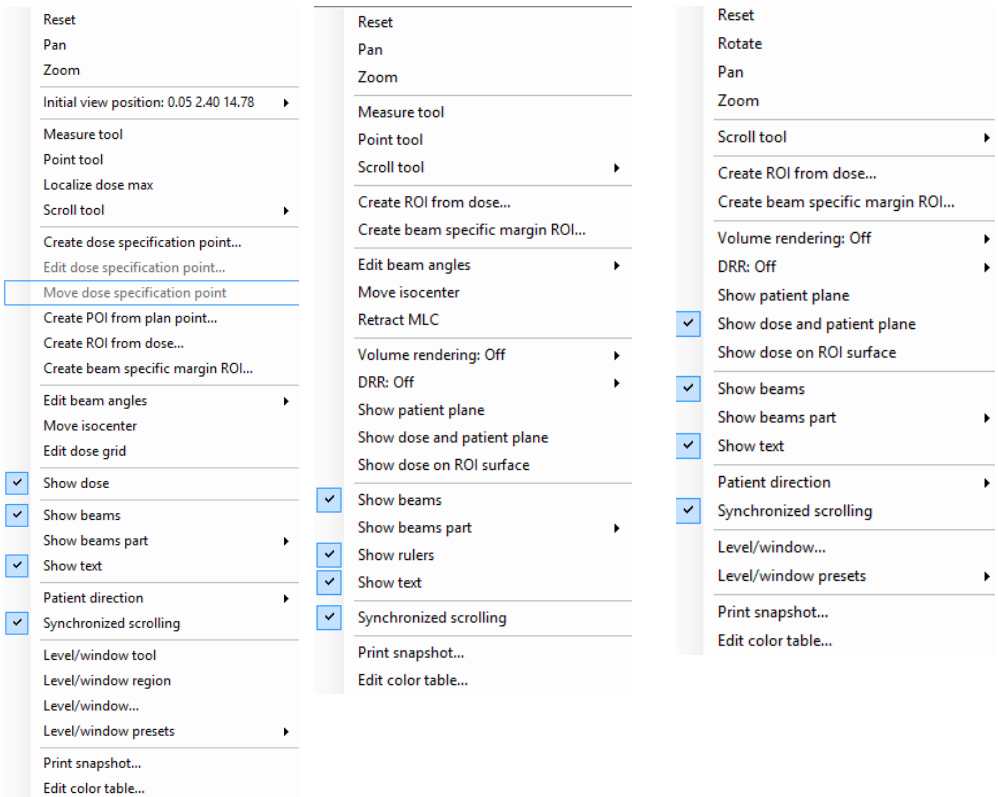


Figure 41. Context menus for 2D, BEV and 3D view in the Plan Setup module.

View manipulation tools

Several tools, e.g. for patient view manipulation, are common throughout the different modules. These tools are found in the upper right corner of a patient view or in a context menu which is made visible by right-clicking in a view.

- **Pan**. Located in upper right corner of patient view or in context menu. Allows translation of a 2D or 3D image by pressing the mouse button and moving the mouse. Pan is also activated when holding down the SHIFT key.

- **Zoom**. Located in upper right corner of patient view or in context menu. Allows to zoom in and out by pressing the mouse button and moving the mouse. Zoom is also activated when holding down the CTRL key.
- **Reset**. Resets image pan/zoom/rotation to default.

Initial view position

The **Initial view position** is the position (x, y, z) that the views are centered around when a plan is opened. The default initial view position is the (first) isocenter for the selected plan. The views in the plan report will (as default) be based on the initial view position.

There are three initial view position options:

1. **Define initial view position**: This option sets the current slice isocenter as the initial view position.
2. **Localize initial view position**: This option centers the views to the initial view position point, i.e., each view will display the slice that intersects the initial view position point.
3. **Clear initial view position**: This option clears the point created using the **Define initial view position** option. The initial view position value will be set to the default value, i.e., the isocenter position for the selected plan.

Display options

Depending on module the context menu offers various options for if and how objects are to be displayed in the views.

- Visibility options. Some modules offer options to toggle visibility on/off for certain objects; ROIs, POIs, beams, (collimator) jaws, (MLC) leaves, fluence, block, etc.
- **Patient direction**. Selection of patient direction in 2D and 3D views (Transversal, Coronal or Sagittal).
- Clicking the Maximize view icon in the upper right corner or double-clicking the mouse button in a view enlarges the current window to the entire workspace. Click the Restore view icon or double-click again to restore the workspace. Keep the SHIFT key down while double-clicking to get Full Screen display.

Navigation options

RayStation 7 provides several tools to orientate and navigate through the patient anatomy:

- **Measure tool**. In 2D images distances may be measured by clicking at the desired start position, moving the mouse to the desired end position and releasing the mouse button.
- **Point tool**. Reads out position, HU and dose when clicking in a 2D image.
- Use the mouse wheel to browse through the image slices.

- In modules displaying beams are options for selection of mouse wheel function; to scroll between image slices, beams, or segments. This is selected via the **Scroll tool** in the Context menu.
- By pressing the middle mouse button (the mouse wheel) somewhere in the patient view, all views will scroll to display the slice containing that point.
- By pressing and holding down the middle mouse button and moving the mouse, it is possible to easily scroll through the image data of the other patient planes. For example to move from the upper part of the rectum to the lower part, middle-click the Sagittal view at the desired position instead of scrolling through all slices.

Print snapshot

The Print snapshot tool enables printing a snapshot of a view at the current state. There are three printing options:

- **Print snapshot**: This option prints the view snapshot directly on a default printer. Requires that a default printer has been defined.
- **Print options**: This option opens the print dialog where a printer can be selected.
- **Save image as**: This option saves the snapshot image to file.

3.10 UNDO AND REDO PROCEDURES

To undo an action, do one of the following:

- Press Undo in the title bar toolbar
- Press Ctrl+Z.

To undo several actions at once, press the arrow next to Undo. In the list, select the actions to undo and press the mouse button. All of the selected actions are reversed.

To redo an action that was undone, do one of the following:

- Press Redo in the title bar toolbar
- Press Ctrl+Y.

To redo several undone actions at once, press the arrow next to Redo. In the list, select the actions to redo and press the mouse button. All of the selected actions are redone.

3.11 CANCEL PROCEDURE

A number of operations that take some time to complete can be cancelled. The cancel button is shown next to the progress bar for the operation.

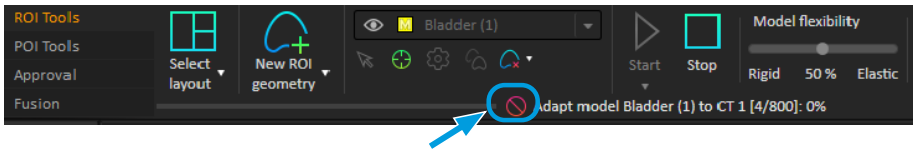
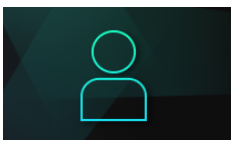


Figure 42. Cancel button example

Note: *Some operations take some time to complete and cannot be immediately cancelled. The operation may need to complete before cancel takes effect.*

4 PATIENT DATA MANAGEMENT

The Patient Data Management planning activity contains the Patient Information module, which presents an overview of the current patient and plan. The module provides functions for opening, editing, saving, importing, exporting and deleting patient data. This is where image set data is managed, for example selection of CT to density conversion tables. For approved plans a plan report can be created, and the treatment adaptation stage can be initialized, to allow for dose tracking.



In this chapter

This chapter contains the following sections:

4.1	Starting RayStation 7	p. 108
4.2	The Patient Information module user interface	p. 110
4.3	Managing patient and case data	p. 111
4.4	Export patient data	p. 132
4.5	Backup and restore procedures	p. 143
4.6	Auto recovery	p. 144
4.7	Change image set properties and create groups	p. 146

4.1 STARTING RAYSTATION 7

The RayStation Launcher application handles startup of the following applications: RayStation, RayPhysics, RayBiology and Clinic Settings. The startup icons will reflect the available licenses.

The manuals and any applicable field safety notice documents are available by clicking the **Documentation** icon.

Click the corresponding icon in the RayStation Launcher application to start the RayStation application.

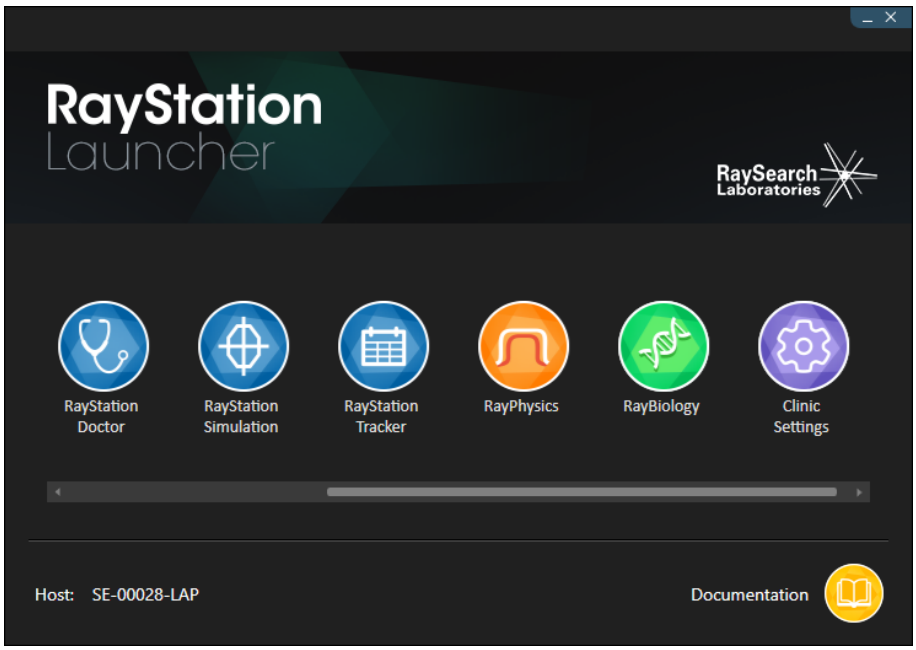


Figure 43. The RayStation Launcher.

When RayStation is started the user is given three options:

- Open a patient (*section 4.3.2 Open patient case on page 119*)
- Import new patient data (*section 4.3.1 Import new patient data on page 112*)
- Open a patient from the **RECENT PATIENTS** list

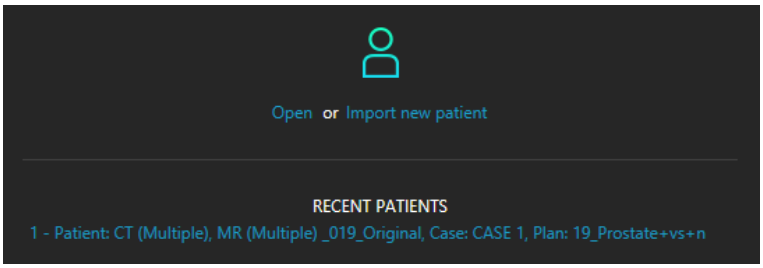
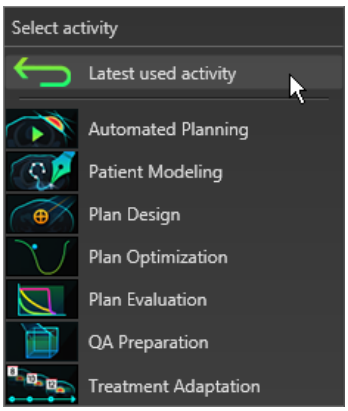

Open or Import new patient
RECENT PATIENTS
1 - Patient: CT (Multiple), MR (Multiple) _019_Original, Case: CASE 1, Plan: 19_Prostate+vs+n

Figure 44. The options to open or import a patient are given at the initial view when starting RayStation.

Most recent patients list

The five most recently opened patients are accessible from the start page and from the RayStation menu. Right click a patient in the **RECENT PATIENTS** list on the start page or click the "..." button to also select an activity to open the patient in. Select menu option **Latest used activity** to directly continue with the activity that was used when the patient was closed or RayStation was closed.



Delete patient data or a plan

It is possible to delete patient data or a plan from the database, see *section 4.3.6 Delete patient data on page 126* or *section 4.3.7 Delete patient data and plan on page 128*.

4.2 THE PATIENT INFORMATION MODULE USER INTERFACE

The Patient Information module workspace

The Patient Information module workspace consists of a main window where patient and plan information is displayed. The upper half of the workspace lists information about the patient and the corresponding treatment plans. Information about treatment adaptation if present/initialized is also listed in this area. The lower part of the workspace contains the image set library.

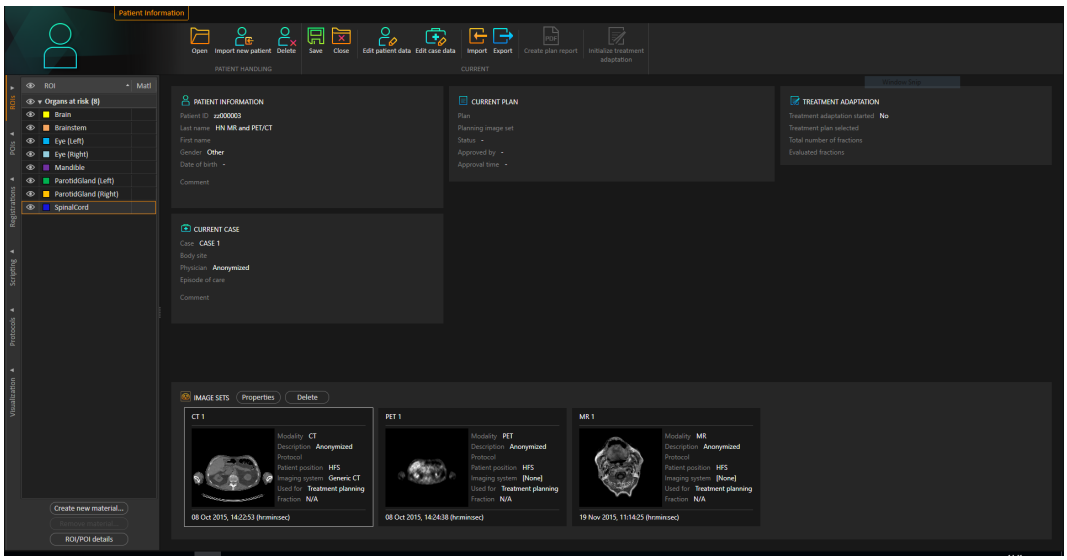


Figure 45. The Patient Information module workspace.

The image set library

The image set library contains all the image sets that have been imported to the patient case. Different types of images can be imported to RayStation, for example CT, MR and PET. Additionally, the user can group several image sets into 4DCT, PET-CT, 4DMR, and MR protocol groups.

To the upper left of the image set library is a **Properties** button. This can be used to change the properties of the image set. For detailed information, see *section 4.7 Change image set properties and create groups on page 146*.

An image set can be deleted from the library using the **Delete** button. This action will delete the image set from the patient case in the database.

4.3 MANAGING PATIENT AND CASE DATA

This section describes the most common procedures for managing patient data such as opening a patient, importing new patient data, saving patient data and deleting patient data.

In this section

This section contains the following sub-sections:

4.3.1	Import new patient data	p. 112
4.3.2	Open patient case	p. 119
4.3.3	Save patient data	p. 122
4.3.4	Edit patient data	p. 123
4.3.5	Edit case data	p. 125
4.3.6	Delete patient data	p. 126
4.3.7	Delete patient data and plan	p. 128
4.3.8	Create a plan report	p. 130
4.3.9	The write-lock	p. 131

4.3.1 Import new patient data

In RayStation patients are created by importing DICOM CT, MR or PET images. This includes patient demographic data such as Patient ID, Name, Gender and Date of birth. Cases are created using the Referring Physician's Name of one of the image sets.

The following methods are possible when importing patient data:

- **Import new patient.** If a conflicting patient exists when importing a new patient, the user must choose to either:
  - Create a new patient with the same Patient ID. This appends a suffix to the Last name.
  - Create a new case for the existing patient.
- **Import to current patient.** When importing data to current patient, it is possible to choose the current case or to create a new case. New cases requires at least one image set to be imported. Import to current patient is restricted to DICOM data that matches the Patient ID. It is possible to override this by checking "Override Patients ID (MRN)".

Import restrictions include, but are not limited to, the following:

- Structure set requires all referenced image instances.
- Beam and Fraction dose require the referenced plan.
- RT Dose with dose type EFFECTIVE will be interpreted as RBE dose and is only possible to import for carbon ions. EFFECTIVE dose must be imported together with the corresponding PHYSICAL dose.
- Spatial Registration requires all referenced image instances.

For more information about DICOM data support and limitations, refer to the *RSL-D-RS-7.0-DCS, RayStation 7 DICOM Conformance Statement*.

WARNING!

Fractionation scheme is discarded in DICOM import. When a DICOM plan is imported to RayStation the fractionation scheme is discarded. As a result, the beam sets created during the import will always be set for sequential delivery even if the original plan indicated an interleaved pattern.

In addition, the delivery order indicated by the beam set order may not match the intended delivery order. As a consequence, no activities that rely on a correct fractionation scheme shall be performed after the import. For example, the biological effect of the imported plan will be incorrectly reported. (119127)

WARNING!

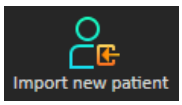
Review frame-of-reference registration before dose computation. It is especially important that frame-of-reference registrations that have been imported or created by treatment position alignment are reviewed before they are used for fraction dose computation in the Dose Tracking module, or when computing dose on additional image sets. (360380)

Note: *When importing a plan using motorized wedges, the two segments (wedge in and wedge out) will be translated into one segment and an effective wedge angle. However, if no matching treatment machine is found in the database, the effective wedge angle will be set to 60 degrees, regardless of the original angle. If a feasible treatment machine is set to the plan, the correct effective wedge angle will be computed.*

Import from files

To perform file based import:

1. Choose import alternative (**Import new patient** or **Import to current patient**) in the DICOM Import sub menu under the RayStation menu.

   This opens the **Import New Patient/Case** dialog.

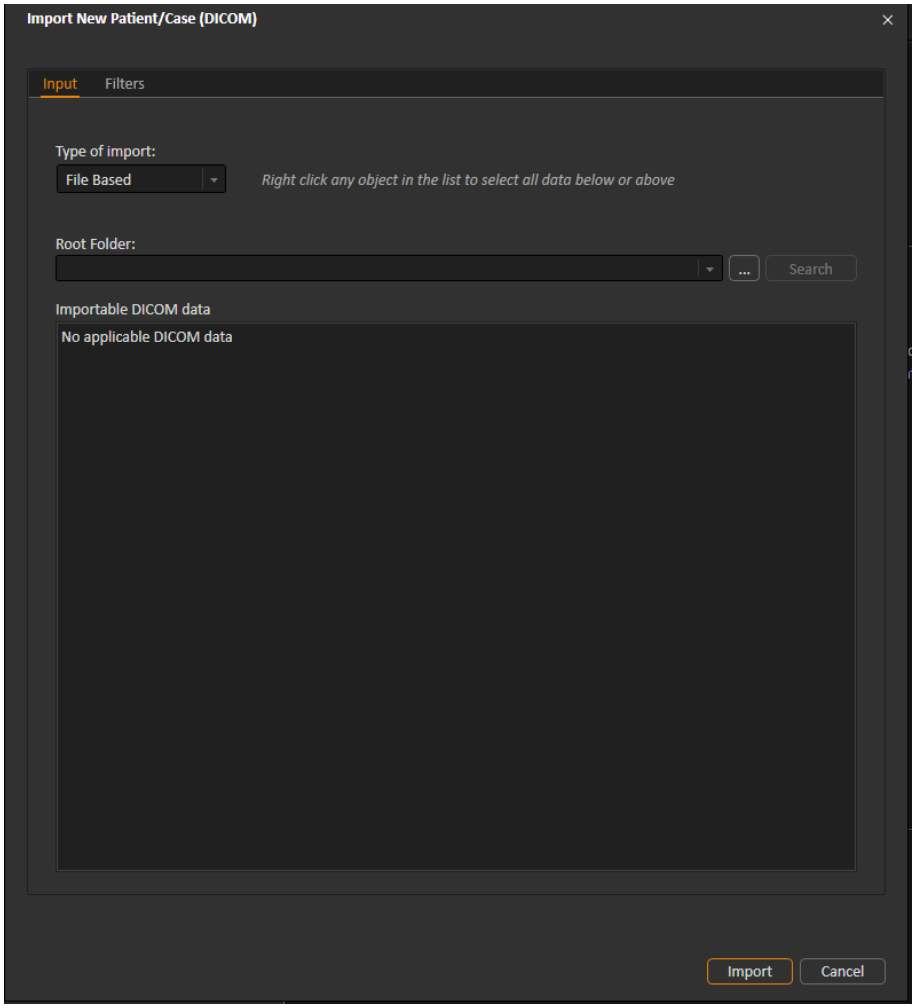


Figure 46. The DICOM Import dialog with type of import set to file based to allow for file based DICOM import.

2. Select **File Based** import.
3. Select **Root Folder**. Open a file browser by clicking the **...** button.
4. Select the DICOM folder and click **OK**.
5. Select the objects to import.
6. Click **Import**.

Note: *When selecting the Import directory, it should be noted that all subfolders will be scanned for DICOM files. It is therefore recommended to avoid choosing folders with many subfolders since the scan can take a considerable amount of time.*

Import from DICOM archive (using query/retrieve)

To import a patient from the DICOM archive:

1. Choose import alternative (**Import new patient** or **Import to current patient**) in the DICOM Import sub menu in the RayStation menu.

   This opens the **Import New Patient/Case** dialog.

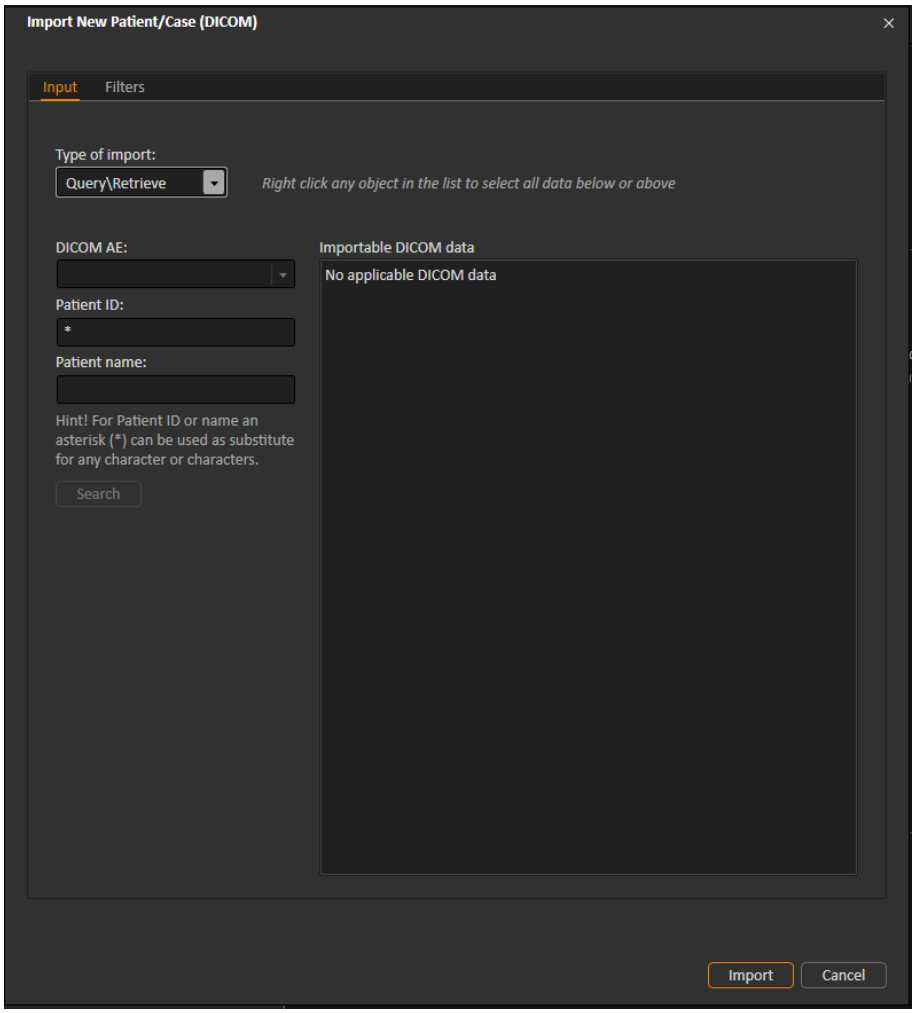


Figure 47. The DICOM Import dialog for Query/Retrieve based import.

2. Select **Type of import: Query\Retrieve**.
3. Select **DICOM AE** in the drop-down list.
4. To search for a specific patient, enter the **Patient ID** and the **Patient name** fields. (Note that to list all patients, some PACS require "*" as patient ID while some require the field to be empty.)
5. Click **Search**.
6. Select the objects to import.
7. Click **Import**.

Storage SCP import

If the RayStation Storage SCP service is installed, it is possible to enable Storage SCP import to RayStation.

Note: *The user which runs the storage service must have write access to the Storage location folder.*

To import a patient from the DICOM Storage SCP folder:

1. Choose import alternative (**Import new patient** or **Import to current patient**) in the DICOM Import sub menu in the RayStation menu.

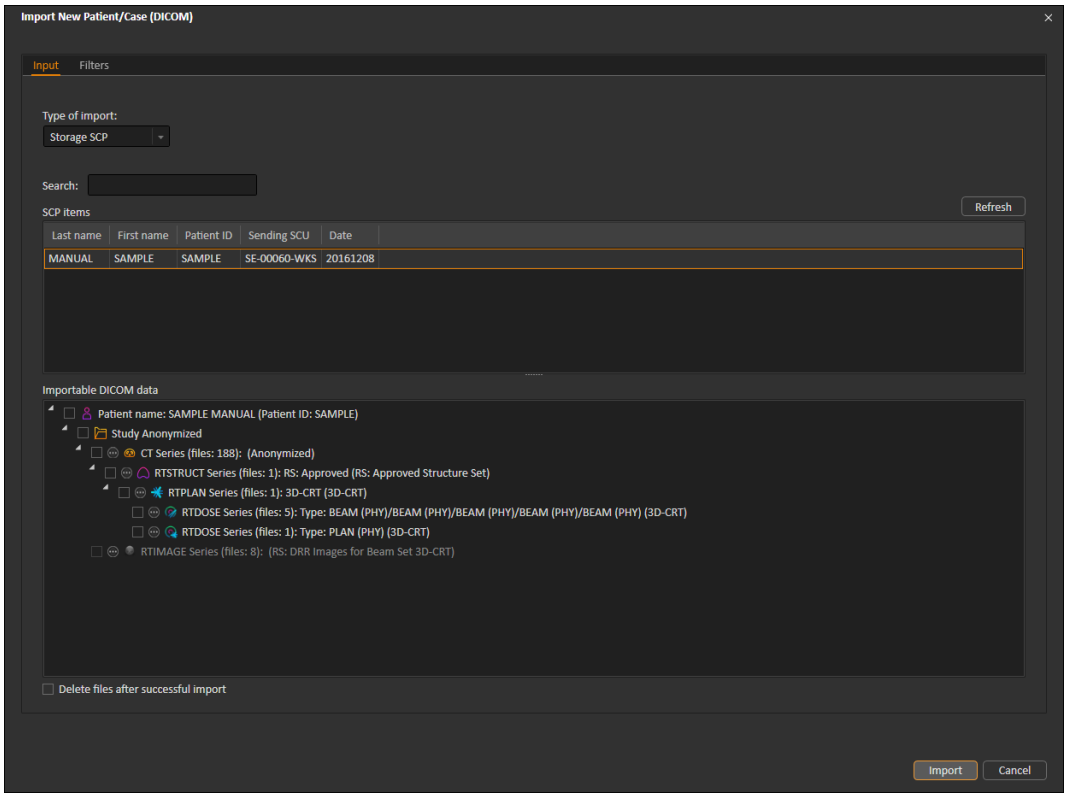


Figure 48. The DICOM Import dialog for Storage SCP import.

2. In the DICOM Import dialog, select **Type of import: SCP**.
3. Select the objects to import.
4. Select to **Delete files after successful import** by checking the corresponding checkbox.
5. Click **Import**.

Note: *Files with same patient ID and SOP Instance UID will be overwritten.*

Import filters

Before the files are imported into RayStation it is possible to apply so-called import filters that modify the DICOM-files in different ways. For example, filters can be used to remove or add a certain attribute or add DICOM transfer syntax to the files. Be aware that the filters are run in the same order as they are listed.

Import filters are only provided by RaySearch Laboratories.

Click the **Filters** tab and select which filters to use by clicking the **Add** button.

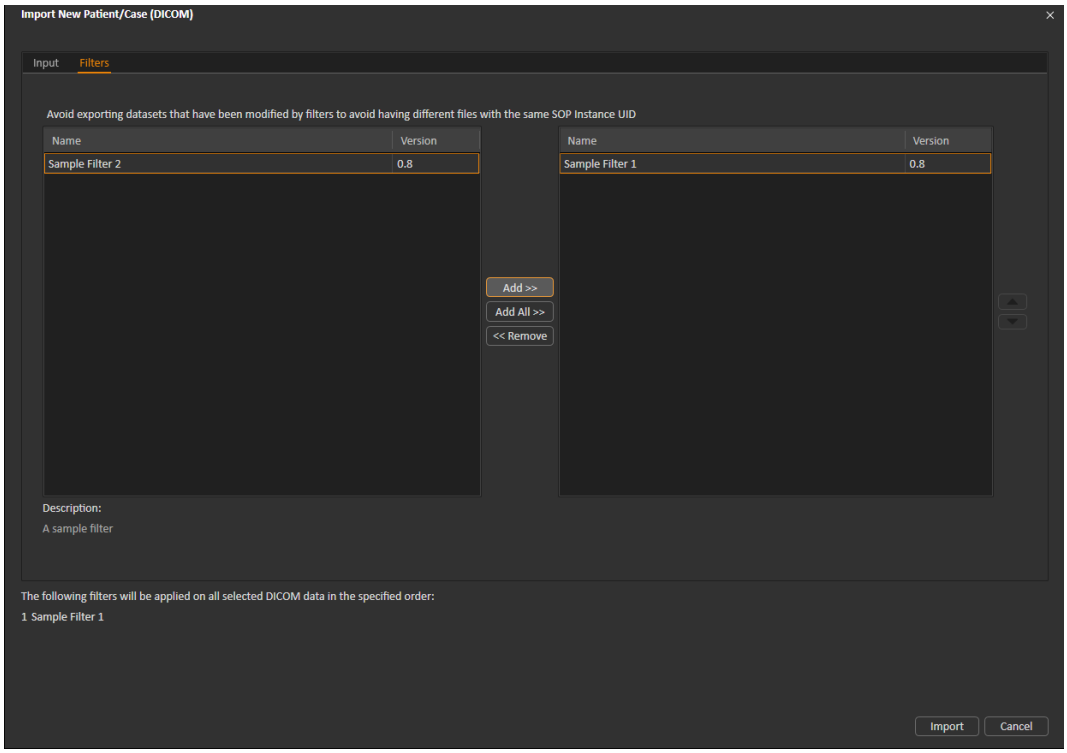
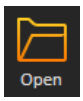


Figure 49. The DICOM Import dialog showing the **Filters** tab.

4.3.2 Open patient case

To open a patient case that is already in the database:

1. Select **Open** from the RayStation menu, click the **Open** button in the title bar toolbar or type Ctrl + O. (This operation is possible from any planning activity.)

   This opens the Open Case dialog.

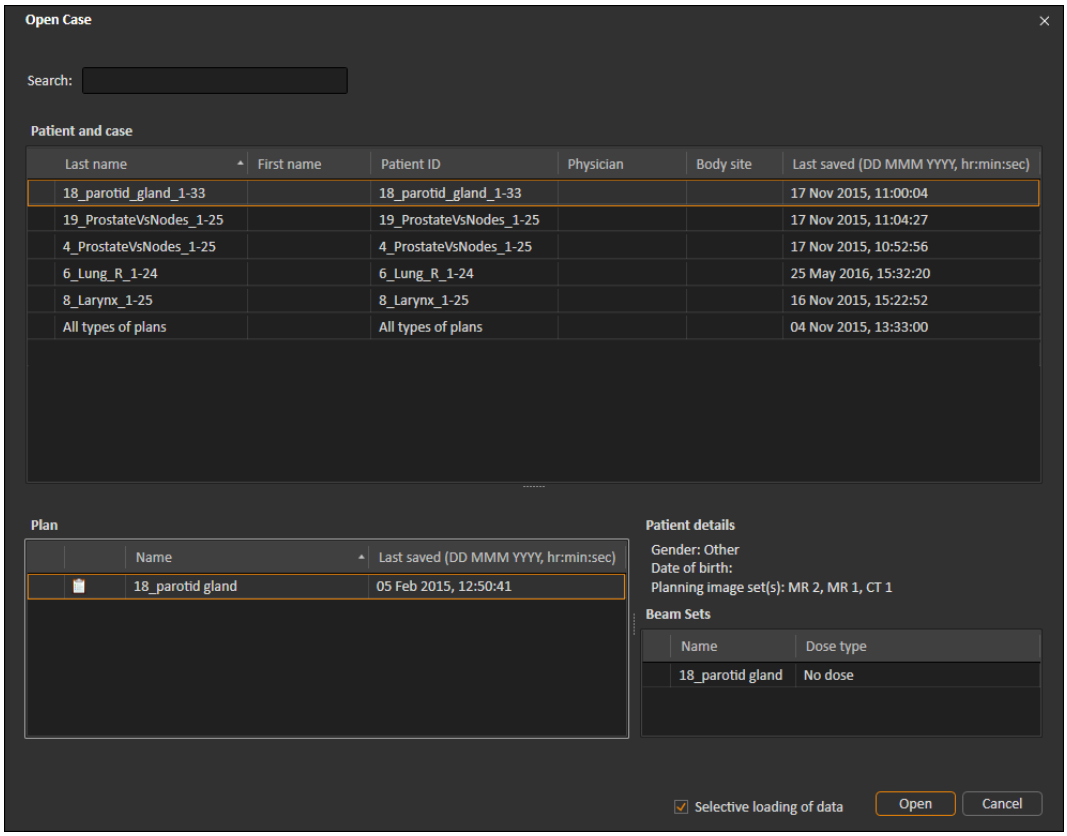


Figure 50. The Open Case dialog.

2. Select a **Patient** from the list. If the patient is not found in the list, search the patient database using the Search field. Patients in the Patient list can be re-sorted by clicking the column headers.

3. Select a **Plan** from the list. This step is optional, it is possible to change the patient plan when the patient is opened.

4. Click the **Open** button. When loaded, the patient and case name should be visible in the top frame of the application window.

Once a patient and a treatment plan has been opened, the patient and case name will be displayed in the main window title bar.

Index service

If an Index service is used, all patients indexed via this service will be displayed in the Open Case dialog. If a patient exists in multiple databases, it will be displayed as one row in the Open Case dialog. A column indicating the databases that the patient exists in will be visible to the left in the **Open Case** dialog.

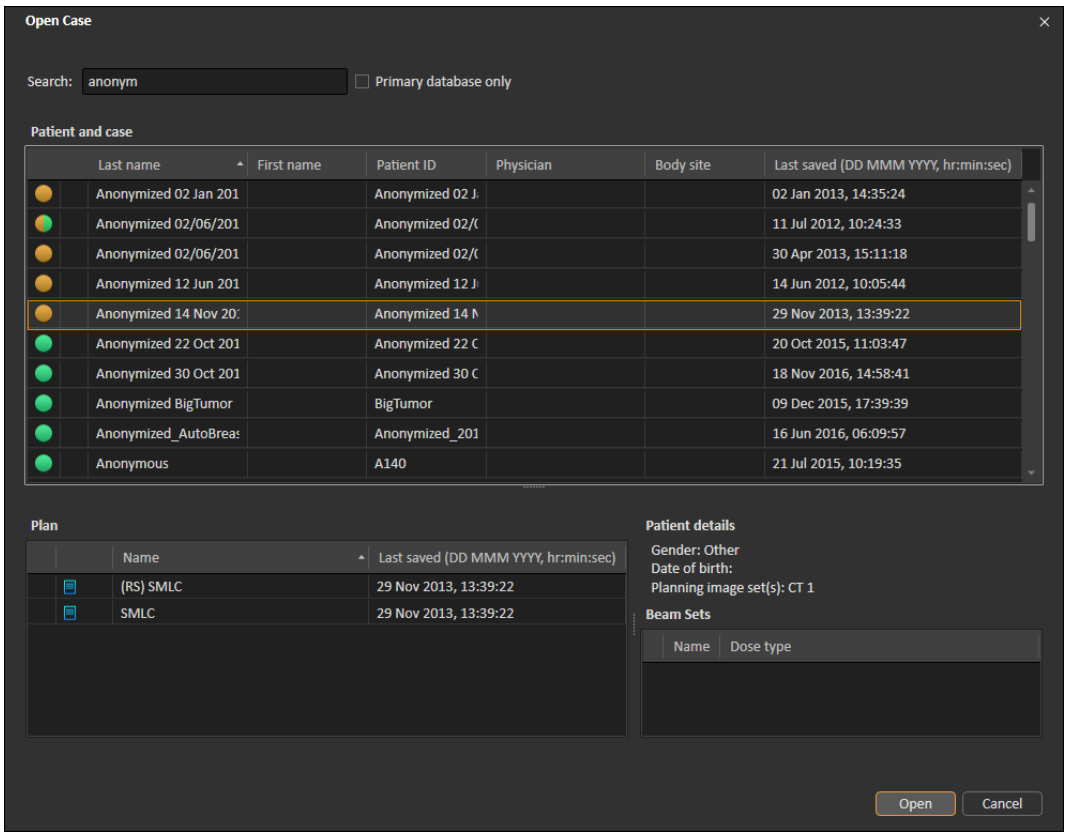


Figure 51. The **Open Case** dialog where an index service is used.

Database status	Description
Green	The patient exists only in the primary database.

Database status	Description
Yellow	The patient does not exist in the primary database, but in a secondary database. If the patient is opened it will be copied or moved to the primary database. • Copying occurs if the secondary database is older (previous version) than the primary database or if the database is a locked archive. • If the secondary database has the same version as the primary database, the patient will be moved.
Green/Yellow	The patient exists in both the primary database and in one or several secondary databases. The patient that is located in the primary database will be opened.
Red	The patient exists in a database with a newer version number and can therefore not be opened.
Green/Red	The patient exists in the primary database and in a newer database version of the database. Note that it is not the newer version that will be opened. It is not recommended to open a patient from this state.
Yellow/Red	The patient exists in an archive and in a newer database version. Note that it is not the newer version that will be opened. It is not recommended to open a patient from this state.

WARNING!

Index service. In RayStation 5 and higher, the index service helps the user to keep track of patients in different databases with different database versions. In earlier RayStation versions this is not possible and there is no warning that a patient might have been migrated to a later database version. (159208)

WARNING!

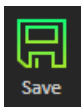
Verify database consistency before upgrade. In the RayStation Storage Tool it is possible to create a new database system based on an existing system. Before creating a new system based on an existing system, make sure to run the ConsistencyAnalyzer tool. (231801)

4.3.3 Save patient data

There are three alternatives for saving patient data:

- Alternative 1: Select **Save** in the RayStation menu.
- Alternative 2: Click the **Save** button in the title bar toolbar.
- Alternative 3: Type Ctrl + S

These alternatives are accessible from any planning activity. In addition to these alternatives a **Save** button is included in the toolbar of the Patient Data Management planning activity.



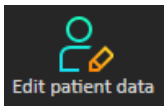
4.3.4 Edit patient data

It is possible to change the patient demographics as long as there are no approved structure sets or beam sets.

The modified patient data will be reflected in the exported DICOM data. This also applies to imported images.

To edit patient data:

1. Click the **Edit patient data** button.



This opens the Edit patient data dialog.

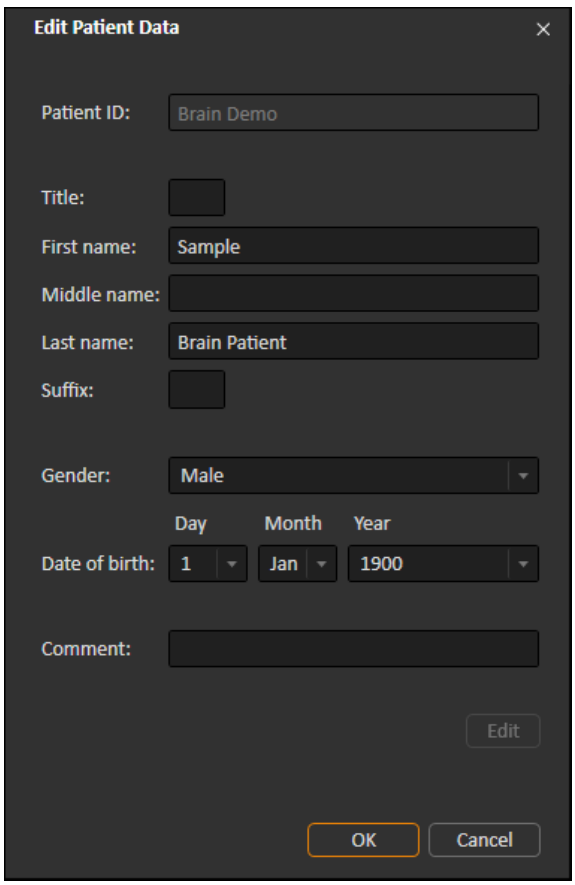


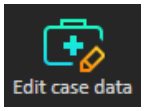
Figure 52. The **Edit patient Data** dialog.

2. Enter new patient demographic data.
3. Click **OK**.

4.3.5 Edit case data

To edit case data:

1. Click the **Edit case data** button.



This opens the **Edit Case Data** dialog.

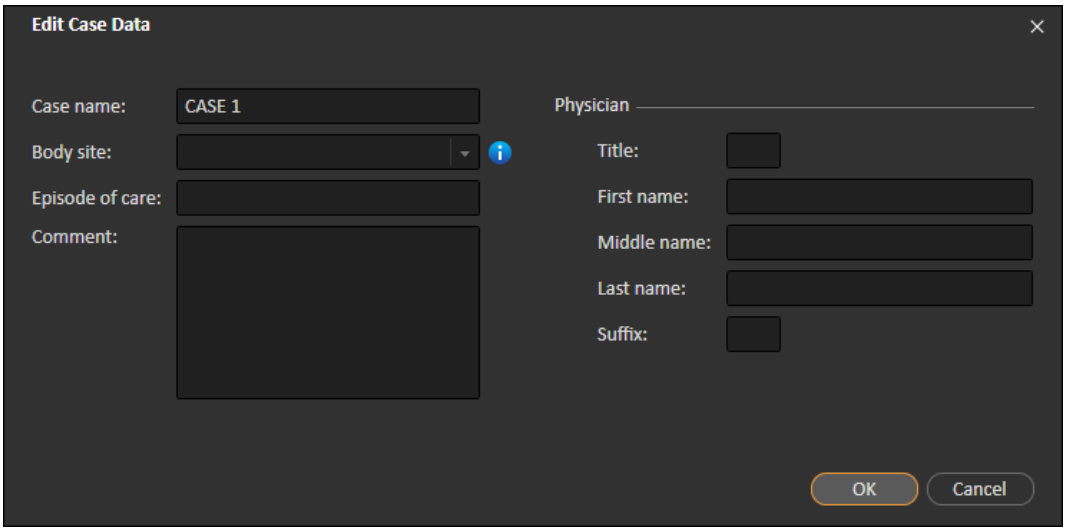


Figure 53. The **Edit Case Data** dialog.

2. Enter the new information for **Case name**, **Body site**, **Episode of care**, **Physician** and **Comment**. A predefined drop-down list of body sites can be defined in Clinic Settings (see *section D.2.2 The Preferences tab on page 922*).

   Body site and physician are searchable in the **Open Case** dialog, and displayed with the comment, together with the rest of the patient information in the Patient Information overview.

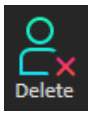
3. Click **OK**.

4.3.6 Delete patient data

Deleting patient data cannot be undone and requires approval and user authentication.

To delete patient data:

1. Select **Delete** in the RayStation menu or click the **Delete** button in the Patient Data Management planning activity toolbar.



This opens the Delete dialog.

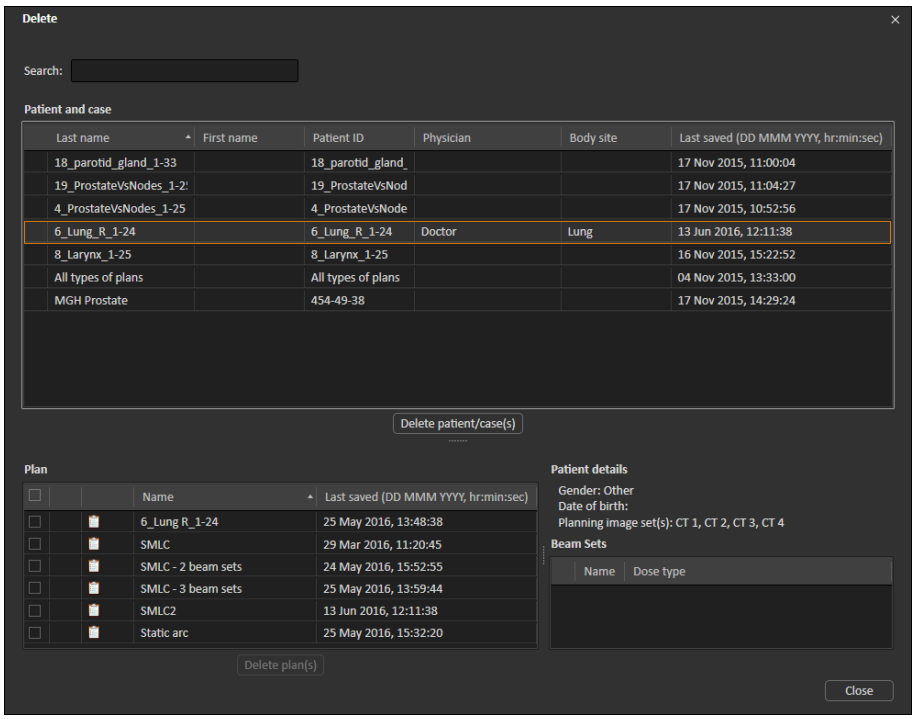


Figure 54. The **Delete** dialog.

2. Select a patient and case from the list and click the **Delete patient/case(s)** button. This opens the Delete patient authentication dialog.

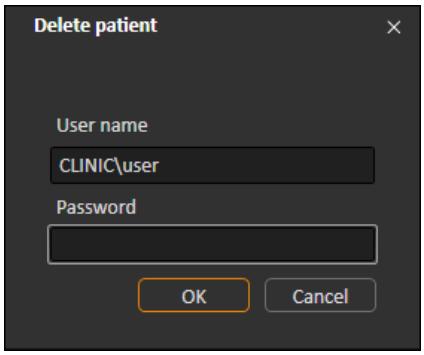


Figure 55. The Delete Patient authentication dialog.

3. Enter **User name** and **Password**.

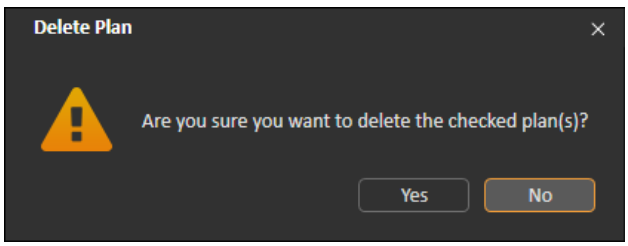


Figure 56. The **Delete Plan** warning dialog.

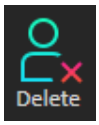
4. Click **OK**. The selected patient and case will be deleted from the RayStation database.
5. Click **Close**.

4.3.7 Delete patient data and plan

Deleting patient data cannot be undone and requires approval and user authentication.

To delete patient data and plan:

1. Select **Delete** from the RayStation menu or click the **Delete** button in the Patient Data Management planning activity toolbar.



This opens the Delete dialog.

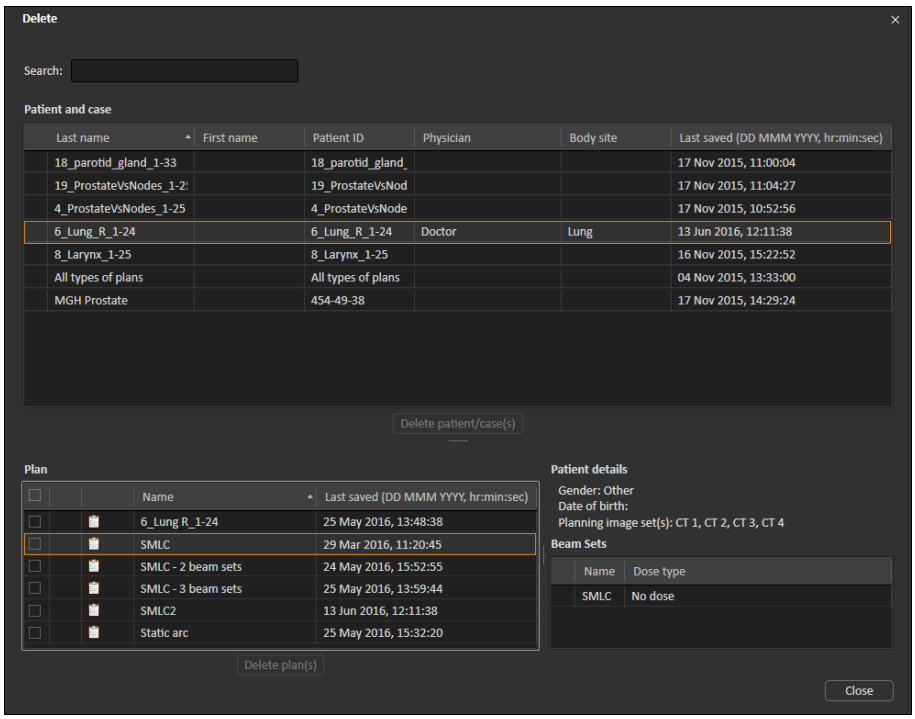


Figure 57. The Delete dialog.

2. Select the desired **Patient**, **Case** and **Plan**(s).
3. Click the **Delete plan(s)** button to delete the selected plan(s) from the RayStation database.

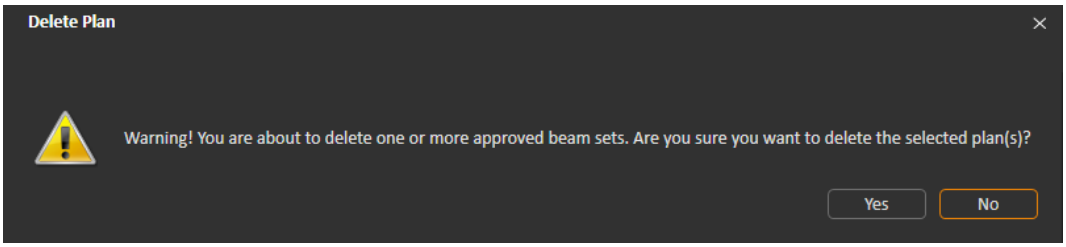

Delete Plan
Warning! You are about to delete one or more approved beam sets. Are you sure you want to delete the selected plan(s)?
Yes
No

Figure 58. The **Delete Plan** warning dialog.

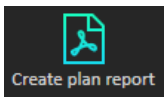
4. Click **OK**. The selected plan will be deleted from the RayStation database.

4.3.8 Create a plan report

A plan report that lists information for the current plan can be created. Report templates can be customized using the RayStation Report Designer, see *Appendix F RayStation Report Designer* for more information.

To create a plan report:

1. Select **Create report** from the RayStation menu, type Ctrl + P or click the **Create plan report** button.

   This opens the Select Report Template dialog.

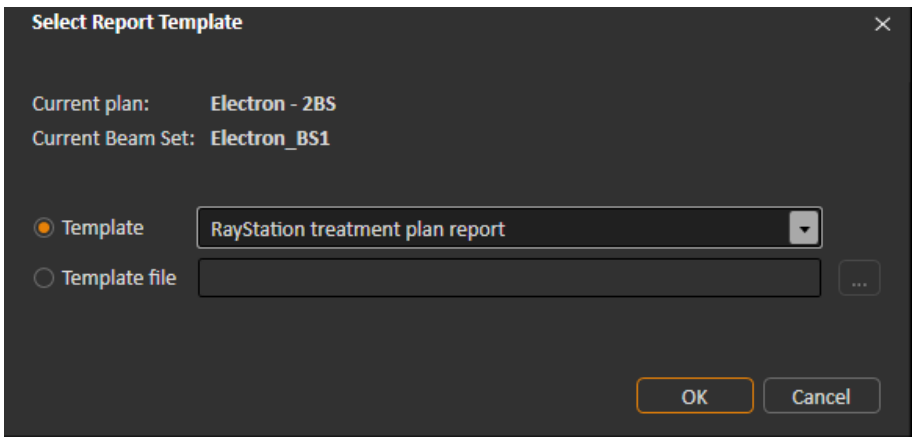
   

   Figure 59. The **Select Report Template** dialog.

2. Select a **Template** from the drop-down list or select to open a local **Template file**.
3. Click **OK**.

4.3.9 The write-lock

RayStation 7 has a safety measure that prevents multiple persons from editing patient or machine data at any time. This is called the write-lock. The user will be notified by the following dialog if the write-lock is triggered.

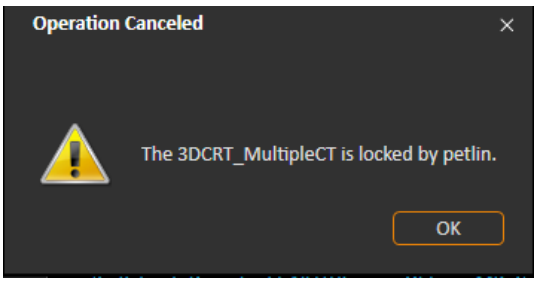


Figure 60. The Write-lock message.

In case the system has crashed and a user tries to load a patient that was opened during the crash the same message may occur. The write-lock will then persist for approximately 30 seconds after the system crash until it is released and the patient can be re-loaded.

4.4 EXPORT PATIENT DATA

RayStation 7 can export patient data to DICOM. This includes:

- Imported CT, MR and PET images (CT, MR, PT)
- 4D-CT Projections (CT)
- Frame-of-Reference registrations (REG)
- Structure Sets (RT Struct)
- Beam Sets (RT Plan)
- Plan Dose and Beam Dose (RT Dose)
- DRR images (RT Image)

For more information about DICOM data support and limitations, refer to the *RSL-D-RS-7.0-DCS, RayStation 7 DICOM Conformance Statement*.

Note: *For VMAT and Conformal Arc plans, DRRs will be generated from the first (zeroed) segment for each beam as opposed to other plans where DRRs are generated from the union segment.*

In this section

This section contains the following sub-sections:

4.4.1	Export to files	p. 134
4.4.2	Export to DICOM archive	p. 136
4.4.3	Export to iDMS	p. 138
4.4.4	Export to ExacTrac Vero and the Vero R&V system	p. 140
4.4.5	Anonymization of patient information	p. 141
4.4.6	Export filters	p. 142

Precautions

WARNING!

DICOM RT Structure set export. The DICOM export of the RT Structure set will convert all ROIs to contours and any structure parts outside the upper or lower image set slice will not be included.

This applies to ROI geometries with mesh or voxel representation. Such geometries are typically created using model-based segmentation, atlas-based segmentation, or by using 3D ROI interaction tools in RayStation. The DICOM export only handles contours on image slices, which means that the parts that extend outside the first or last slice of the image set will not be included in the export. Thereby they will not be identical after a DICOM export/import roundtrip into RayStation or an external system. (118239)

WARNING!

DICOM export of Vero plans. Extra care must be taken when DICOM exporting a plan with multiple isocenters to the Vero R&V system. It is necessary to perform the DICOM export twice, once with the ExacTrac Vero checkbox checked and once with the checkbox unchecked. (125706)

WARNING!

The user must verify that ion block/MLC/compensator DICOM data is correctly transformed from isocenter to physical plane. The user must verify that their receiving systems use the same transform to achieve the physical block/MLC/compensator as RayStation, based on the tags for VSAD, isocenter to tray distances and properties on the isocenter exported in DICOM. This must be verified for a number of collimator angles, if the machine supports a rotated collimator (snout). (370896)

4.4.1 Export to files

To export patient data to files:

1. Select **DICOM Export** from the RayStation menu. This opens the **DICOM Export** dialog.

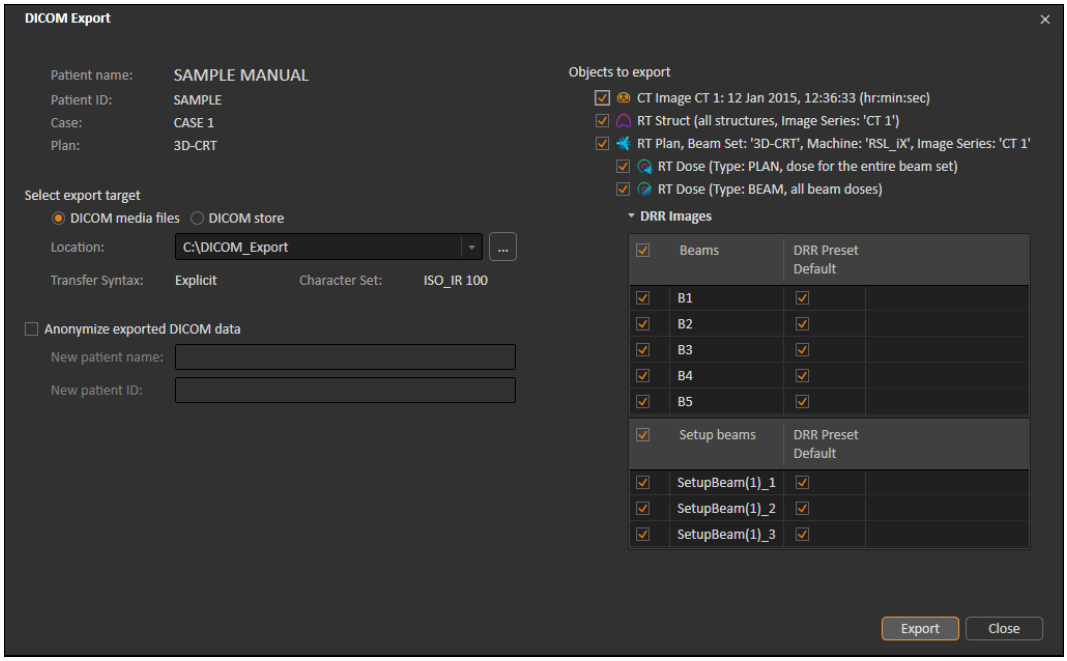
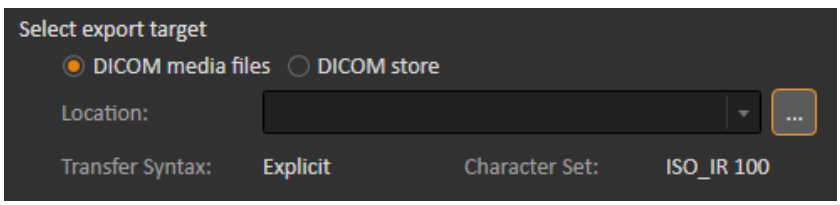


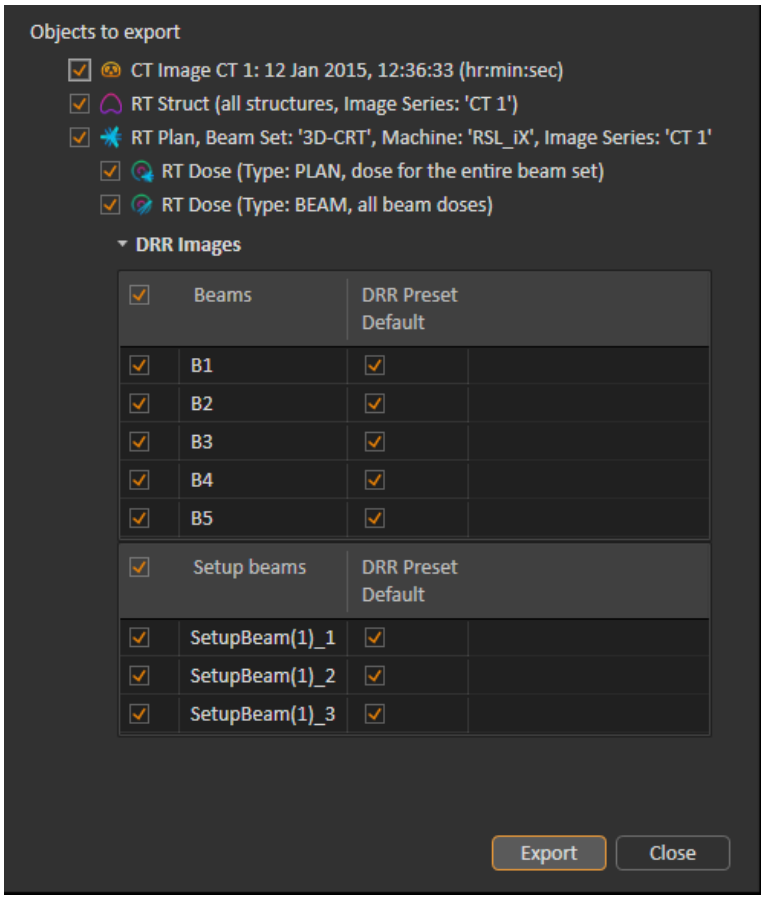
Figure 61. The **DICOM export** dialog for patient data export to file.

2. Make sure that the correct patient, plan and machine are displayed in the **DICOM Export** dialog.
3. Select **DICOM media files** as export target.



4. Open a file browser by clicking the "**...**" button.
5. Select the DICOM folder and click **OK**.

6. Select **Objects to export,** by checking the corresponding checkboxes.



7. Click **Export**. A message is displayed notifying the outcome of the export.

4.4.2 Export to DICOM archive

1. Select **DICOM Export** from the RayStation menu. This opens the **DICOM Export** dialog.

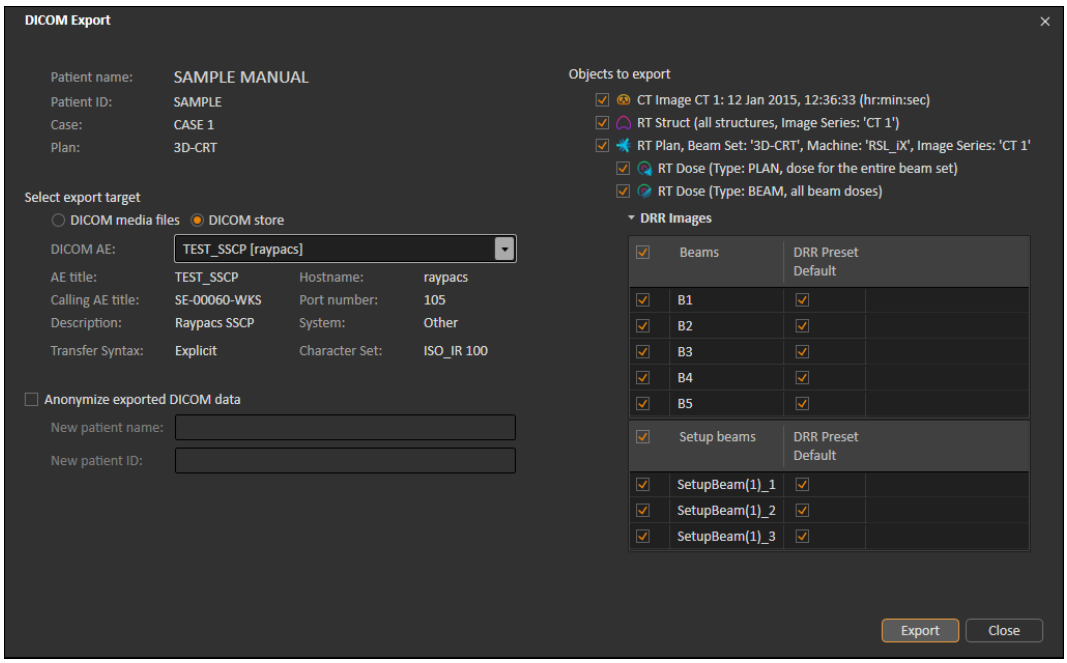
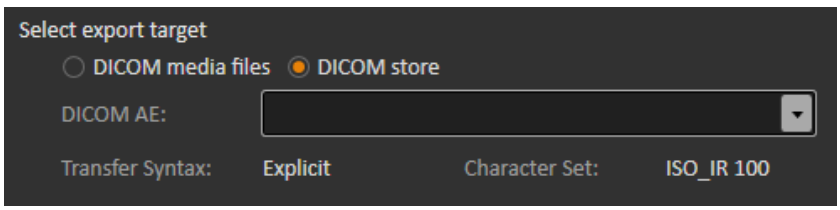


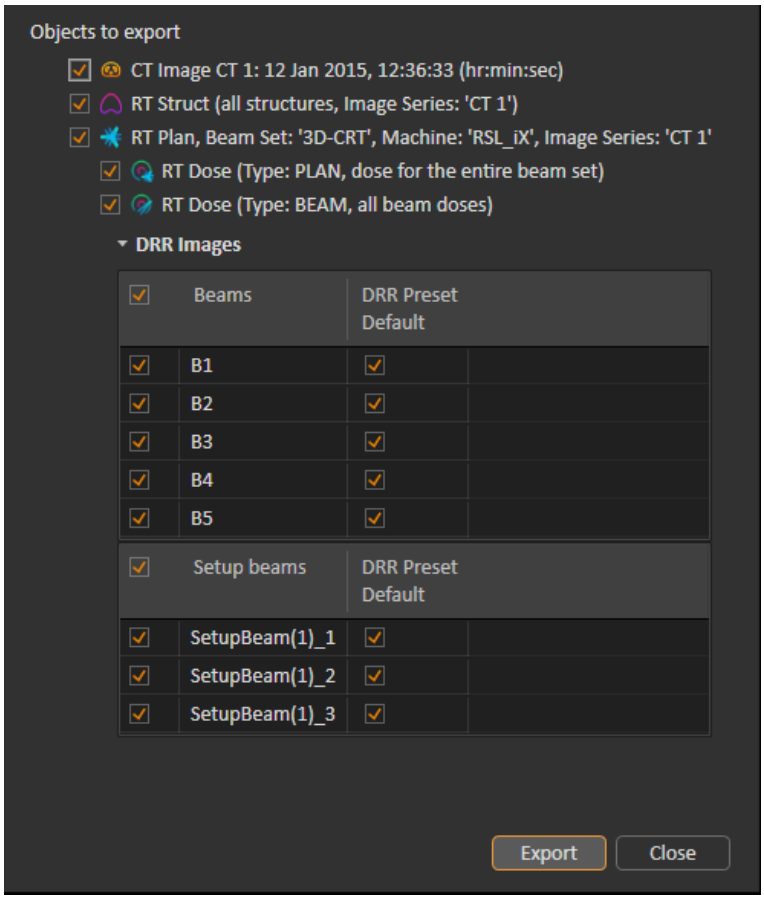
Figure 62. The **DICOM Export** dialog for patient data export to DICOM archive.

2. Make sure that the correct patient, plan and machine are displayed in the **DICOM Export** dialog.
3. Select **DICOM store** as export target.



4. Select **DICOM AE** from the drop-down list.

5. Select **Objects to export** by checking the corresponding checkboxes.



6. Click **Export**. A message is displayed notifying the outcome of the export.

4.4.3 Export to iDMS

In order to export a plan to iDMS, at least one RayGateway connection with the target set to iDMS must be set up via the Clinic Settings application (see *RayGateway Connections on page 931*). The current plan also needs to have at least one beam set with treatment technique TomoHelical.

The **Objects to export** are structured differently when selecting iDMS as export target compared to when selecting DICOM media files or DICOM store. When selecting iDMS, the **Objects to export** are grouped into exportable packages. An exportable package is the treatment plan and its dependent image set and structure set and the resulting beam set dose. The plan name in IDMS will be a combination of the "Treatment plan name" and the "Beam set name".

To export data to iDMS:

1. Select **DICOM Export** from the RayStation menu. This opens the **DICOM Export** dialog.

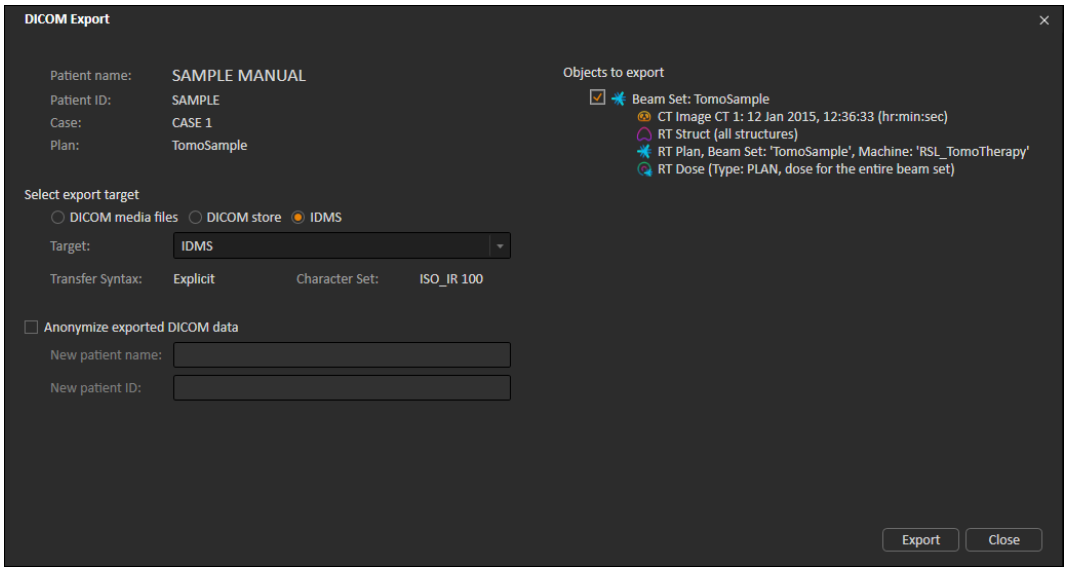
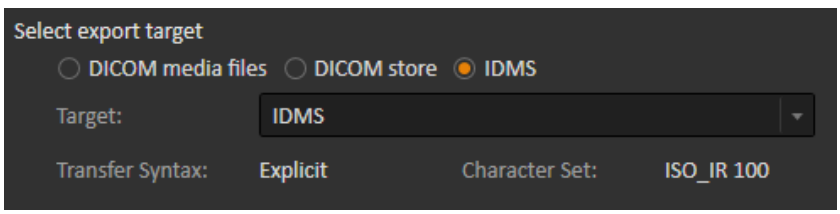


Figure 63. The **DICOM Export** dialog for patient data export to iDMS.

2. Make sure that the correct patient, case, plan and machine are displayed in the **DICOM Export** dialog.
3. Select **IDMS** as export target.



4. In the **Target** drop-down list, select the desired RayGateway connection (that has been set up in Clinic Settings).

   If multiple RayGateway connections are available with the **Target** set to "IDMS" in Clinic Settings, the desired connection can be selected in the **Target** drop-down list in the **DICOM Export** dialog.

5. Select **Objects to export** by checking the corresponding checkboxes.

6. Click **Export**. A message is displayed notifying the outcome of the export.

4.4.4 Export to ExacTrac Vero and the Vero R&V system

Plans with multiple isocenters

For plans with multiple isocenters, it is necessary to perform the DICOM export twice, once with the **ExacTrac Vero** checkbox checked and once with the checkbox unchecked.

- When the **ExacTrac Vero** checkbox is checked, one plan is exported containing all isocenters and all beams. This plan should be sent to ExacTrac.
- When the **ExacTrac Vero** checkbox is unchecked, one plan for each isocenter is exported. These plans should be sent to the Vero R&V system.

If the **ExacTrac Vero** checkbox is unchecked and the export target is **DICOM store**, it is only possible to select an AE that has been configured with system set to ExacTrac in the **DICOM Application Entities** tab in ClinicSettings.

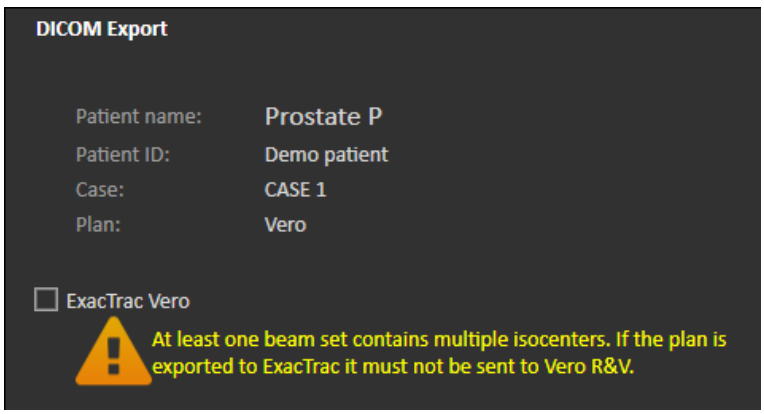


Figure 64. The DICOM Export options for a multiple isocenter plan.

Note: *There is no support in the QA Preparation module to handle export of QA plans with multiple isocenters to the Vero R&V system. If QA is to be performed with multiple isocenters, use the patient plan for delivery also during QA.*

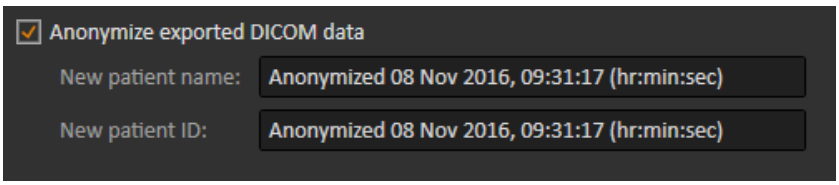
Plans with a single isocenter

For plans with a single isocenter, the **ExacTrac Vero** checkbox is not displayed. However, if using DICOM store it is still necessary to perform the DICOM export twice: once for the ExacTrac AE and once for the Vero R&V AE.

4.4.5 Anonymization of patient information

The anonymization option makes it possible to change patient demographic information in the exported DICOM objects.

To anonymize the exported DICOM objects, check the **Anonymize exported DICOM data** checkbox in the **DICOM Export** dialog. Enter the new patient name and patient ID to be used in the anonymized data. Patient birth date will be set to today's data, and the patient sex will be set to 'O' (Other).

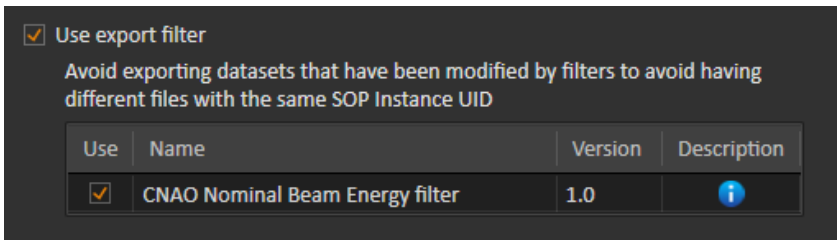

Anonymize exported DICOM data
New patient name:
Anonymized 08 Nov 2016, 09:31:17 (hr:min:sec)
New patient ID:
Anonymized 08 Nov 2016, 09:31:17 (hr:min:sec)

4.4.6 Export filters

Before the files are exported from RayStation it is possible to apply export filters that modify the DICOM files in different ways. For example, filters can be used to modify, remove or add attributes. It is only possible to apply one export filter at a time.

Filters have to be written and signed by RaySearch in order to run in clinical versions of RayStation.

When filters are available they will appear in the **Use export filter** list in the **DICOM Export** dialog. To use a specific filter, select it in the **Use export filter** list in the **DICOM Export** dialog.


Use export filter
Avoid exporting datasets that have been modified by filters to avoid having different files with the same SOP Instance UID
Use
Name
Version
Description
CNAO Nominal Beam Energy filter
1.0

4.5 BACKUP AND RESTORE PROCEDURES

The backup and restore functionality allows export, to disk, of a complete copy of the state in the database for a patient. The exported patient may later be imported into another RayStation system. The feature should primarily be used for communicating patients between a clinic and RaySearch, e.g. if there are problems related to a specific data set.

To backup or restore a patient, select **Backup/restore** in the RayStation menu.

Note: *At this point there is no guarantee that it will be possible to restore a backed up patient in a future release of RayStation.*

Treatment machines can be backed up and restored in the same way, from the Beam Commissioning module in the RayPhysics application. See the *RSL-D-RS-7.0-RPHY, RayStation 7 RayPhysics Manual* for more information.

The treatment machines and CT machines used for the patient are backed up and can be restored together with the patient.

RBE models can be backed up and restored together with patients that have carbon ion plans.

RBE models can be backed up and restored from the RBE Model Administration module in the RayBiology application. See *Appendix E RayBiology* for more information.

Note: *When restoring a treatment machine or a CT machine together with a patient, it will not be accessible in the machine tree in RayPhysics in an already open instance of the application. The RayPhysics application has to be restarted or the user can enter the Beam Commissioning module and click the Refresh machine list button in order to display the restored CT machine.*

Note: *When restoring an RBE model together with a patient, it will not be accessible in the RBE model tree in RayBiology in an already open instance of the application. The RayBiology application has to be restarted or the user can enter the RBE Model Administration module and press the Refresh RBE model list button in order to display the restored RBE model.*

4.6 AUTO RECOVERY

When RayStation executes, data is collected for all user-performed actions. If RayStation is terminated in an uncontrolled way and then restarted, RayStation offers a way to recover unsaved changes before RayStation terminated.

Recovery data (patient, phantom, machine, imaging system or RBE model) is personal and saved individually for each user. In order to recover changes, the same user must start RayStation with the same profile (icon) in RayStation Launcher. If another user opens data with unsaved changes, there will be a warning about it. If the other user selects to continue, recovery data will be deleted if the other user selects to save. Recovery data can only be restored in one instance of RayStation.

Recovery data will be presented to the user when RayStation starts or when opening data. In the **Recover Unsaved Changes** dialog, the user has the possibility to:

- **Recover** specific unsaved changes, or
- **Discard** the changes, or
- **Postpone** the decision and leave the recovery data untouched.

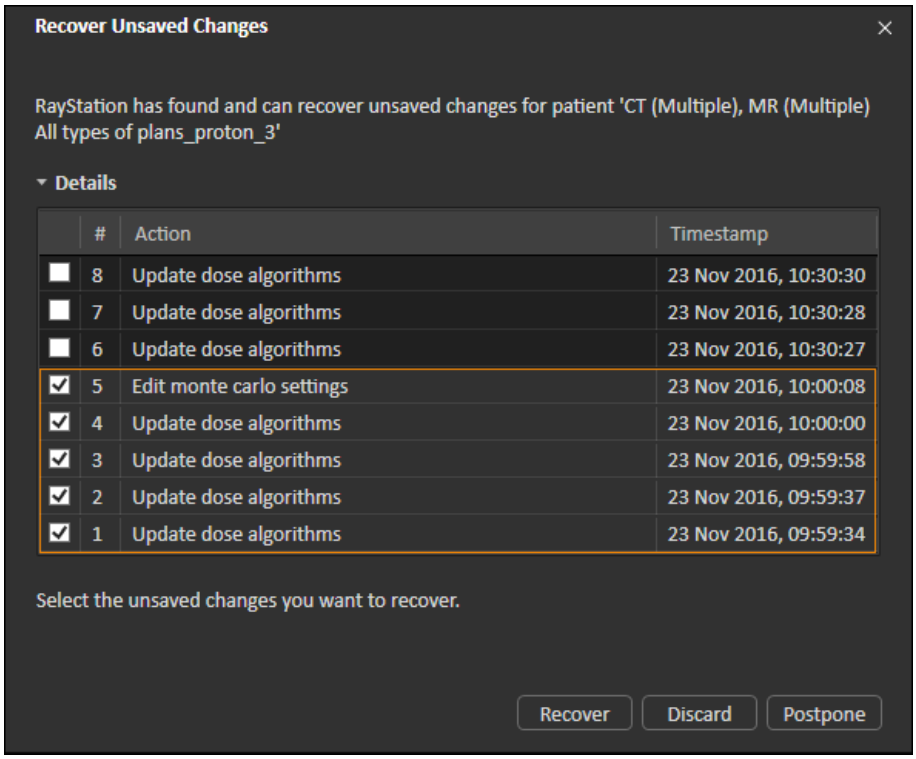

Recover Unsaved Changes
RayStation has found and can recover unsaved changes for patient 'CT (Multiple), MR (Multiple) All types of plans_proton_3'
Details
Action Timestamp
8 Update dose algorithms 23 Nov 2016, 10:30:30
7 Update dose algorithms 23 Nov 2016, 10:30:28
6 Update dose algorithms 23 Nov 2016, 10:30:27
5 Edit monte carlo settings 23 Nov 2016, 10:00:08
4 Update dose algorithms 23 Nov 2016, 10:00:00
3 Update dose algorithms 23 Nov 2016, 09:59:58
2 Update dose algorithms 23 Nov 2016, 09:59:37
1 Update dose algorithms 23 Nov 2016, 09:59:34
Select the unsaved changes you want to recover.
Recover
Discard
Postpone

Figure 65. The **Recover Unsaved Changes** dialog with the expanded **Details** list. Select the unsaved changes to recover in the dialog and click recover.

If the user selects to **Recover** the unsaved changes, the default is to recover all actions. If the last action(s) have been undone in the previous session, they will still be performed. After restoration the user has a chance to view the changes before saving.

4.7 CHANGE IMAGE SET PROPERTIES AND CREATE GROUPS

This section describes how to change the properties for image sets acquired for treatment planning or for fraction images and how to create and manage 4DCT, PET-CT, 4DMR, and MR protocol groups.

In this section

This section contains the following sub-sections:

4.7.1	Setting image set properties for CT image sets	p. 147
4.7.2	Setting image set properties for CBCT image sets	p. 151
4.7.3	Setting image set properties for other modalities	p. 159
4.7.4	Treatment position alignment	p. 160
4.7.5	Create and manage image set groups	p. 163
4.7.6	Create 4DCT projections	p. 166

4.7.1 Setting image set properties for CT image sets

For CT image sets, it is possible to edit the **Image set name** and the **Imaging system**. The imaging system is connected to an image set type, for example CT, CBCT etc. The imaging system specifies which CT to density table that will be used to determine the densities in the image data. The imaging system and the corresponding CT to density table are created in RayPhysics. For more information, refer to the *RSL-D-RS-7.0-RPHY, RayStation 7 RayPhysics Manual*.

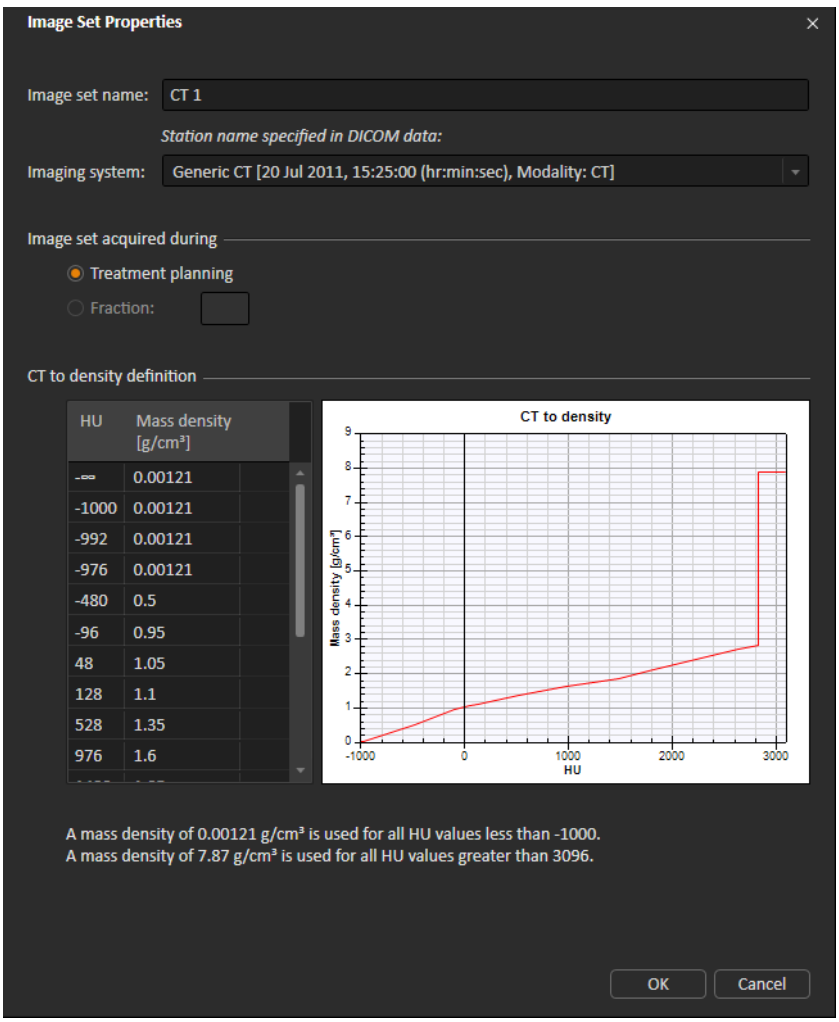


Figure 66. The Image Set Properties dialog where the Image set name and the CT to density table are displayed.

Note: *For automatic mapping of a CT-dataset to a specific CT during DICOM import, use the same name for the CT as used in the DICOM-data tag [Station name; 0008,1010]. In order to use different CT to density tables for different protocols, use the name convention StationName:ProtocolName, where protocol name corresponds to the DICOM-data tag [Protocol name; 0018,1030]. CT machine version information is not available in DICOM, mapping will be done to the latest machine version with that name.*

Rescale density table

If the CT machine was commissioned with the "Require HU scaling" option checked in RayPhysics, the Rescale density table section will be shown in the Image Set Properties dialog.

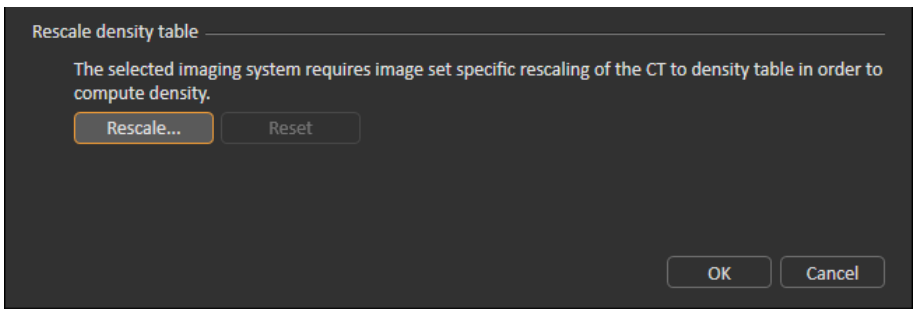

Rescale density table
The selected imaging system requires image set specific rescaling of the CT to density table in order to compute density.
Rescale...
Reset
OK
Cancel

Figure 67. The Rescale density table section.

In order to compute density and dose, an image specific calibration must be made. This is done by rescaling the Hounsfield unit (HU) interval of the density table to an interval specific to the selected image set.

To rescale the density table:

1. Click the **Rescale...** button. This opens the Rescale Density Table dialog.

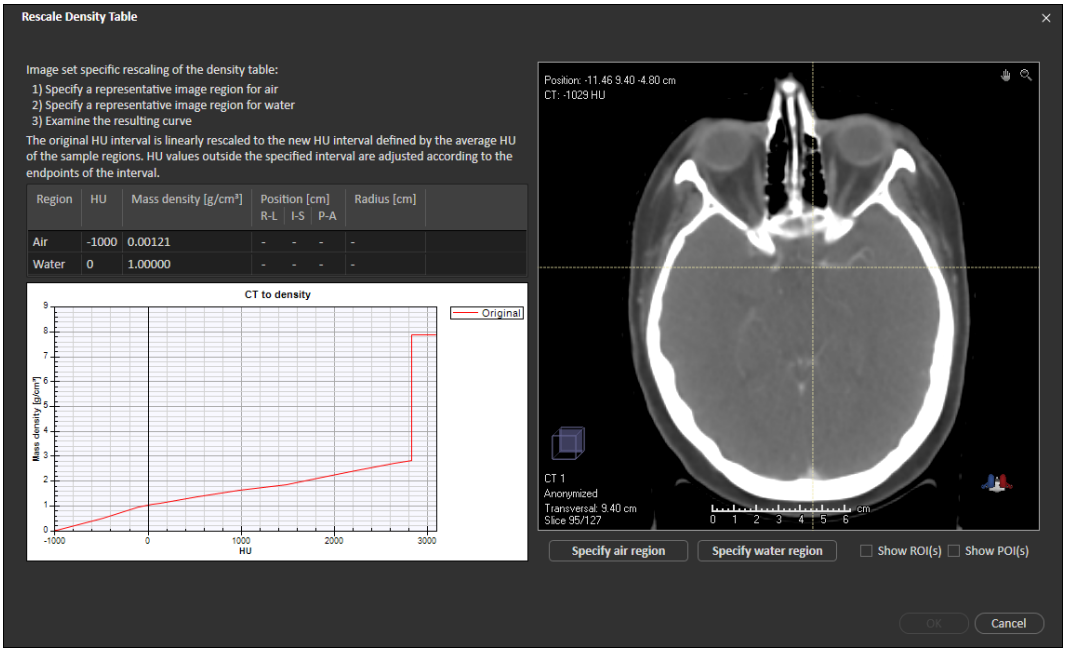


Figure 68. The Rescale Density Table dialog.

2. Click the **Specify air region** button and use the mouse to draw a circular region containing pixels representative for air in any slice.

   Result: The table row for Air is updated.

3. Click the **Specify water region** button and use the mouse to draw a circular region containing pixels representative for water in any slice.

   Result: The table row for Water and the graph are updated.

4. Evaluate the rescaled graph (use the mouse to zoom in).

5. Click **OK**.

   Result: The graph in image set properties is updated with the rescaled curve and table.

6. Click **OK** in the Image Set Properties dialog.

The calibration may be reset by clicking the **Reset** button in the Image Set Properties dialog.

WARNING!

Image specific density table obtained through HU rescaling. When using an image set specific density table obtained through HU rescaling it is highly important that the user reviews the resulting density table properly before using it for dose computation. The rescaled density table will directly affect the dose computation. (125272)

4.7.2 Setting image set properties for CBCT image sets

For CBCT image sets, it is possible to edit the Image set name and the Imaging system. It is also possible to create a rigid registration of a CBCT image to a planning image based on CBCT treatment position alignment and to create a density table for the CBCT image.

Note: *The DICOM modality tag does not differentiate between CT and CBCT. This means that a CBCT image set will be assigned image modality CT during import. Once a CBCT imaging system has been selected, the image set will internally in RayStation have image modality CBCT.*

To edit the CBCT image set properties:

1. Select the desired image set in the image set library and click the **Properties** button. This opens the Image set properties dialog.

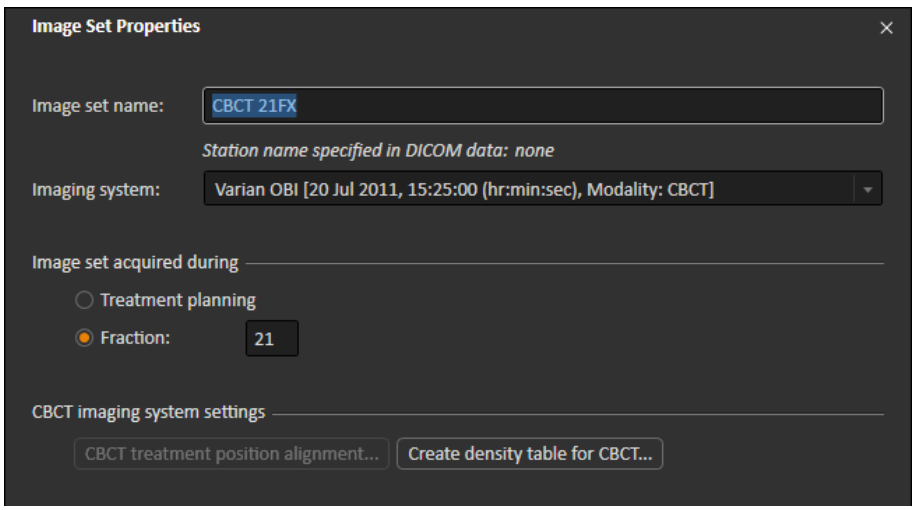


Figure 69. The Image Set Properties dialog, the image set has been assigned to a fraction.

2. Edit the **Image set name**. All CBCT image sets will be imported as a CT. Rename the CBCT as desired.
3. Select the CBCT **Imaging system** used to acquire the image.
4. Select and input the **Fraction** number of the image set. Only available for selection if Treatment Adaptation has been initialized.
5. If desired, select to **Create a CBCT treatment position alignment** by clicking the corresponding button. For more information, see *Create a rigid registration to a CBCT image set based on treatment position alignment on page 160*.

Density table for CBCT

As opposed to CT image sets, where a CT to density table is specified in RayPhysics, CBCT image sets requires that a density table is created manually for each image set in the Patient Information module. In addition, a piece-wise constant transfer function which maps the CBCT values to HU-like values is also created. The transfer function is used in the Patient Modeling planning activity (e.g., model based segmentation, Create external ROI on limited FOV data) as well as for level & window presets.

The acquisition parameters for kV CBCT affect the image quality and voxel value distribution. Moreover, the magnitude of scatter and artifacts are affected by the scanned object size. Therefore, it is not possible to do a calibration of a CBCT machine to give voxel values in HU. The approach taken in RayStation 7 is to provide a user interface where a density table easily can be defined for a specific image acquisition setting. The user defines gray level thresholds which divides the image set into regions of air, lung, adipose, tissue, cartilage/bone and high density (such as fiducial markers). The corresponding densities will be used for dose calculations:

Tissue	Mass density [g/cm3]
Air	0.00121
Lung	0.26
Adipose	0.95
Tissue	1.05
Cartilage/Bone	1.6
Other	3

These densities are set in RayStation 7 and cannot be edited by the user.

An automatic algorithm to divide the image into the above mentioned regions are used to give the user an initial suggestion on how to set the gray level thresholds. The algorithm is illustrated by the following figures:

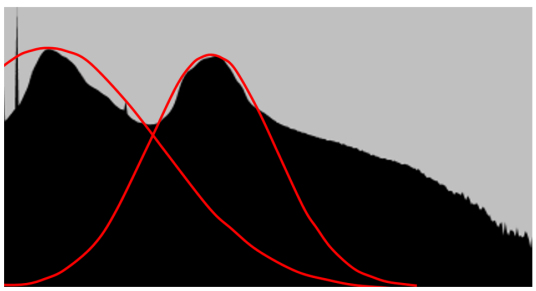


Figure 70. Model the histogram as two normal distributions (μ_1, σ_1) (μ_2, σ_2).

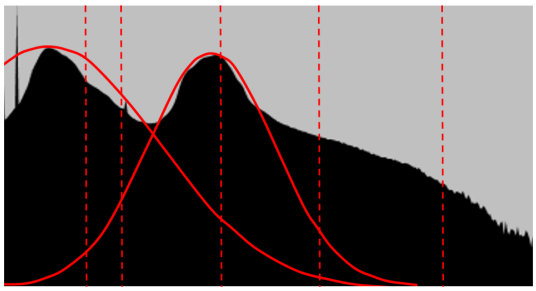


Figure 71. Use the normal distributions to generate initial threshold values.

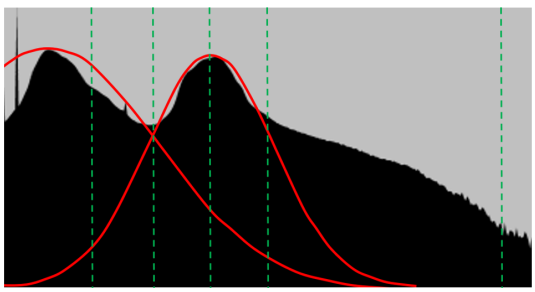


Figure 72. Combine thresholding and mathematical morphology to adjust the initial thresholds, e.g., analysis of the gray levels at the lung boundaries, bone-tissue interface etc.

In most cases, the automatic algorithm will generate good results but it is also possible for the user to modify the result.

If more than one image set acquired using the same CBCT machine is available in the same case, the density table defined for the previous image sets will be suggested for the new image set (i.e, fraction -1, fraction -2 etc.). Alternatively, the density table defined for another image set acquired using the same machine will be suggested. The user will have to verify that it is correct with each of the image sets.

Note: *If opening old database data, i.e. data where the mass density for bone is set to 2.0 g/cm^3, the views will display data according to the old value even if the mass density table in the Create density table for CBCT dialog specifies cartilage/bone as 1.6 g/cm^3. When the segmentation is changed, the patient views will be updated according to the new cartilage/bone mass density.*

WARNING!

CBCT dose calculation. Dose calculation using a CBCT imaging system may be less accurate than using a CT imaging system since there is a limited set of density levels specified for a CBCT compared to what is normally specified for a CT. The accuracy of the dose calculation using CBCT relates to the tuning of the CBCT scale to density, and how well the real density maps against the selected CBCT density. This must be validated by the clinic before using CBCT doses for clinical decisions. Dose calculation on CBCT image data sets is not supported for protons, electrons or carbon ions. (117843)

Create density table for CBCT

To create a density table:

1. Click the **Create density table for CBCT...** button. This opens the **Create density table for CBCT** dialog.

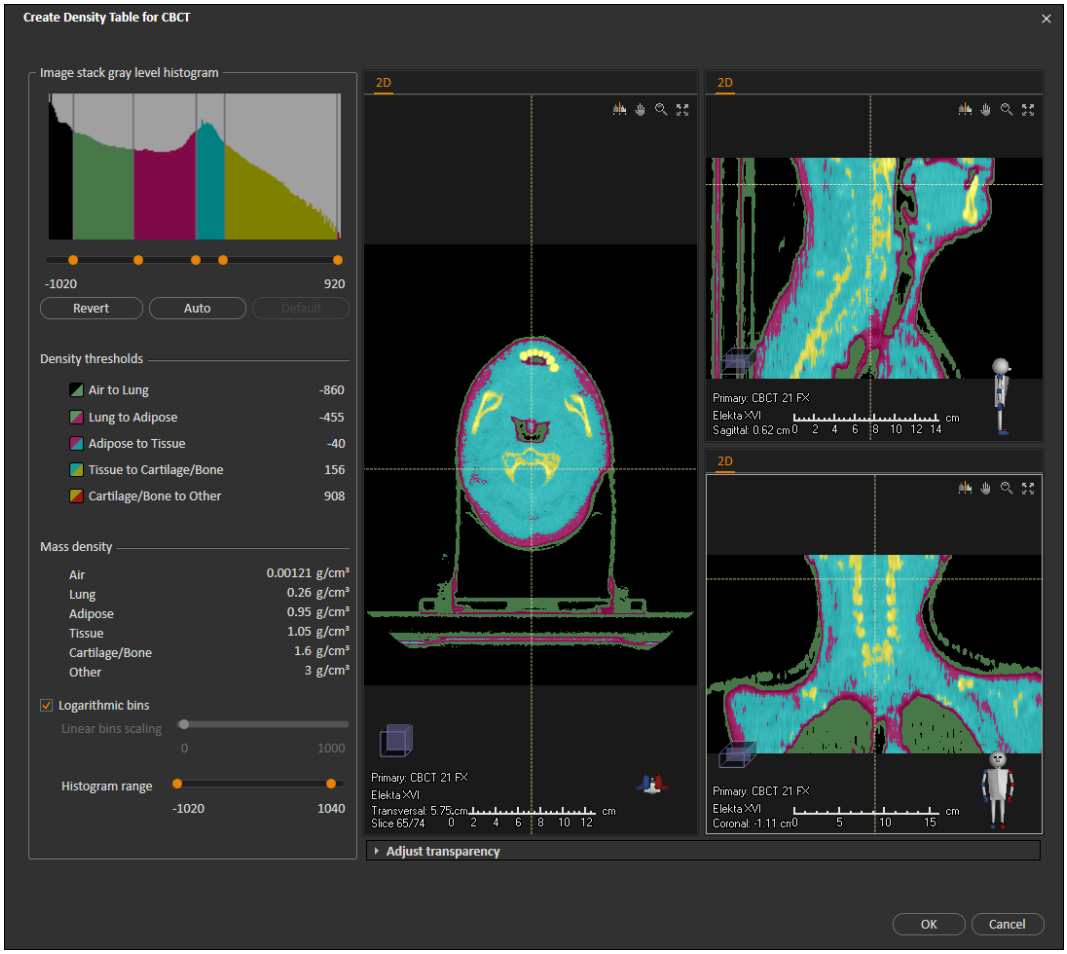


Figure 73. The Create density table for CBCT dialog.

2. Adjust the **Density thresholds** by moving the sliders below the **Image stack gray level histogram**.

   There are three buttons in the **Image stack gray level histogram** area.

   - **Revert**: Revert to previously saved/entered threshold values. When clicking the Revert button, the threshold values will be reverted to the same state as when the dialog was opened.
   - **Auto**: Calculate new threshold values.
   - **Default**: Get threshold values from another image set.

3. If desirable, check the **Logarithmic bins** checkbox. Use the slider to change the **Linear bins scaling**.

4. Change the **Histogram range** by moving the sliders.
5. Select to **Adjust transparency** by moving the sliders.
6. Click **OK**.

Verify that the thresholding is accurate

As the density table is used in dose calculation, it is important to verify that the thresholding is accurate. The suggested workflow is to:

1. Start from the automatic thresholding.
2. Adjust the sliders for **Air to Lung** and/or **Lung to Adipose** (these should be collapsed to one if lungs are not present in the image) in order to capture the patient outline.
3. Check that the region for **Other** only is present if needed.
4. Adjust the slider for **Tissue to Cartilage/Bone** in order to capture the bone.
5. If considered necessary, adjust the slider for **Adipose to Tissue**.

Note: *The most important is to capture patient outline, bone and other as the difference between their densities are large and will have the most influence on the dose calculation.*

Note: *The automatic algorithm handles for instance regions where no lungs are present, i.e., the thresholds air-lung and lung-adipose coincides, as well as give expected results also for CT images.*

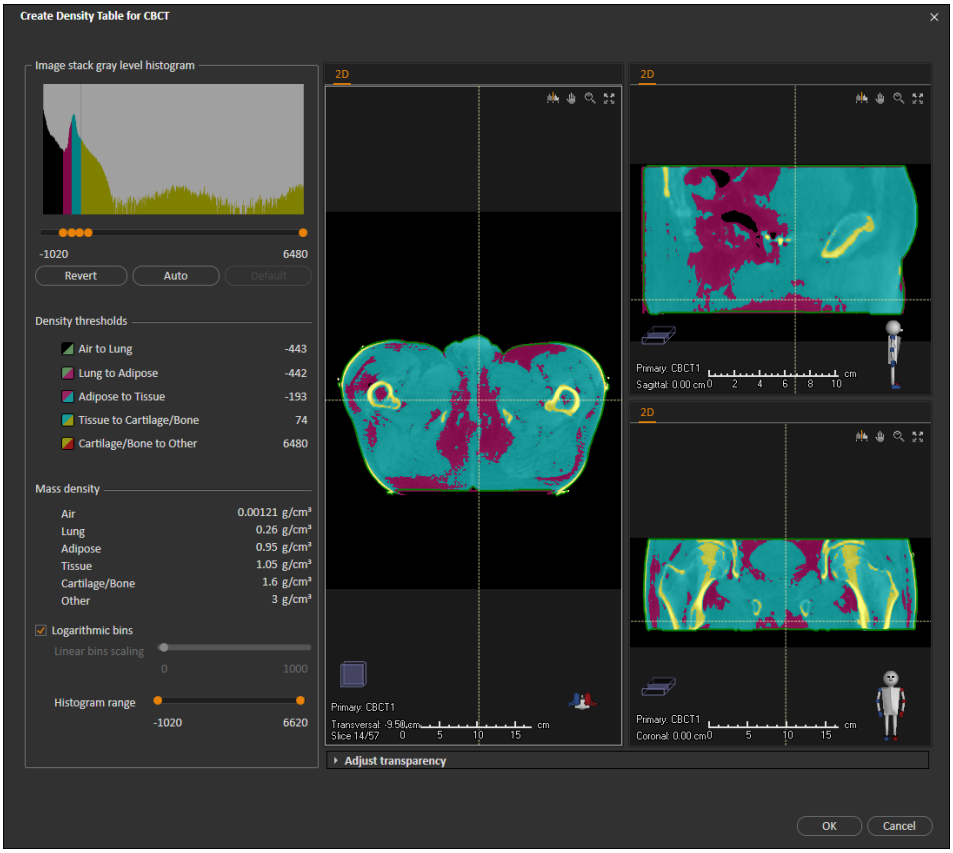


Figure 74. No lungs present, i.e., thresholds for air-lung and lung-adipose coincides.

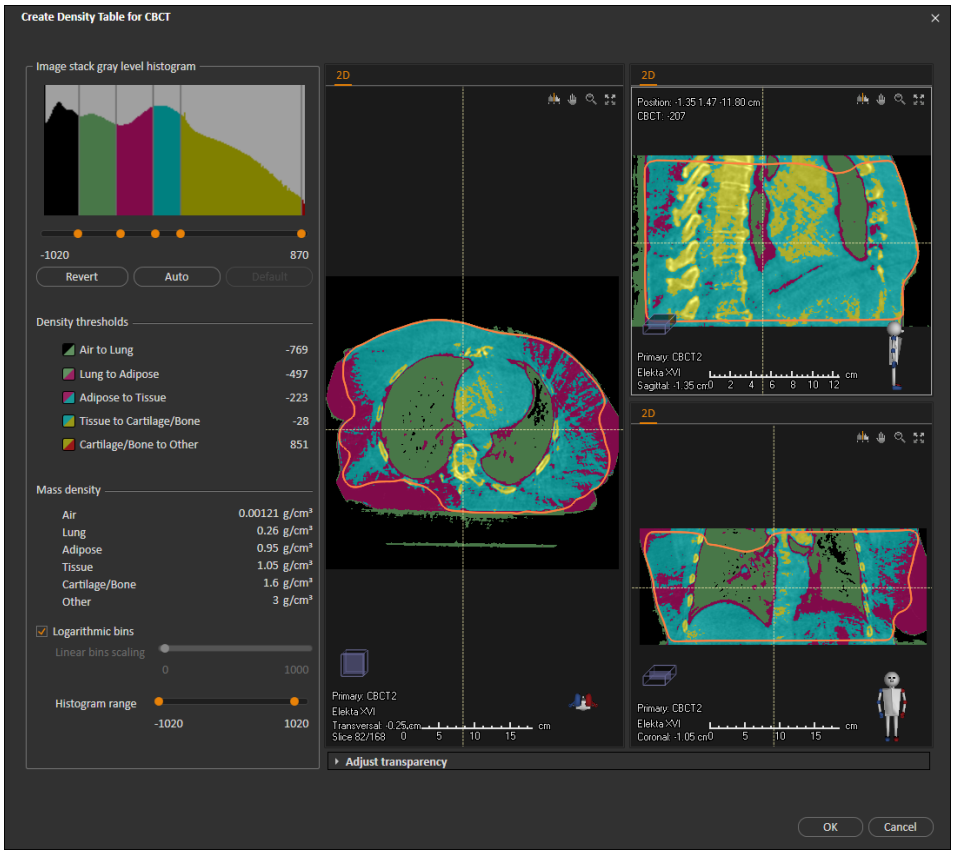


Figure 75. CBCT automatic thresholding applied to thoracic CT data.

WARNING!

CBCT values to density table. RayStation uses an image-specific CBCT values to density table. Always review the density table before it is used in dose computation. The review can be performed through spot check of selected slices in the Create Density Table for CBCT dialog where the effect of the density table is visualized. (55998)

4.7.3 Setting image set properties for other modalities

For other image modalities such as PET or MR it is possible to change the image set name and to specify if the image set was acquired during treatment planning or fraction.

4.7.4 Treatment position alignment

If the relationship between the planning image set and the actual treatment position during the fraction is known, a frame-of-reference registration between the fraction image set and the planning image set can be set up as treatment position alignment in RayStation.

WARNING!

Review frame-of-reference registration before dose computation. It is especially important that frame-of-reference registrations that have been imported or created by treatment position alignment are reviewed before they are used for fraction dose computation in the Dose Tracking module, or when computing dose on additional image sets. (360380)

Create a rigid registration to a CBCT image set based on treatment position alignment

For CBCT fraction image sets it is possible to create a rigid registration to a CBCT image set based on treatment position alignment in the Create treatment position alignment dialog. The CBCT isocenter can be entered together with, if applicable, post setup correction of the couch. The default suggestion for the CBCT isocenter is the middle of the image set, but it is also possible to select the isocenter of the plan. To be able to create a treatment position alignment, the plan that treatment adaptation has been initialized for has to be active in RayStation. Additionally, the CBCT fraction image set has to be assigned to a fraction in this plan, i.e., it is set to "acquired during fraction" and has a valid fraction value.

To create a rigid registration of a CBCT image set:

1. Select the desired image set in the image set library and click the **Properties** button. This opens the Image set properties dialog.
2. Click the **CBCT treatment position alignment…** button. This opens the CBCT treatment position alignment dialog.

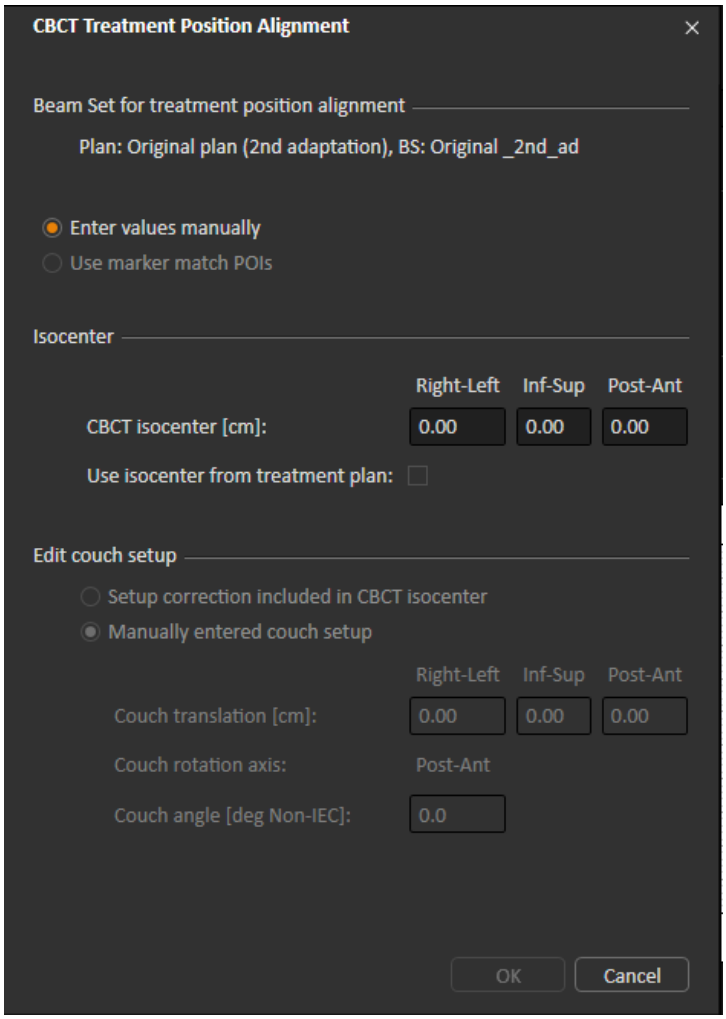


Figure 76. The CBCT treatment position alignment dialog.

3. Select to **Enter values manually** or to **Use marker as match POIs**. The Use marker as match POIs can be used for Varian OBI imaging systems when a RT struct with 'Acquisition isocenter' and 'Initial match isocenter' POIs has been imported.
4. Select **Isocenter** by entering values in the CBCT isocenter fields or select to **Use isocenter from treatment plan**.
5. Select **Couch setup**. The options are **Setup correction included in CBCT isocenter** or **Manually entered couch setup**.
6. Click **OK**.

Set rigid registration as treatment position alignment

It is also possible to set an existing registration as treatment position alignment. This is useful if the registration has been imported or set in the Image Registration module. It can be used for any image modality. This is possible by using the script method SetRegistrationAsTreatmentPositionAlignmentRegistration. For more information about scripting methods, refer to the *RSL-D-RS-7.0-SG, RayStation 7 Scripting Guideline*.

Note: *A treatment position alignment corresponds to the relationship between the planning image set and the actual treatment position during the fraction. Hence, only set a frame-of-reference registration corresponding to the relationship between the planning image set and the actual treatment position as being treatment position alignment.*

4.7.5 Create and manage image set groups

Image set groups can be used to group image sets that belong together according to the group type definition. Common for all group types is that they require that the image sets are defined in the same Frame of Reference (FoR), i.e., that they are acquired with the same machine at the same time. The image set groups are displayed in the image library and can be expanded or collapsed.

There following group types are available:

- **4DCT.** The 4DCT group can contain CT (or CBCT) image sets defined in the same FoR. The intended use is to group image sets acquired over time, e.g., phases in a breathing cycle.
- **4DMR.** The 4DMR group can contain MR image sets defined in the same FoR. The intended use is for MR image sets of the same sequence acquired over time.
- **PET-CT.** The PET-CT group can contain a CT image set and a PET image set defined in the same FoR.
- **MR protocol.** The MR protocol group can contain MR image sets in the same FoR. The intended use is for MR image sets acquired at the same time using different sequences.
- **Organ motion.** The organ motion group type is used to group deformed image sets generated using simulated organ motion. See *section 5.4.14 Simulated organ motion on page 288*.

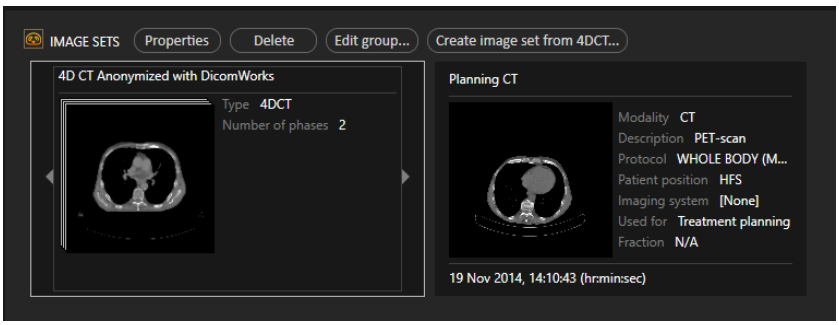


Figure 77. The image set library showing a 4DCT group and another image set.

Add image set(s) to a group

To add image sets to a group:

1. Click the **Edit group…** button. This opens the Edit group dialog.

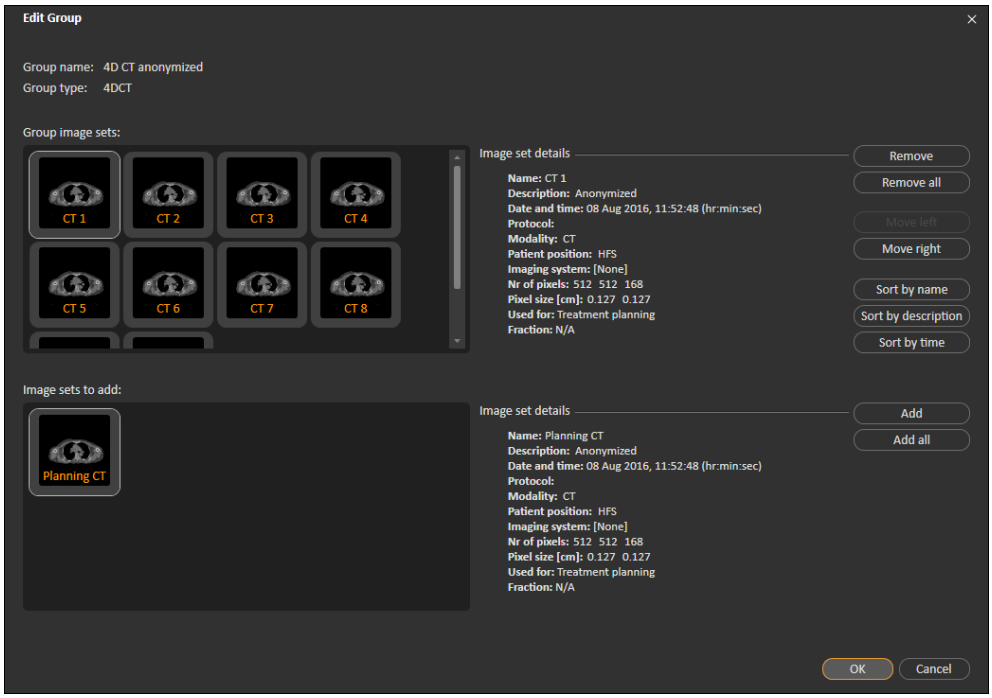


Figure 78. The **Edit group** dialog.

2. Select an image set from the **Image sets to add** list and click the **Add** button. The image set will be added to the **Group image sets** list.

   It is also possible to select an image set from the **Image sets to add** list and drag and drop it to the **Group image sets** list.

3. Click **OK**.

Note: *Image sets not in the same Frame of Reference as the image sets in the Group image sets list are automatically sorted out from the Image sets to add list.*

Remove image set(s) from a group

To remove an image set from a group:

1. Click the **Edit group…** button. This opens the Edit group dialog.
2. Select an image set from the **Group image sets** list and click the **Remove** button. The image set will be removed from the list and visible in the **Image sets to add** list.

   It is also possible to select an image set from the **Group image sets** list and drag and drop it to the **Image sets to add** list.

3. Click **OK**.

Sort image sets

All image sets that are included in a group can be sorted by name, time or by just moving them from left to right.

To sort the image sets:

1. Click the **Edit group...** button. This opens the Edit group dialog.
2. Select a phase in the **Group image sets** list and click the **Move left** or **Move right** button. It is also possible to drag and drop phases to a desired position in the list.

   The phases can also be sorted by name, time or description by clicking the corresponding **Sort by name**, **Sort by time** or **Sort by description** button.
3. Click **OK**.

4.7.6 Create 4DCT projections

For a 4DCT group it is possible to create projections from 4D to 3D using average-, maximum-, or minimum intensity projection. An image set created this way is defined in the same frame of reference as the image sets in the group and appears in the image set library like a regular image set.

WARNING!

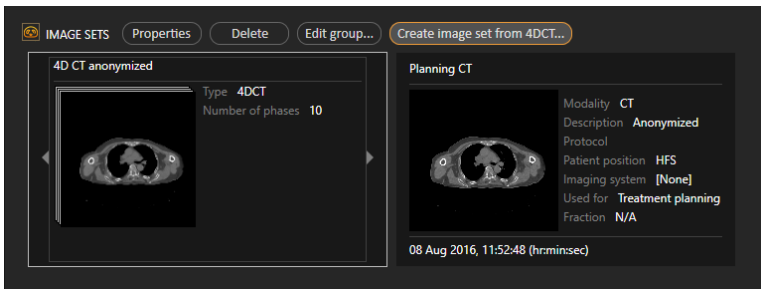
Review 4DCT projections. The user shall review the resulting image set from a 4DCT projection before using it for treatment planning or evaluation purposes. The projected image set shall be compared against the image sets in the 4DCT group in order to verify that the Hounsfield Units and corresponding densities are as expected. This can be performed by examining HU values in the patient views and by computing evaluation doses in the Plan Evaluation module.

The geometrical properties of the projected image set, such as orientation, position and size shall also be compared against the original 4DCT. This can be performed by fusing the projected image sets with the original 4DCT image sets in the Structure Definition module or the Image Registration module and verify that they are aligned correctly. (117566)

Create a 4DCT projection

To create a 4DCT projection:

1. Select a 4DCT group.



2. Click the **Create image set from 4DCT...** button. This opens the Create Image Set from 4DCT dialog.

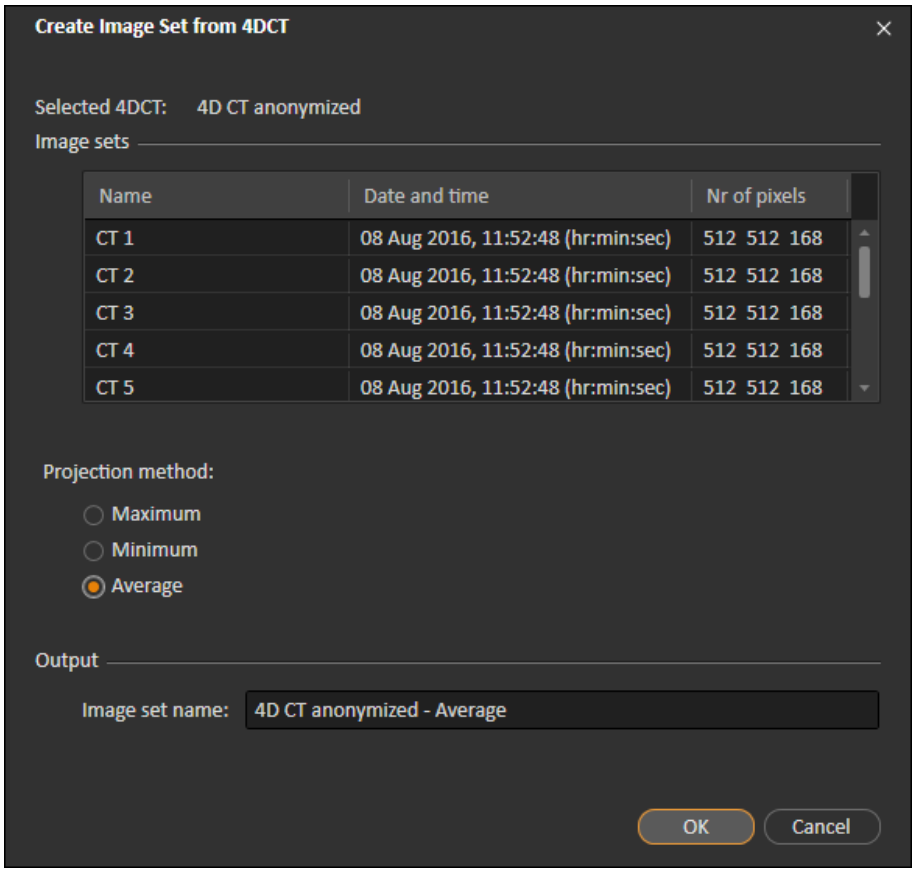
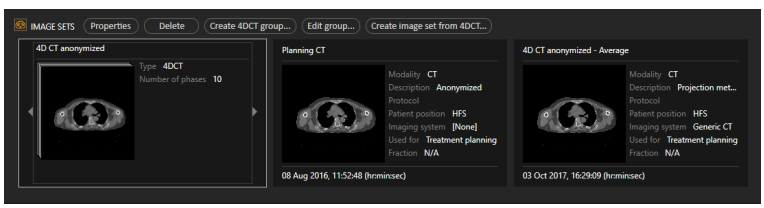


Figure 79. The Create Image Set from 4DCT dialog.

3. Select **Projection method** and **Image set name**. The default name is based on the group name and the selected projection method.
4. Click **OK**. The new image set is created and appears in the image set library.



The size of the projected image set is based on the group. Image slices that are not present in all image sets in the group will be discarded.

5 PATIENT MODELING

The Patient Modeling planning activity contains modules for image registration, structure definition and deformable registration.

In this chapter

This chapter contains the following sections:

5.1	The Image set library	p. 172
5.2	The Image Registration module	p. 173
5.3	The Structure Definition module	p. 186
5.4	The Deformable Registration module	p. 252

Precaution

WARNING!

Automatic ROI generation and modification. Always verify the outcome of automatic ROI generation and modification. (360372)

WARNING!

Automatic image registration. Always verify the outcome of automatic image registration. (360374)

WARNING!

Modifying imported POIs intended for treatment position alignment. Modifying imported POIs intended for treatment position alignment with types 'Acquisition isocenter' and 'Initial match isocenter' before performing 'CBCT treatment position alignment' will result in an erroneous alignment. (360378)

WARNING!

Image set slice spacing and extrapolation of contours. In RayStation, the 3D reconstruction of an ROI from contours assumes that the first and last contours extend half a slice distance. The first and last contours of an ROI are therefore extrapolated half a slice distance from the outermost drawn contours. Note that there is no limit for this extrapolation, it is always half a slice distance. For typical image sets with a slice distance of about 2-3 mm this means that RayStation extrapolates 1-1.5 mm, but in an image set with wide slice spacing, this extrapolation may lead to unexpected behavior. It is therefore highly recommended to always use planning CTs reconstructed with a slice spacing less than or equal to 3 mm. (125440)

WARNING!

Missing intermediate ROI contours. If there are missing intermediate ROI contours, the gap is NOT filled in automatically.

If there are image slices with missing contours between the outermost contours of the ROI geometry, no automatic interpolation is performed between the contours. This applies to imported contours as well as contours generated in RayStation. (360375)

WARNING!

ROI geometry extending outside the image set. When performing a contour operation (e.g., manual drawing, simplify contours etc.) on an ROI that extends outside the top or bottom of the image set, the ROI will be cut at the top and bottom slices of the image set. (240137)

WARNING!

Review the deformable registration. Always review the deformable registration before it is used to deform dose by:

- evaluating the registration in the Fusion view.
- evaluating the deformed grid in the Deformed grid view.
- evaluating mapped structures between reference and target image sets.

This is especially important for dose tracking and when deformed dose is used as background dose during optimization of an adapted plan. Note that biomechanical deformable registrations are not guaranteed to be invertible and should therefore be evaluated extra thoroughly. (360376, 10544)

WARNING!

Review the accuracy of mapped structures. Before mapped structures are used for treatment planning or evaluation purposes, make sure to always review the accuracy of structures mapped between image sets using deformable registrations. Note that biomechanical deformable registrations are not guaranteed to be invertible and should therefore be evaluated extra thoroughly. (360379)

5.1 THE IMAGE SET LIBRARY

The image set library lists the image sets of the current case. The library is available in the image registration and structure definition modules and allows selection of a primary and a secondary image set. The primary image set is always visible in patient views and is where structures are defined when working in structure definition. The secondary image set is shown in fusion views. In image registration, the primary image set is the reference image and the secondary is the floating image. When image sets are grouped together (4DCT, PET-CT, 4DMR or MR protocol), the library displays a group item that can be expanded in order to view the image sets within the group. The image set library can be hidden by clicking the tab header.

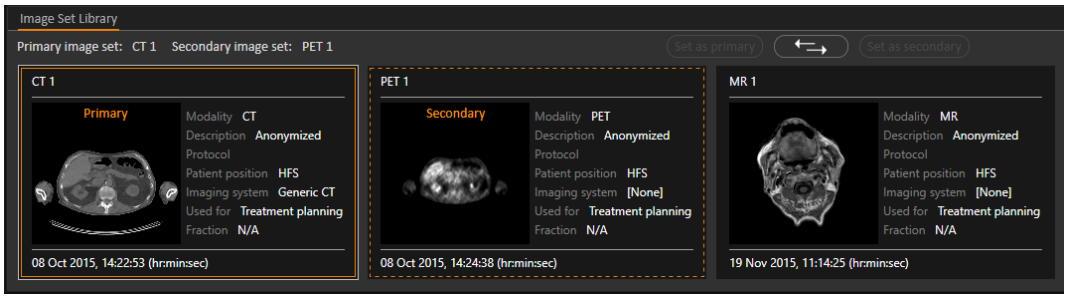
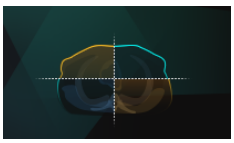


Figure 80. The Image set library, with a Primary image set and a Secondary image set.

5.2 THE IMAGE REGISTRATION MODULE

In the Image Registration module different image sets can be transformed into one common coordinate system. Registrations can be made with several different methods, both automatic and manual. This module supports rigid-body transformations only.



In this section

This section contains the following sub-sections:

5.2.1	The Image Registration workspace	p. 174
5.2.2	Automatic image registration	p. 176
5.2.3	Manual image registration	p. 181
5.2.4	Rigid transformation	p. 182
5.2.5	Image fusion	p. 184

5.2.1 The Image Registration workspace

The Image Registration workspace is divided into three main views for patient data display;

- The **Reference view** shows the Reference image set.
- The **Floating view** shows the Floating image set.
- The **Fusion view** shows both the Reference and Floating image sets combined.

The bottom area contains the **Image set library** where the Reference and Floating image sets are selected.

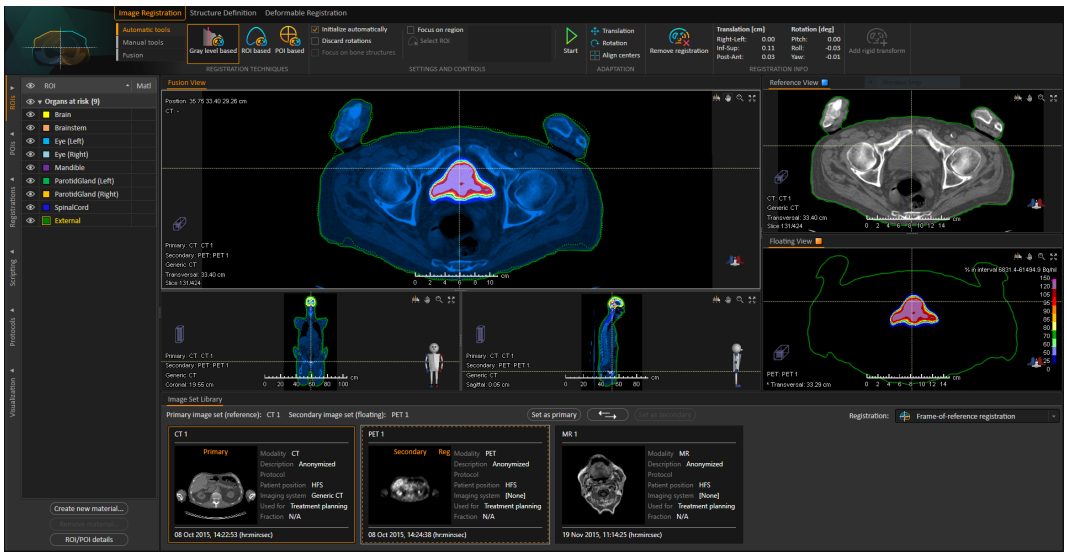


Figure 81. The Image Registration module workspace.

Note: *For image sets that have the same Frame of Reference UID (i.e. where the coordinate system and the patient position is the same in both sets) all registration tools are disabled.*

Note: *For some combinations of modalities some selections can be disabled. For example, focus on bone is only enabled for CT / CBCT.*

Note: *The registration of the following combination of modalities has been verified using spot checks of image registrations: CT-CT, CT-CBCT, CBCT-CBCT, CT-MR, MR-MR and PET-CT. The user must always inspect the registration, regardless of which modalities that are registered.*

Graphical User Interface

For more information about the tools, operations and various view types in the Graphical User Interface, see *chapter 3 The Graphical User Interface*.

The context menu

The context menu is accessed by right-clicking in any patient view. The menu contains view and visualization settings, such as pan, zoom and level/window etc. For more information about view settings, see *section 3.6 Common views on page 71*.

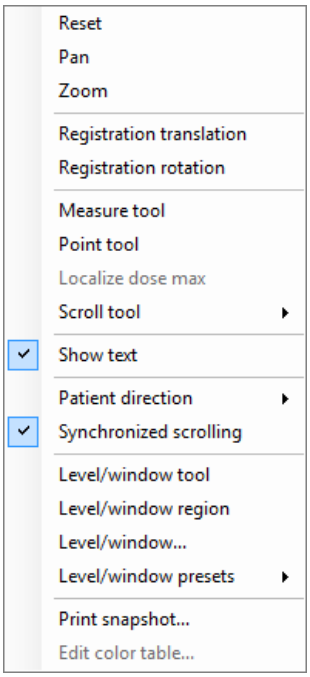


Figure 82. The Image Registration module Context menu.

Register image sets

To register image sets:

1. Select the image set to use as reference for the registration and click the **Set as primary** button. The reference image set will be displayed in the Reference view and in the three Fusion views.
2. Select the image set to use as floating set and click the **Set as secondary** button. The floating set will now be displayed in the Floating view as well as in the Fusion view.
3. If the floating image set has its origin far away from the reference image set's origin, the floating image set might not be visible in the fusion views until it is zoomed out. By using the **Align centers**, see *Other registration options on page 180*, a good starting point for the registration is obtained.

5.2.2 Automatic image registration

The Automatic tools tab in the toolbar contains options for automatic image registration. There are three different techniques for automatic image registration in RayStation 7:

- Gray level based registration (See *Gray level based registration on page 176*)
- ROI based registration (See *ROI based registration on page 177*)
- POI based registration (See *POI based registration on page 178*)

Gray level based registration

The gray level based registration technique makes a registration based on the gray levels of the two image sets. The gray level based image registration algorithm performs best when the patient external is defined both in the reference image and the floating image.

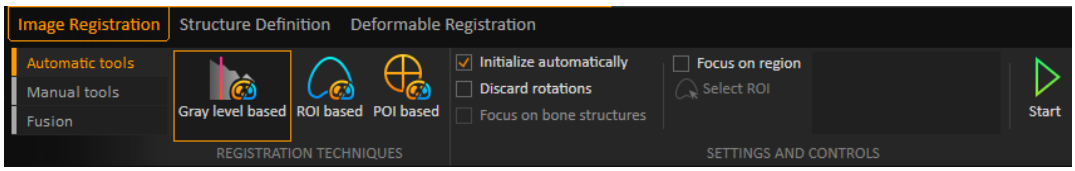


Figure 83. The gray level based image registration tools.

To perform gray level based registration:

1. In the **Image set library**, select the image sets to register.
2. Click the **Gray level based** button in the toolbar.

3. Click the **Start** button.

Optional settings for gray level based registration:

- **Initialize automatically**. When selected the system will try to find the best possible starting point before the registration process starts. When deselected the registration process will start with the image sets in their current positions.
- **Discard rotations**. When selected the system will not rotate the image sets during the registration.
- **Focus on bone structure**. The registration will be focused on the bone structures in the images.
- **Focus on region**. One or more reference ROIs can be selected to focus the registration to a certain region in the primary image set. To select image region, check the **Focus on region** checkbox and click the **Select ROI** button to be able to select ROI(s) from a list.

ROI based registration

The ROI based technique makes a registration based on ROIs that have geometries defined in both image sets.

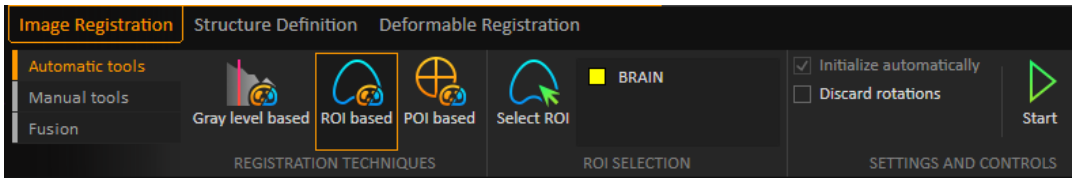
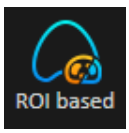


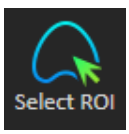
Figure 84. The ROI based image registration tools.

To perform ROI based registration:

1. In the **Image set library**, select the image sets to register.
2. Click the **ROI based** button in the toolbar.



3. Click the **Select ROI** button.



This opens the Select ROI dialog.

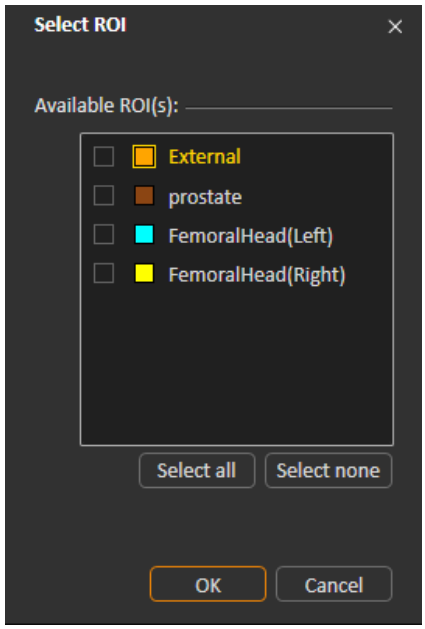


Figure 85. The Select ROI dialog.

4. Select the ROIs to be matched and click **OK**.
5. Click the **Start** button.

There is also an optional setting:

- **Discard rotations**. When selected the system will not rotate the image sets during registration.

POI based registration

The POI based registration technique makes a registration based on POIs that are defined in both image sets.

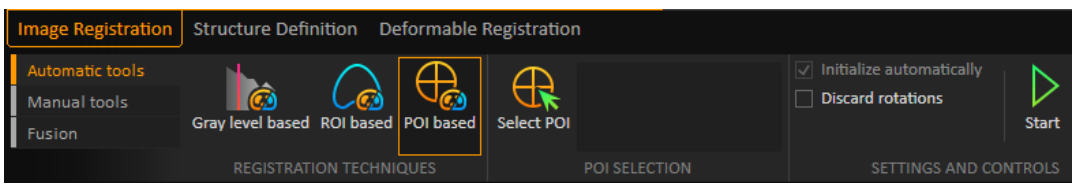


Figure 86. The POI based image registration tools.

To perform POI based registration:

1. In the **Image set library**, select the image sets to register.

2. Click the **POI based** button in the toolbar.

3. Click the **Select POI** button.

This opens the Select POI dialog.

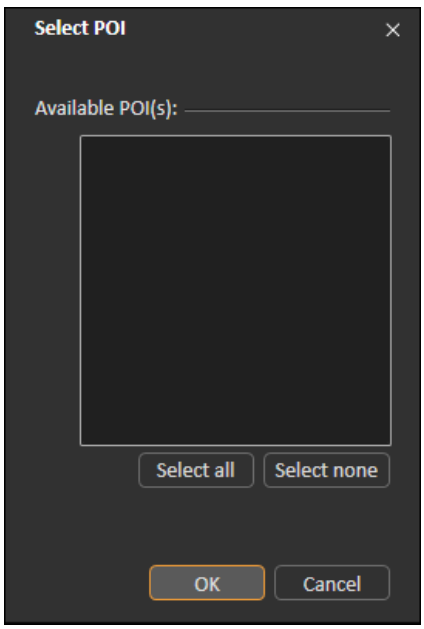


Figure 87. The **Select POI** dialog.

4. Select the POIs to be matched from the **Available POI(s)** list and click **OK**.
5. If desirable, select to **Discard rotations**. If this option is selected, image sets will not be rotated during registration.
6. Click the **Start** button.

Other registration options

To the right in the toolbar are a set of tools for manual image registration; **Translation**, **Rotation**, and **Align centers** (see *View manipulation tools on page 102*), as well as the options **Remove registration** and **Add rigid transform**.

To the far right, the current rigid transformation is presented. For more information, see *section 5.2.4 Rigid transformation on page 182*.

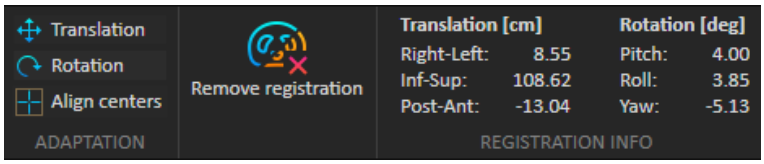


Figure 88. Options for manual image adaption a deletion of a registration.

The **Add rigid transform** tool defines the rigid transform manually for an image set that is treatment position aligned. Only one extra rigid registration can be applied.

This extra registration can be selected in the fusion view in the Structure Definition module and can be used to map ROIs and when creating deformable registrations. It is not used for fraction dose computation in the Dose Tracking module or when computing dose on additional sets.

5.2.3 Manual image registration

To access the manual image registration tools, click the **Manual** tools tab.

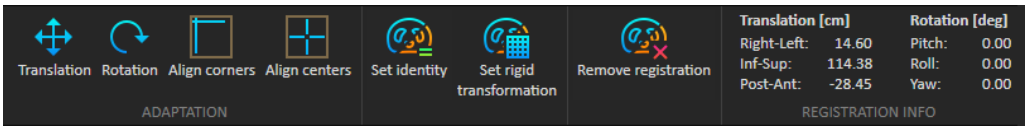
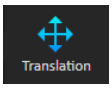


Figure 89. The manual image registration tools.

The manual image registration tools

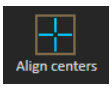
The **Manual tools** tab in the toolbar contains the following tools:



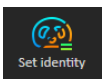
The **Translation** tool enables moving of the Floating series by click and drag in the fusion views.

The **Rotation** tool enables rotation of the Floating series by click and drag in the fusion views.

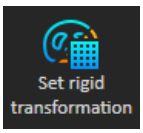
The **Align corners** tool aligns the corners of the images.



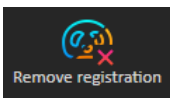
The **Align centers** tool aligns the centers of the image sets.



The **Set identity** tool registers the image sets as they were imported. (This is for image sets that are aligned but not recognized as such by the system.)



The **Set rigid transformation** tool defines the rigid transformation manually, see *section 5.2.4 Rigid transformation on page 182*.



Remove registration. Removes an existing registration. This is possible only if there exists an explicit registration between the images, not if they are implicitly registered.

5.2.4 Rigid transformation

A rigid transformation in RayStation is defined between two frame of references (FoRs) given by the secondary (floating) image and the primary (reference) image set. The rigid transformation maps points from the floating FoR to the reference FoR. The transformation consists of translations and rotations and is represented by a 4 x 4 transformation matrix M. When presented to the user, a more intuitive representation is derived from the matrix. This representation consists of a translation (T), three rotation angles (yaw, pitch, roll), and a rotation center point (c). The default rotation center point is always the floating image set origin.

The rotation angles are defined as follows:

- **Pitch** – Rotation about the patient's Right-Left axis. For an HFS patient, a positive pitch angle corresponds to a clockwise rotation when observed from the right.
- **Roll** – Rotation about the patient's Inferior-Superior axis. For an HFS patient, a positive roll angle corresponds to a clockwise rotation when observed from the feet.
- **Yaw** – Rotation about the patient's Posterior-Anterior axis. For an HFS patient, a positive yaw angle corresponds to a counter-clockwise rotation when observed from above.

The order of transformations is:

1. Negative rotation center shift (T_{-c})
2. Yaw rotation (R_{yaw})
3. Pitch rotation (R_{pitch})
4. Roll rotation (R_{roll})
5. Positive rotation center shift (T_c)
6. Translation (T)

In matrix form, this becomes

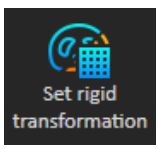
$$M = T \cdot T_c \cdot R_{roll} \cdot R_{pitch} \cdot R_{yaw} \cdot T_{-c}$$

where T_{-c} and T_c are translation matrices corresponding to the rotation center shifts, R_{roll}, R_{pitch} and R_{yaw} are rotation matrices, and T is the translation matrix.

Set rigid transformation

To manually specify the rigid transformation:

1. Click the **Set rigid transformation** button.

   This opens the **Set Rigid Transformation** dialog.

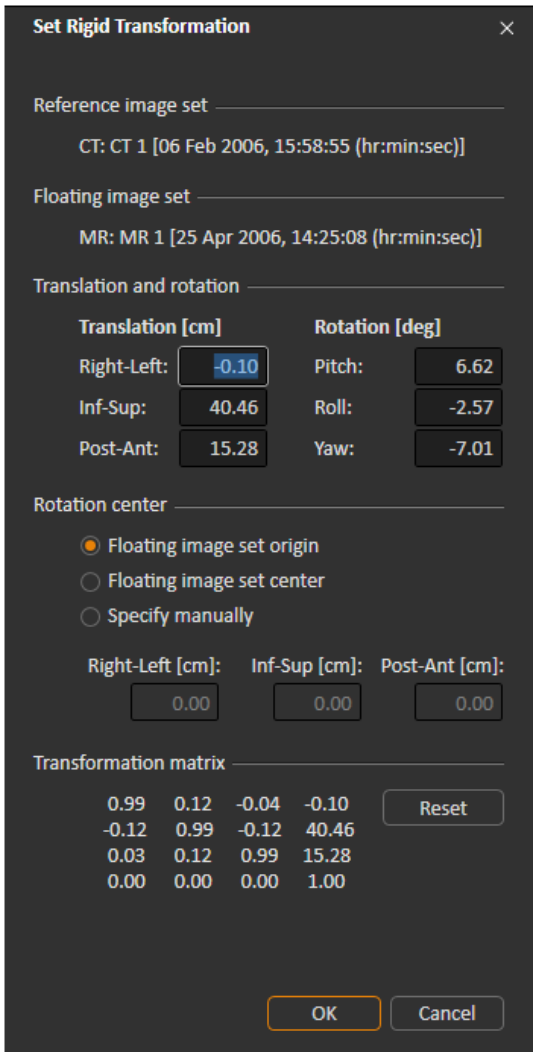


Figure 90. The **Set Rigid Transformation** dialog.

2. Select Translation distances [cm] in the **Right-Left**, **Inf-Sup** and **Post-Ant** directions.
3. Select Rotation angles [deg] in the **Pitch**, **Roll** and **Yaw** directions.
4. Select **Rotation center**. Select either **Floating image set origin**, **Floating image set center** or **Specify manually**.
5. Click **OK**.

5.2.5 Image fusion

In the **Fusion** tab in the toolbar it can be selected how the image fusion shall be displayed. There are several display modes and color schemes to choose from. The fusion settings can also be accessed from the **Visualization** tab (described in *section 3.4.5 The Visualization tab on page 62*).

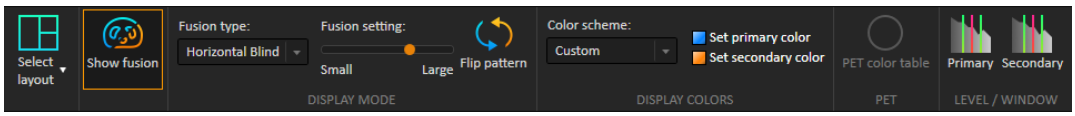
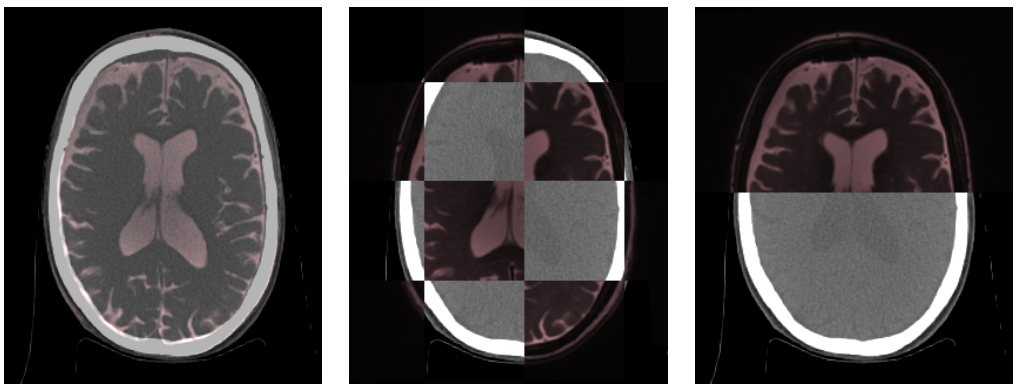


Figure 91. The image fusion tools in the **Fusion** tab.

Display mode

The following fusion types can be selected from the **Fusion type** drop-down list: **Overlay**, **Checkers**, **Horizontal blinds** and **Vertical blinds**.



A B C

Figure 92. Examples of fusion display modes. A) Overlay, B) Checkers, C) Horizontal blinds.

When **Overlay** is the selected **Fusion type** in the **Fusion** tab, the **Fusion setting** slider is used to set the transparency of the two image sets:

- When the slider is in the middle, the two image sets are overlaid.
- When the slider is to the far to the left, only the primary image set is displayed.
- When the slider is set to the far right, only the secondary image set is displayed.

When checkers or blinds are used the **Fusion setting** slider is used to change the size of the patterns.

To move the selected pattern in the image, press and hold down the mouse button and the ALT key while moving the mouse.

To flip the selected pattern, do one of the following:

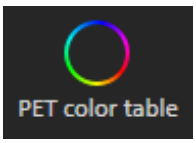
- Press the space bar on the keyboard.

- Click the **Flip pattern** button in the Fusion tab.
- Click the **Flip** button in the **Visualization** tab.

Display colors

There are several sets of display colors to use from in the **Color scheme** drop-down list. It is also possible to define custom display color sets by clicking the **Set primary color** or **Set secondary color** buttons. If PET images are registered, colors can be set from the PET color map.

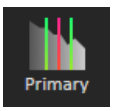
Click the **PET color table** button to access the Adjust color tables dialog.



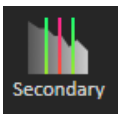
Level/Window

The Level/Window tools can be used to change the contrast of the image data. For more information, see *section 3.8.1 Level/window on page 94*.

Click the **Primary** button to open the Adjust Level & Window dialog for the reference image set.



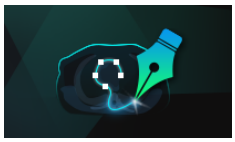
Click the **Secondary** button to open the Adjust Level & Window dialog for the floating image set.



5.3 THE STRUCTURE DEFINITION MODULE

In the Structure Definition module ROIs can be created and modified by manual drawing using the RayStation 7 contouring tools and by using the automatic ROI generation tools. ROIs can also be created using Model Based Segmentation (MBS).

Note: *For carbon ions: Only the RBE dose is shown in the Structure Definition module.*



In this section

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5.3.1 The Structure Definition user interface

Workspaces

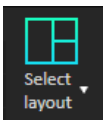
In the Structure Definition module, the user can choose between two different workspace layouts for displaying the image data and structure sets from a primary image set and an optional secondary image set.

Classic - Three 2D image views where each view can be switched to a 3D view using the 3D tab in the view's upper left corner. By default, the main window shows the transversal slices, and the two smaller windows show sagittal and coronal reconstructions.

Side-by-side – Two synchronized 2D views where the primary and secondary image set are displayed next to each other. When drawing contours, they are visualized on both image sets.

Independent of workspace layout, the bottom area contains the **Image Set Library** where the primary image set, and possibly a secondary image set for image fusion or side-by-side display, is selected.

To select workspace layout, click the **Select layout** button in the toolbar.



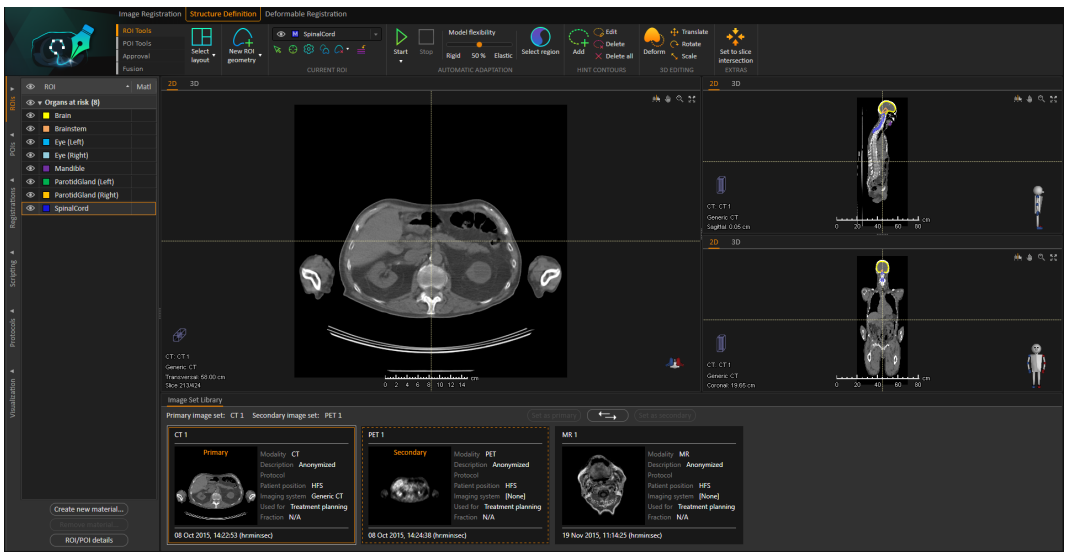


Figure 93. The Structure Definition module with the **Classic** workspace layout.

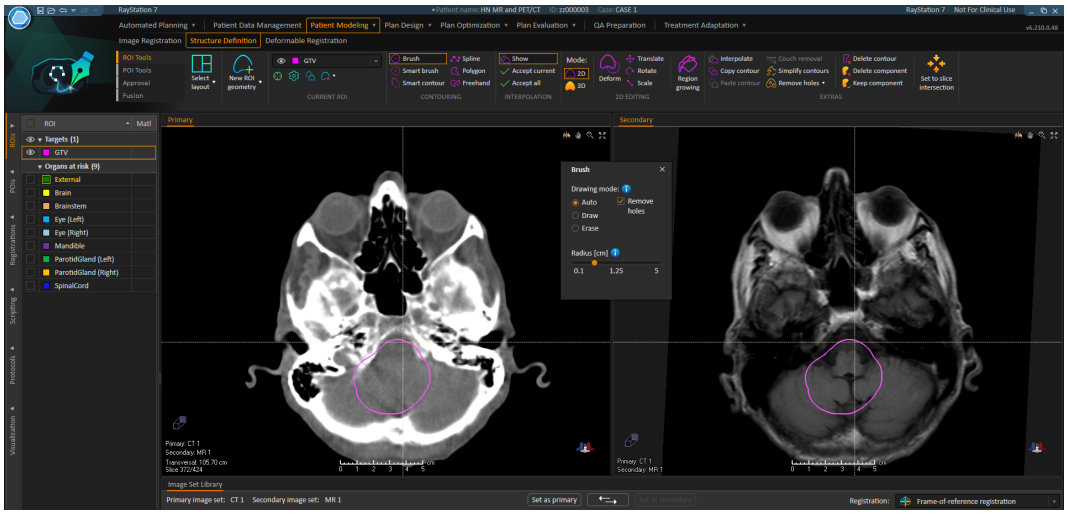


Figure 94. The Structure Definition module with the **Side-by-side** workspace layout.

Graphical User Interface

For more information about the tools, operations and various view types in the Graphical User Interface, see *chapter 3 The Graphical User Interface*.

The Context menu

The context menu is made visible by right-clicking in any patient view, see *View manipulation tools on page 102*. The menu for 2D views contains:

- **Translation** - 3D ROI Translation
- **Rotation** - 3D ROI Rotation
- **Scaling** - 3D ROI Scaling
- **Deformation 3D** - 3D ROI Deformation
- **Delete component (3D)**
- **Pick tool** - Pick an ROI for editing.
- **Create beam specific margin ROI...** - The Create Beam Specific Margin ROI function provides tools for automatic extension of ROI geometries based on beam directions. For more information, see *Create Beam Specific Margin ROIs on page 217*.
- **Show dose** - Displays the dose in the view. Only applicable if a dose has been computed for the current plan and the active image set is the same as in the selected plan. Note that in the Structure Definition module default visualization of dose is off. In order to show dose, the user has to select **Show dose** in each view separately.
- **Show dose on ROI surface** - It is possible to visualize the dose distribution on the ROI surfaces. This option **Show dose on ROI surface** is accessible from the 3D view context menu.

- **Localize dose max** - The slice intersection will be set to the position of the global maximum dose value for the current dose type (plan dose, beam set dose or beam dose).
- **Create ROI from dose** - Only applicable if a dose has been computed for the current plan and the active image set is the same as in the selected plan. Select to create an ROI based on dose threshold values.

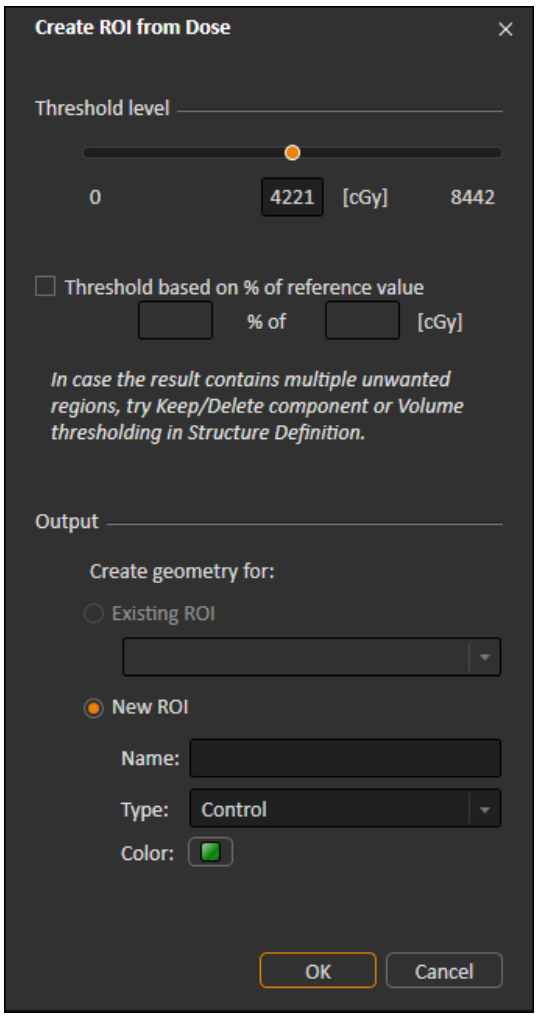


Figure 95. The **Create ROI from dose** dialog.

- **Start and Stop adaptation** - Only available when an MBS ROI is selected.

Navigation tools

Use the mouse wheel to browse through the image slices

- By pressing the middle mouse button (the mouse wheel) somewhere in the patient view, all views will scroll to display the slice containing that point. By pressing and holding down the middle mouse button and moving the mouse, it is possible to easily browse through the image data of the other patient planes.
- For 4DCT and 4DMR groups, a navigation wheel will be displayed in the 2D patient views. The navigation wheel contains a play button and a pie chart representing the image sets in the group. Press the play button to automatically show the image sets as a sequence or click the different components of the pie chart to switch to the corresponding image set. The pie chart can also be controlled using the mouse scroll wheel. Note that using the pie chart actually changes the selected primary image set and structures, while the play button only changes the image grayscale.

Image set library

The image set library lists the image sets of the current case. To set the primary working image set, select the image set in the library and click the **Set as primary** button or double-click the image set. The primary image set now will be displayed in the patient views.

If the case contains multiple image sets that are registered with each other, a secondary image set for fusion view can be selected from the Image set library (Set as secondary set). ROI geometries will be defined on the primary image set, but the secondary image can be helpful when drawing the contours.

If there are multiple registrations, rigid or deformable, it is also possible to select which registration to use. The primary and secondary images will be set automatically depending on the selected registration. This means that if a deformable registration is selected, it is possible to draw contours guided by the deformed image set.

The image set library can be hidden by clicking the **Image Set Library** tab.

5.3.2 Introduction to ROIs and ROI geometries

In RayStation an ROI (Region of Interest) consists of two parts:

- the patient-wide ROI definition (name, type, color, tissue name, material, derived expression etc.)
- the ROI geometry which is the image set-specific geometric representation of the ROI

Consider a prostate patient with a CT and an MR. Prostate and Rectum are the relevant structures, with two instances each, one for each image set. In RayStation-terminology we have two ROIs (Prostate and Rectum) each with two ROI geometries, one for each image set.

Create and manage ROIs

The left part of the ROI tools tab in the toolbar contains the ROI administration tools. The **New ROI geometry** button expands a menu with various options for creation of ROIs and ROI geometries. The **Current ROI** drop-down list is for selecting current ROI. In the ROI drop-down list the visibility for individual ROIs can also be toggled on or off. If the colored square before the ROI is only half-filled, the ROI lacks geometry for the active image.

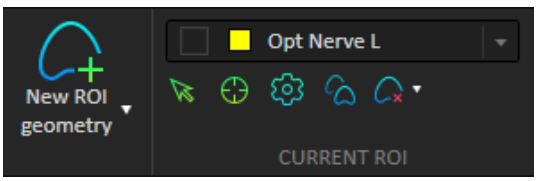


Figure 96. The 'OPT Nerve L' ROI is currently activated and subject to the editing tools. The eye indicates that the ROI is visualized in the image views.

The current ROI tools:

The **Pick tool** allows to point at an ROI in a patient view to make it the current one for editing.

The **Localize ROI** tool re-positions all patient views to the center of the current ROI.

The **ROI properties** tool opens the ROI properties dialog.

The **Copy ROI** tool opens the Copy ROI dialog.

- Select the ROI that the copied ROI will be based on.
- Select to create a new geometry for an Existing ROI or for a New ROI.

The **Delete** tool has options to delete either the entire ROI or the current ROI geometry.

To copy one or several ROI geometries from one image set to one or several other image sets, select **Copy ROI geometries...** from the **New ROI geometry** button menu. (This function is available only if the image sets have been registered with each other.)

In dialogs for ROI creation the options to create a new geometry for an Existing ROI (this is for example to delineate the organ in an additional image set) or for a New ROI are given.

ROI types

When creating a new ROI, the relevant ROI type needs to be selected, e.g., GTV, CTV or PTV for targets and Organ for organs at risk, etc. The default value is Organ.

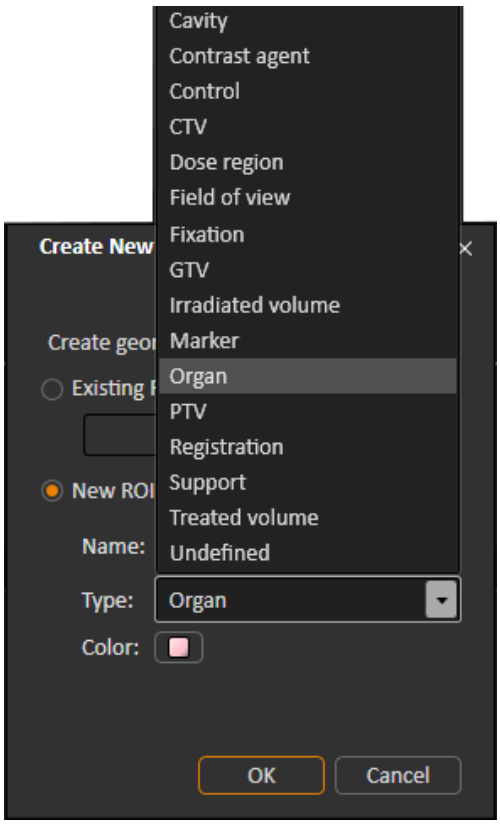


Figure 97. The **Create New ROI** dialog showing some of the ROI type options.

Setting the correct ROI type is important since it sets the Organ type that determines which ROIs can be treated or protected in Treat and Protect (for 3D-CRT, Virtual Simulation, Electron Beam Design and Proton Beam Design). It also determines which optimization functions can be applied (for Plan Optimization and MCO).

The dose computation is performed inside the External ROI, except for the ROI types Bolus, Fixation and Support. ROIs of type Bolus must be fully outside the External ROI, while ROIs of type Fixation

and Support must be at least partially outside the External ROI to be included in the dose computation. They must also have a material override (see *Material override on page 193*). For ROIs that are inside the External ROI, always use other ROI types.

Patient fixation and support objects that were not included in the CT scan but of significance to the dose computation, can be added as ROI type Fixation or Support in order to calculate dose through these objects.

The volume not covered by any External, Bolus, Fixation or Support ROIs are treated as vacuum in the dose calculation.

Material override

Objects that do not follow the ordinary HU to mass density curve, e.g., prostheses, inserts or contrast agents, should be given a material override. If an ROI requires an override of the material, it can be set from the **ROI Properties** dialog or from the **ROI/POI Details** dialog.

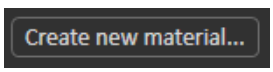
An ROI with a material override will be indicated with a star in the ROI list. For more information about material override, see the *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual*.

It is also possible to create a new custom material based on an existing material in which the name and mass density can be changed.

Note: *It is not possible to use custom materials for ROIs used in electron calculations. Use only the pre-defined material in these cases.*

To create a new custom material:

1. Click the **Create new material** button (available in the **ROI** list, the **ROI/POI details** dialog and the **ROI properties** dialog).

   This opens the **Create New Material** dialog.

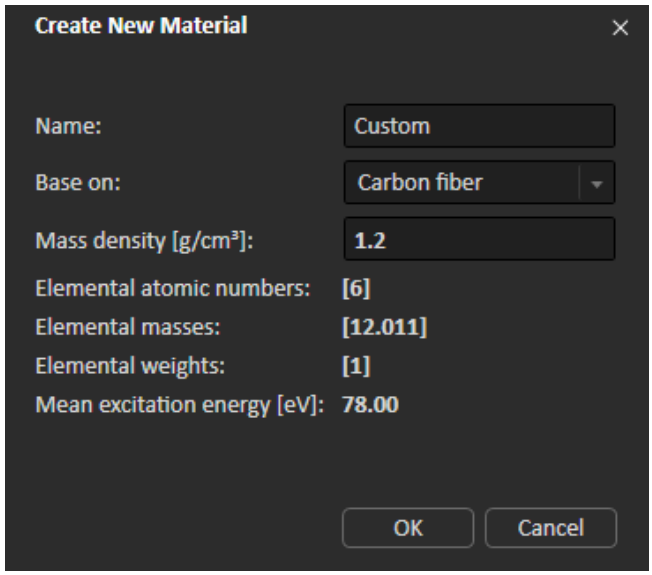


Figure 98. The **Create New Material** dialog.

2. Enter a **Name** for the new material.
3. Select a pre-defined material to base the new material on. Hovering over the material gives the element information of the material.

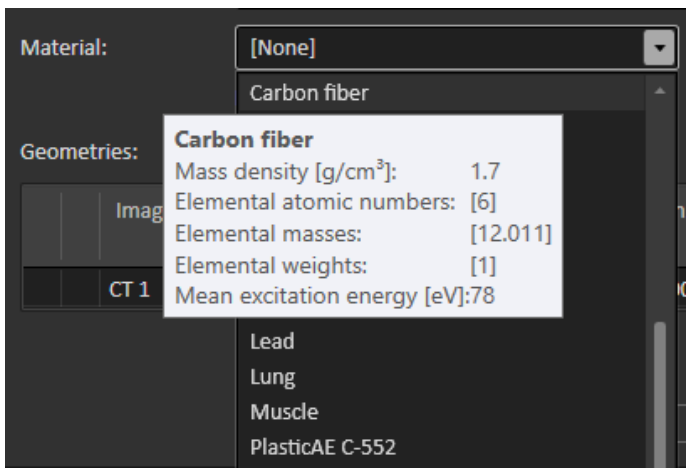


Figure 99. Hovering over a material in the pre-defined list gives the element information of the material.

4. Enter the new **Mass density [g/cm³]**.

Note: *A custom density of 0 g/cm^3 is not accepted in the dose computation. For mass densities of 0 g/cm^3, use the pre-defined air value instead.*

5. Click **OK**.

   The new material will now be available for selection.

To delete a custom material:

1. Click the **Remove material** button (available in the **ROI** list, the **ROI/POI** details dialog and the **ROI properties** dialog

   This opens the **Remove material** dialog.

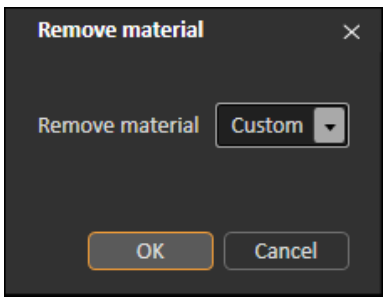
   

   Figure 100. The **Remove material** dialog

2. Select the material to delete.
3. Click **OK**.

ROI representation types

An ROI geometry can have any of the following representation types;

- Contours
- Voxels
- Triangle Mesh
- MBS mesh

Contour ROIs are created and modified by manual drawing (see *Create and manage ROIs on page 191*). Voxel ROIs can be derived from other ROIs using tools for creating margins, ROI walls, and ROI algebra. MBS ROIs are created using Model-Based Segmentation (MBS). The MBS tool allows for semi-automatic delineation of structures based on 3D template models, see *section 5.3.8 Introduction to Model-Based Segmentation on page 232*.

Conversion between the different representation types happens automatically depending on the operation that is to be performed. For example, to perform Deform 3D, the representation type has to be Triangle mesh or MBS mesh, for contouring the type has to be Contours, and for Create Expanded ROI the type has to be Voxels. The representation type is visible in the ROI properties dialog, see *section 3.4.1 The ROI list on page 54* for more information. The conversions are described in detail in *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual*.

Create new ROI

To create a new ROI:

1. Click the **New ROI geometry** button and select **Create new ROI...**.

   This opens the **Create New ROI** dialog.

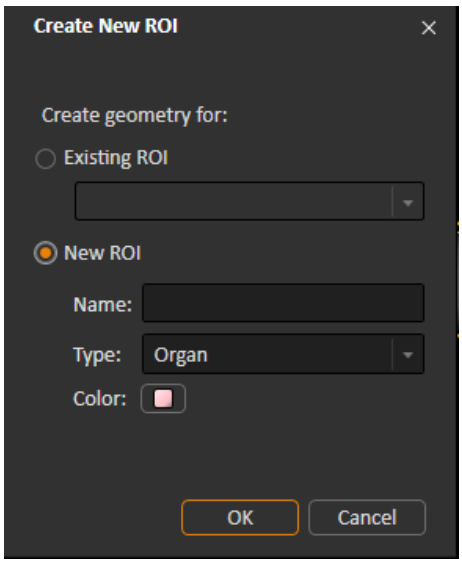
   

   Figure 101. The **Create New ROI** dialog.

2. Select to create a geometry for an **Existing ROI** or select **New ROI**.
3. If a **New ROI** has been selected, select a ROI **Type**. For more information, see *ROI types on page 192*.
4. Click **OK**.

   The new ROI will automatically be displayed in the ROI list as the current ROI. The new ROI does not have any contours; they need to be added with the drawing tools.

5.3.3 The ROI modification tools

The ROI modification tools includes the 3D editing tools, the contouring tools, the 2D editing tools and some extra ROI modification tools.

The 3D editing tools

The 3D ROI tools are accessible for all ROI types. The 3D ROI tools are turned into a pick tool when hovering other ROIs than the selected, which makes it possible to switch the current ROI directly from the view. The 3D tools can be used if the 3D button is toggled.

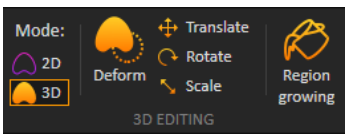


Figure 102. The 3D editing tools.

The 3D editing tools are described below.

The **Deform** tool deforms the ROI. It can be used in all of the patient planes. When using this tool, the mouse pointer is shown as a diamond with a dashed ring around it. The size of the cursor ring is proportional to the extent of the deformation. Move the cursor to the ROI contour, click and move the mouse to deform the contour. To change the size of the deformation tool, use the slider in the Deform tool settings dialog, press the + and - keys on the keyboard, or use the mouse wheel while pressing the CTRL key.

The **Translate** tool moves the whole ROI. It can be used in all of the patient planes. Put the mouse pointer on the contour of the ROI that is to be moved, press the mouse button and move the mouse to move the ROI to the desired position.
Select several ROIs in the ROI list (**ROIs**) by holding down the Shift key and clicking the desired ROIs in the list. Click the **Translate** button and move all the selected ROIs to a desired position.

The **Rotate** tool rotates the ROI. It can be used in all of the patient planes. Put the mouse pointer on the contour of the ROI that is to be rotated, press the mouse button and move the mouse to rotate the ROI into the desired position. Select several ROIs in the ROI list (**ROIs**) by holding down the Shift key and clicking the desired ROIs in the list. Click the **Rotate** button and move all the selected ROIs to a desired position.

The **Scale** tool scales the ROI. It can be used in all of the patient planes. Put the mouse pointer on the contour of the ROI that is to be scaled, press the mouse button and move the mouse inwards or outwards of the ROI contour to make it smaller or larger.

The **Region growing** tool opens the **Region growing** dialog.

- Select seed points by clicking in the image. The **Threshold levels** interval will be set to the min and max values for all seed points within the tool radius.
- Adjust the **Threshold level** sliders to grow the region.
- Click the **Clear region** button and click again in the image to get new seed points.
- Check the **Use limiting volume** in order to delimit the area where the region can grow. Adjust the area by moving the sides of the bounding box that appears in the patient views.
- Click the **Reset** button to undo the changes made to the bounding box.

Note: *It is not possible to set seed points in the secondary view in Side by side layout.*

The contouring tools

The contouring tools can be used in all patient directions, i.e. in the transversal, coronal and sagittal 2D patient views.

The **Spline**, **Polygon**, and **Freehand** drawing tools can be used in three modes:

- **Auto.** Creates a new contour if the drawn contour does not intersect an existing contour. Cuts an existing contour if the drawn contour intersects it and the first point of the drawn contour is outside the existing contour. The longest part is kept. Extends the existing contour if the drawn contour intersects it and the first point of the drawn contour is inside the existing contour.
- **Extend.** Creates new contours and extends existing contours.
- **Subtract.** Cuts parts of existing contours.

Note: *To allow for contouring in an oblique image set the Patient direction has to be set to Slice aligned from the patient view context menu.*

Note: *It is recommended to work in a single patient direction when contouring a ROI geometry. Switching patient direction will cause a conversion of all the contours in that geometry to the new direction.*

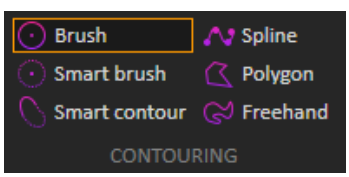
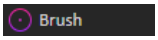


Figure 103. The contouring tools.



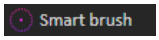
The **Brush** tool is used to create new contours and to modify existing contours by pushing the contour lines. The size of the brush can be adjusted using a slider (Brush tool settings dialog), by pressing the + and - keys on the numerical keyboard, or by using the mouse wheel while pressing the ALT key.

- Click the **Brush** button.
- Click and keep the left mouse button pressed down – add or modify contours by pushing the contour lines.

The **Brush** tool can be used in three drawing modes:

- **Auto** (default). In this mode, the tool adds a new contour or modifies existing contours. The behavior depends on where the tool is positioned in relation to existing contours. To extend an existing contour, click the left mouse button inside the contour and push the contour lines from the inside. To reduce an existing contour, click the left mouse button outside the contour and push the contour lines from the outside.
- **Draw**. Draws new contours and extends existing contours. When in auto mode, hold down the ALT key to force draw mode.
- **Erase**. Erases existing contours or creates holes inside existing contours. When in auto mode, hold down the Z key to force erase mode.

There is also an option to automatically remove holes which are created when the drawing is connected in both ends.



The **Smart brush** extends the functionality of the standard brush by changing shape according to edges in the image. For CT and CBCT images there are five different edge detection settings:

- **None** - works like the standard brush, no image dependence
- **Bone** - used for contouring of bone structures
- **Dark**- used for contouring of structures which is (mainly) darker than the surroundings
- **Air** - used for contouring of air structures
- **Bright** - used for contouring of structures which is (mainly) brighter than the surroundings

Except from the smart setting "Bone", the tool performs best when the image intensities of the structure is approximately constant with well defined edges. For structures that appear noisy, the user can adjust the "Sensitivity" slider. A lower sensitivity value means that the smart brush will be less sensitive to edges in the image and it becomes easier to contour structures with a noisy interior and well defined edges. The smart brush depends on level/window settings which means that the user can influence the behavior of the tool by adjusting level/window. For MR images, only smart settings None, Bright and Dark are possible to use.
For Smart brush it is possible to use *smart interpolation*. Smart interpolation will interpolate the user defined contours to a 3D ROI and adapt the ROI surface to image data according to the Edge detection setting. The progress of the computations can be seen in the progress bar and the interpolated contours in the patient views will be continuously updated during the computations. It is possible to draw new contours before the computation has finished. The computation will then restart taking into account the new contours.

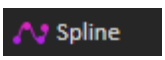
The **Smart contour** tool snaps to the grey-scale gradient in the image, and is efficient when creating contours around consistently colored areas. The tool depends on the current level/window setting. When the X key is pressed, the tool switches to polygon contouring.

- Click the **Smart contour** button.
- Click to define the starting point. For bright objects on a dark background: contour the object clockwise. For dark objects on a bright background: contour the objects counter clockwise.
- Move the mouse – the tool renders the line that will be drawn the next time the mouse button is pressed.
- Click the left mouse button to set a new starting point and thereby fix the latest segment.
- Right-click to exit drawing mode, the first and the last points in the slice will be connected.

There are three options for the **Smart contour** tool:

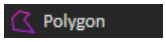
- **Training mode**. Helps to define the current gray-scale gradient.
- **Use training**. When this option is checked the tool uses the gray-scale as defined in training.
- **Lasso mode**. The remaining part of the contour is estimated and shown as a dashed line. Right-click to accept. If the lasso mode is turned off by unchecking the checkbox, it is accessible by holding down the Shift key while drawing.

Note: *It is not possible to use the Smart contour tool in the Secondary view in Side by side layout.*



Add a **Spline** contour for the current ROI one slice at a time. The **Spline** tool adds smoothly curved lines between the points marked by a click.

- Click the **Spline** contour button
- Click to add a curved contour line
- Right-click to exit drawing mode, the first and the last points in the slice will be connected



Add a **Polygon** contour for the current ROI one slice at a time.

- Click the **Polygon** contour button
- Click to add a contour line
- Right-click to exit drawing mode, the first and the last points in the slice will be connected

Add a **Freehand** contour for the current ROI one slice at a time.

- Click the **Freehand** contour button.
- Click and keep the mouse button pressed down – draw contour in slice, when the mouse button is released the start and the end of the curve are connected.

The interpolation tools

When using the contouring tools or the 2D editing tools it is also possible to view derived interpolated contours (dashed lines) on slices where no contours have been drawn. The interpolated contours will also be displayed in all patient views, transversal, sagittal and coronal, and can be accepted one slice at a time or all at once. When the contours have been accepted, they can also be saved.

The interpolation is recomputed every time the ROI geometry is modified.

Note: *Interpolated contours are not saved unless accepted, they are only for visualization.*

Note: *Linear contour interpolation between two contours assumes lateral overlap.*

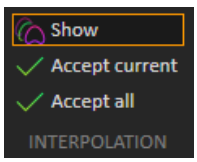
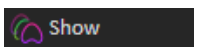
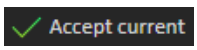


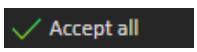
Figure 104. The interpolation tools.



Click the **Show** interpolation button to show the interpolated contours.



Click the **Accept current** interpolation button to accept the interpolated contour on the current slice.



Click the **Accept all** interpolation button to accept the interpolated contours on all slices.

The 2D editing tools

The 2D editing tools can be used if the **2D** button is toggled. All the 2D editing tools can be used in all patient directions, i.e. in the transversal, coronal and sagittal 2D patient views.

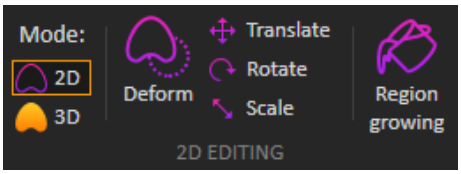


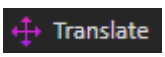
Figure 105. The 2D editing tools.

The **Region growing** tool opens the Region growing dialog.

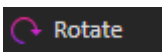
- Select seed points by clicking in the image. The **Threshold levels** interval will be set to the min and max values for all seed points within the tool radius.
- Adjust the **Threshold level** sliders to grow the region.
- Click the **Clear region** button and click again in the image to get new seed points.

Note: *It is not possible to set seed points in the secondary view in Side by side layout.*

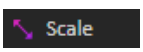
The **Deform** tool deforms the contour. The size of the cursor ring is proportional to the extent of the deformation. Move the cursor to the contour, press the mouse button and move the mouse to deform the contour. To change the size of the deformation tool, use the slider in the tool page, press the + and - keys on the keyboard, or by using the mouse wheel while pressing the CTRL key.



The **Translate** tool allows translation of a contour by clicking its border and moving the mouse.



The **Rotate** tool allows rotation of a contour by clicking its border and moving the mouse.



The **Scale** tool allows scaling of a contour by clicking its border and moving the mouse.

The extra tools

The extra tools are located to the right in the toolbar. All the 2D editing tools, except the Simplify contours tool, can be used in all patient directions, i.e. in the transversal, coronal and sagittal 2D

patient views. The latest patient view used specifies the current direction (see the tooltip for the selected tool for the current direction).

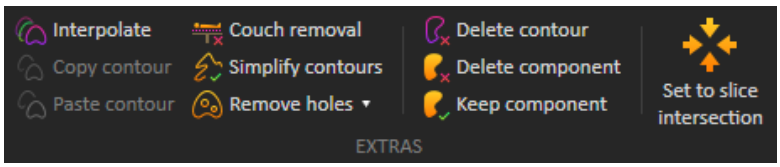


Figure 106. The extra tools.

The **Interpolate** tool fills in missing contours using linear interpolation. Contours are created on slices without contours that are between the uppermost and lowermost drawn contours.

Note: *Linear contour interpolation between two contours assumes lateral overlap.*

The **Copy contour** tool can copy contours for the selected ROI from the current slice.

The **Paste contour** tool pastes the copied contours on to the current slice.

The **Delete contour** tool. When activated, click inside a contour for the current ROI, in a patient view, to delete it.

The **Remove holes** tool removes holes in the current slice or on all slices.

The **Simplify contours** tool can remove holes, remove small contours or reduce the maximum number of points to a specified number. Click the Simplify contours button. This opens the Simplify Contours dialog.

- **Remove holes**: Remove holes on all slices.
- **Remove small contours**: Remove all contours having an area less than the specified area threshold on all slices for the current ROI.
- **Reduce the maximum number of points**: Reduce the maximum number of points in each contour to a specified value.

The **Delete component** tool deletes a coherent volume for the current ROI when clicking on it in one of the patient views.

The **Keep component** tool keeps a coherent volume for the current ROI and removes all others when clicking on it in one of the patient views.

The **Set to slice intersection** tool is used to move the current ROI to the intersection of the transversal, sagittal, and coronal views.

Use the coronal view to select where to cut the external contour (by moving the slice indicator, which is done by pressing and holding down the middle mouse button) and then click the **Couch removal** icon. The tool can only be activated if the External ROI is selected. Note that it is only necessary to use this tool if the External ROI includes part of the CT-couch.

5.3.4 Generate External ROI

The Create External ROI function creates an ROI surrounding the patient outline. The ROI created will automatically be set as the external ROI of the patient. The External ROI generation uses the image data to find the body outline.

Note: *The quality of the automatically generated External ROI depends on the image type. Sometimes it is necessary to manually edit the contours.*

Create External ROI

To create an External ROI:

1. Click the **New ROI geometry...** button and select **Create External ROI...**.

   This opens the **Create External ROI** dialog.

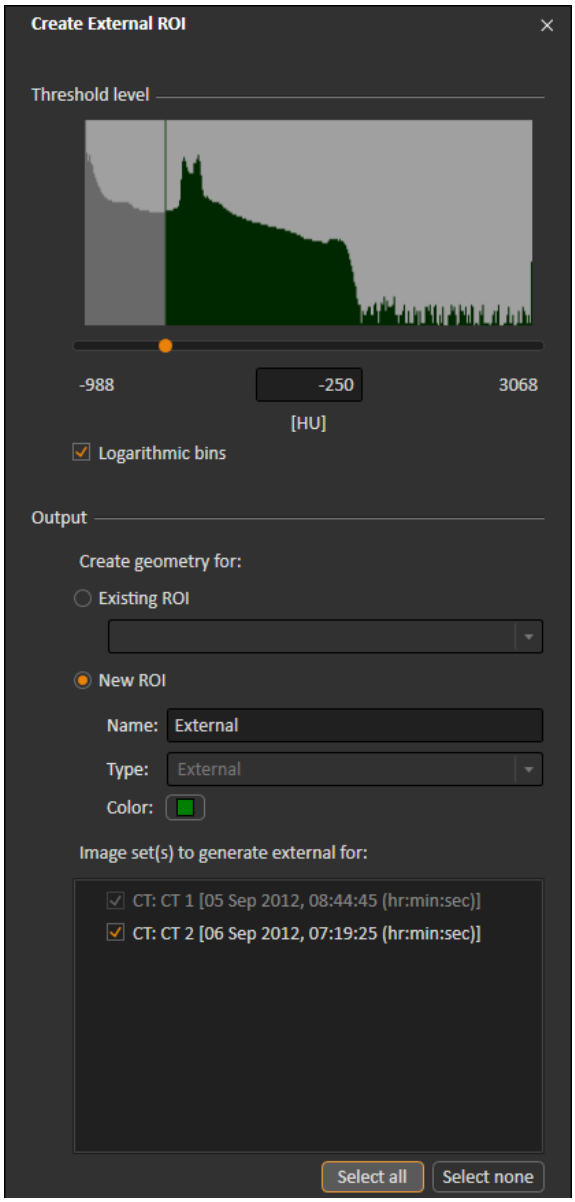


Figure 107. The **Create External ROI** dialog.

Initially, a default threshold value is calculated. Most of the time this value is desired, but sometimes manual adjustment is needed. The patient views indicate the effect of the threshold value. Note that the threshold only serves as a base for the external computation. The result will be the thresholded region followed by hole removal and other computations where everything that is not associated with the largest object will be removed.

2. Select to create geometry for an **Existing ROI** or for a **New ROI**.
3. Select **Image set(s)**.
4. Click **OK**.

WARNING!

Ensure that the correct ROI has been assigned as the External ROI. Always verify that the External ROI covers all target ROIs and OARs. Dose volume histograms might be computed erroneously if the entire ROI is not included in the External ROI. (6299)

5.3.5 Derived ROIs

When creating ROIs based on other ROIs, e.g., margins and algebra ROIs, it is possible to save the ROI definition in order to edit it later or to update it automatically when any source ROI changes. This is called a Derived ROI and is indicated in the ROI list with a white circle.

Note: *The derived expression applies to all image sets in the current case.*

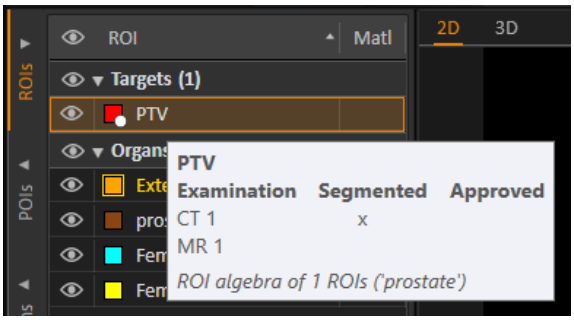


Figure 108. The ROI list where a derived ROI has been selected.

When a derived ROI is selected in the ROI properties dialog, it shows the definition of the derived ROI as well as buttons for editing and updating the derived ROI (see **Edit** and **Update** below).

Figure 109. The ROI properties dialog where a derived ROI has been selected.

In a specific image set, the geometry for a derived ROI can have different status:

Up to date: The geometry is up to date with respect to its dependent geometries. This is indicated with a green circle.

Needs update: One or several dependencies have been modified, the derived geometry must be updated. It is not possible to approve a derived geometry with this status. This is indicated with a red square.

Overridden: The derived geometry has been overridden by the user (by manual modification). This is indicated with a yellow triangle.

When a derived ROI is selected in structure definition, an extra tool panel field becomes visible.

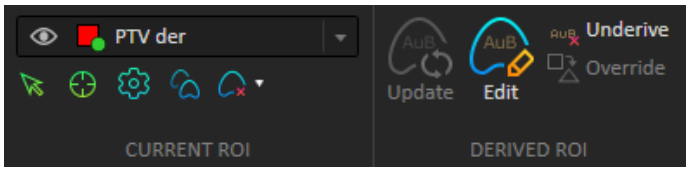
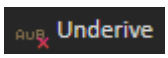


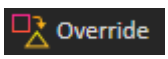
Figure 110. The Derived ROI toolbar.

By clicking **Edit**, the dialog box used when the ROI was created is opened, and it is possible to redefine the derived ROI expression, e.g., by adjusting margins.

A derived geometry that is not up to date can be updated by clicking **Update**. If there are dependencies on multiple levels, all levels are updated simultaneously. If multiple derived ROIs are selected, all will be updated.



Underive discards the ROI definition and the ROI will behave as a standard ROI.



Override performs a manual override for the geometry in the currently selected image set.

Create Expanded/Contracted ROI

This tool is for generation of ROI margins – both as expansions and contractions of an ROI. It is possible to define non-uniform margins.

The Margin operations are performed on voxel representation of the ROIs.

- If the margin is uniform, the operation is performed on relative voxel volumes using Fast Marching Distance transform (Fast Marching Methods , J.A Sethian, SIAM Review, 41,2, 1999, pp. 199-235.)
- If the margin is non-uniform, relative voxel volumes are thresholded at 50% level to binary voxels and a binary structure element is applied. The structure element is an ellipsoid with axes corresponding to the non-uniform distances.

To create an Expanded/Contracted ROI:

1. Click **the New ROI geometry…** button and select **Algebra and margins: Create Expanded/Contracted ROI...**.

   This opens the **Create Expanded/Contracted ROI** dialog.

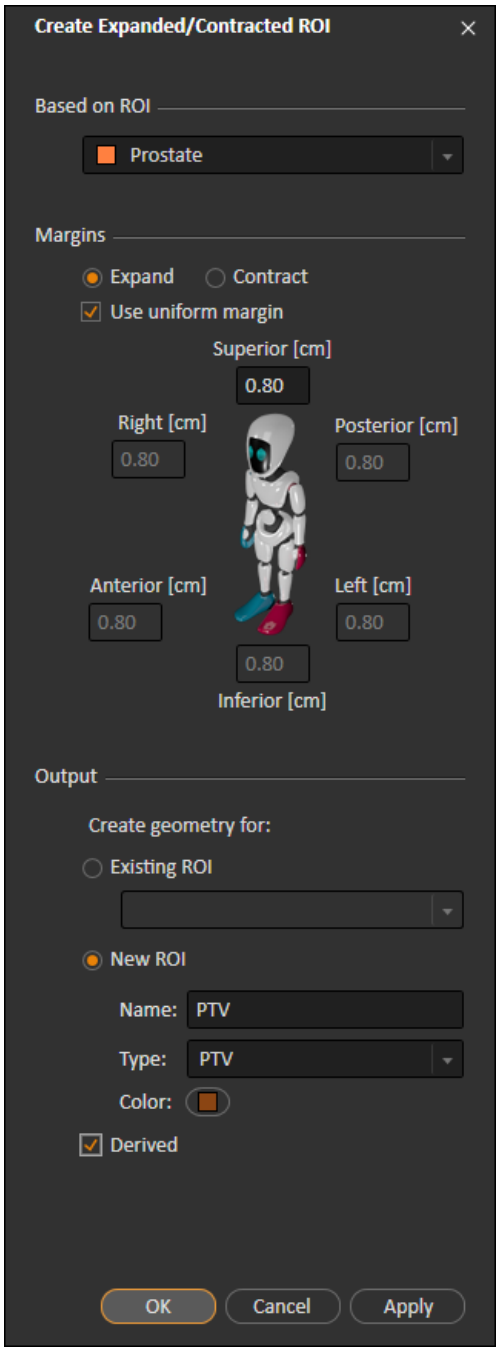


Figure 111. The **Create Expanded/Contracted ROI** dialog.

2. Select the ROI that the Expanded/Contracted ROI should be based on.
3. Enter **Margins** and if they should **Expand** or **Contract**.

   To use uniform margins in all directions, check the **Use uniform margin** checkbox.
4. Select **Output**; either **Existing ROI** or **New ROI**.
5. In order to make the resulting ROI a derived ROI, make sure that the **Derived** checkbox is checked.
6. Click **OK**.

Create wall

The **Wall** tool is a margin tool where it is possible to create a wall-geometry by selecting a base ROI and specifying the outward and inward distances. Select **New ROI geometry: Algebra and margins: Create wall...** to open the **Create Wall** dialog. In order to make the resulting ROI derived, make sure that the **Derived** checkbox is checked.

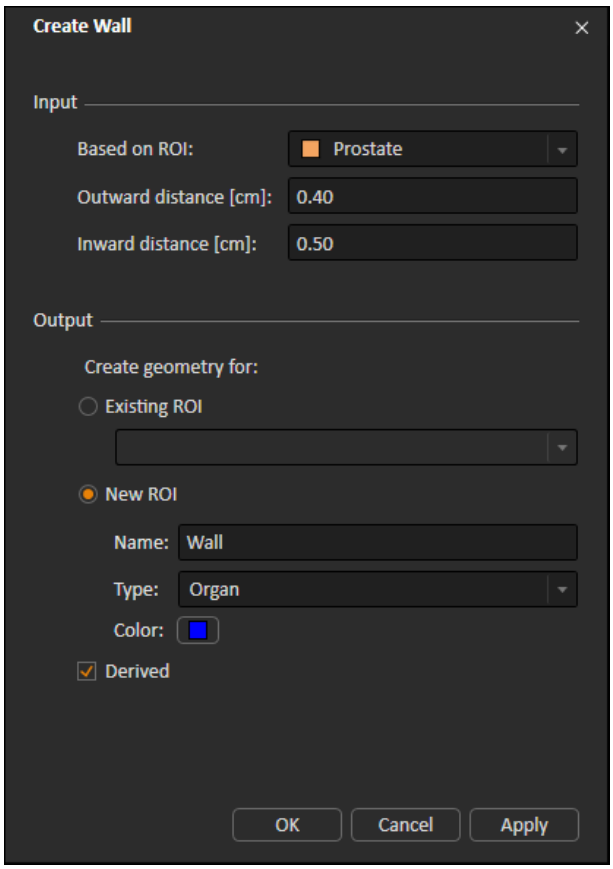


Figure 112. The **Create Wall** dialog.

ROI algebra

The ROI algebra tool provides a way of creating more complex expressions. It is possible to create new ROIs based on the union, intersection or subtraction of existing ROIs with optional margins. In the ROI Algebra dialog it is possible to specify two expressions, Expression A and Expression B.

Each expression has the form:

$$Expression\{A,B\} = Margin(Operation(sourceRoi0, sourceRoi1, \ldots)), \quad \text{[Eq. 1]}$$

where Margin is an expansion or contraction as in the Expand/Contract dialog and Operation is either Union or Intersection. At least one source ROI must be selected.

When the two expressions have been defined, they are combined by the resulting operation (in the middle) which is either Union, Intersection, or Subtraction. Finally, a resulting margin can be applied, i.e.:

$$Result = Margin(Operation(ExpressionA, ExpressionB)). \quad \text{[Eq. 2]}$$

All margin functions are default set to zero. If the result operation is set to **None**, only Expression A is used.

Algorithms used for ROI algebra

- ROI algebra operations are performed slice wise on contour representations of the ROIs.
- The margin operations are described in *Create Expanded/Contracted ROI on page 210*.

To create a new ROI geometry:

1. Click **the New ROI geometry...** button and select **Algebra and margins: ROI algebra...**.

   This opens the **ROI Algebra** dialog.

Figure 113. The **ROI Algebra** dialog.

2. Select the **Source ROIs** and **Margins** for Expression A. If several ROIs are selected in Expression A, make sure to select the desired operation for the ROIs; Union or intersection.

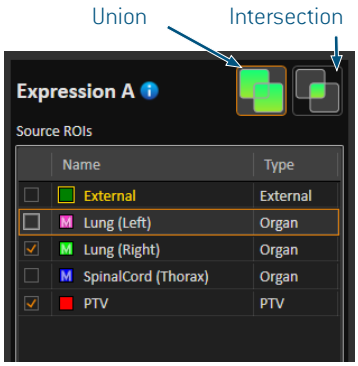


Figure 114. Operation options for Expression A.

3. Select the **Source ROIs** and **Margins** for Expression B. If several ROIs are selected in Expression B, make sure to select the desired operation for the ROIs; Union or intersection.

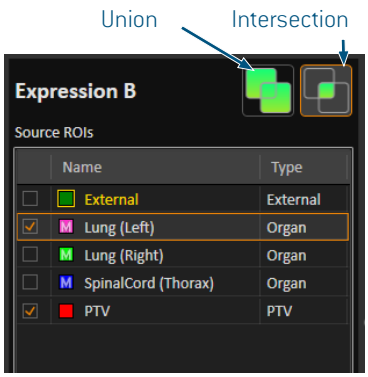


Figure 115. Operation options for Expression B.

4. Select resulting operation for the combination of Expression A and Expression B (in the middle of the dialog):

   Union
   The resulting ROI will be the union of Expression A and Expression B.

   Intersection
   The resulting ROI will be the intersection between Expression A and Expression B.

   Subtraction
   The resulting ROI will be Expression B subtracted from Expression A.

   None

   The **Clear expressions** button will clear the selected ROIs and margins and reset selected operations.

5. Enter the **Result margins** for the combination of Expression A and Expression B.

   To use uniform margins in all directions, check the **Use uniform margin** checkbox.

6. Select **Output**; either **Existing ROI** or **New ROI**.

7. In order to make the resulting ROI a derived ROI, make sure that the **Derived** checkbox is checked.

8. Click **OK** or **Apply**.

5.3.6 Additional ROI geometry options

This section describes additional ROI geometry options that can be selected from the **New ROI geometry** button.

Create Beam Specific Margin ROIs

The Create Beam Specific Margin ROI function provides tools for automatic extension of ROI geometries based on beam directions. An ROI geometry can be uniformly expanded in the distal, proximal and radial direction relative to a chosen beam and a source ROI geometry. The margin directions are determined by the beam angles and the margin distances are geometrical, not radiological.

In order to create a Beam Specific Margin ROI there must be at least one non-empty ROI geometry and a selected plan containing at least one beam.

Note: *There is no dependency between the resulting margin ROI geometry and the source ROI geometry or the selected beam. If any of those are changed, the margin ROI geometry becomes absolute and must be regenerated.*

Select **New ROI geometry: Algebra and margins: Create beam specific margin ROI...** to open the **Create Beam Specific Margin ROI** dialog.

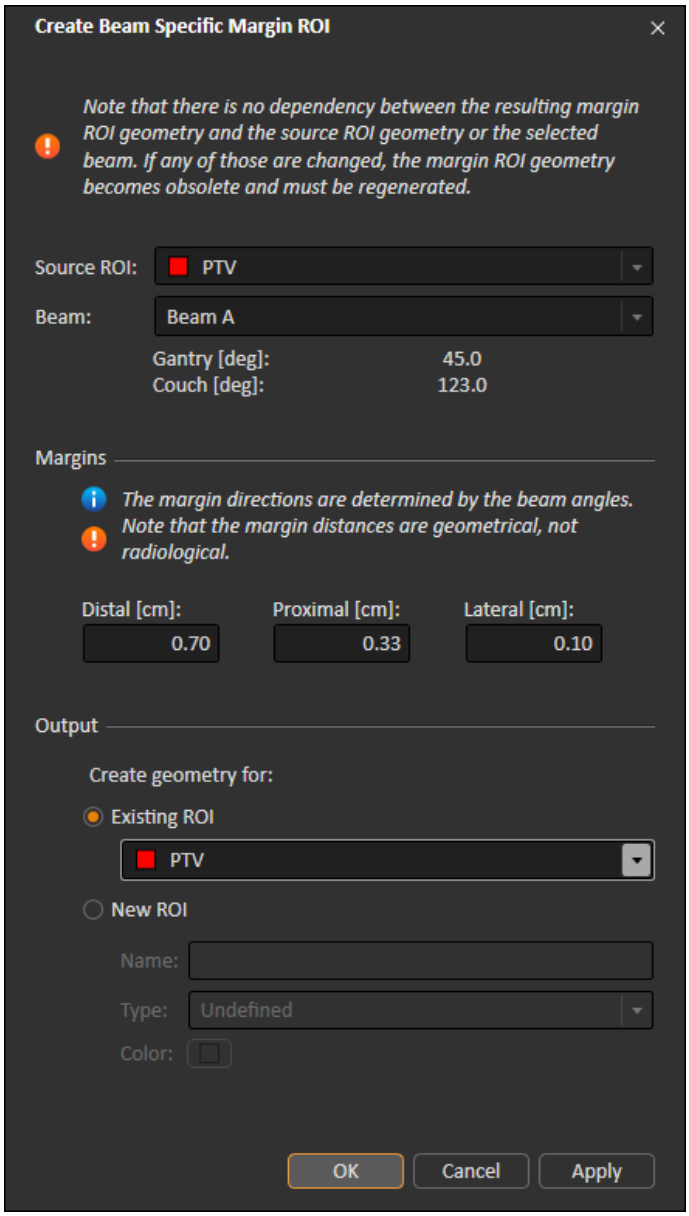


Figure 116. The **Create Beam Specific Margin ROI** dialog.

Create ITV

The ITV tool creates an ROI of the union of all or a subset of the geometries for an ROI in a 4DCT or 4DMR group. It is also possible to set a margin (inner or outer) on the result. Select **New ROI geometry: Algebra and margins: Create ITV…** to open the Create ITV dialog.

Create Box, Cylinder or Sphere ROIs

ROIs can be created with the shape of a box, a cylinder or as a sphere. This is useful for evaluation purposes in for example the QA Preparation module. Boxes and cylinders are created aligned with the coordinate axes. These options can be selected by clicking **New ROI geometry: Basic shapes**.

Create Bone ROI

The Create bone ROI tool creates an ROI based on the gray-level threshold for the selected image set. Select **New ROI geometry: Create Bone ROI...** to open the Create bone ROI dialog.

Create Field-of-View ROI

If the image set has limited field of view (FOV), that is when parts of the body are outside the FOV, an ROI can be created for the FOV. This ROI can later be used for calculating the external on the limited FOV data. Select **New ROI geometry: Limited FOV tools: Create Field-Of-View ROI...** to open the Create Field-of- view ROI dialog. This option is enabled for CT and CBCT image sets.

Note: *When creating a field-of-view ROI on a CBCT image set, the piece-wise linear transfer function maps the CBCT values to HU-like values calculated from the density table for the CBCT. Hence, for optimal performance, the user should have created a density table before using this method.*

Generate external ROI on limited FOV data

If the image set has limited FOV data and an ROI has been created for the FOV, an external ROI can be created for the image set using the FOV ROI and an External ROI from another image set as model. This allows for dose calculation on the image set with limited FOV data. When the External-FOV ROI has been created, it is possible to set a material for the ROI. The material will be used for that specific area in dose calculations. Select **New ROI geometry: Limited FOV tools: Create External ROI On Limited FOV data...** to open the Create external ROI on limited FOV data dialog.

The result is an external contour, an external mesh and an external – FOV. The default material used for the override of the External – FOV region is water, but can be edited to any preset or user defined material.

Note: *When creating an External ROI on limited FOV data on a CBCT image set, the piece-wise linear transfer function maps the CBCT values to HU-like values calculated from the density table for the CBCT. Hence, for optimal performance, the user should have created a density table before using this method.*

Create an ROI based on the gray level threshold

An ROI can be created based on the gray levels in the image histogram. For PET images where SUV can be computed, the threshold values can be specified in SUV units. Select **New ROI geometry: Thresholding: Gray Level Threshold...** to open the Gray Level Threshold dialog.

Create an ROI based on volume threshold

An ROI can be created based on volume thresholds. Select **New ROI geometry: Thresholding: Volume Threshold...** to open the Volume Threshold dialog.

5.3.7 Structure templates

It is possible to save the current structure set (or a subset of it) as a template. The template can later be used to create ROIs and POIs and their geometries on structure set for different patients. This gives the possibility to create structures with consistent name, color and type each time. Materials and derived ROI dependencies are also included in the template. A typical use-case of structure templates is to store couch models or similar structures with multiple geometries having different material properties.

The image set associated with the structure set is also saved in the template making it possible to use rigid and deformable image registration for initialization of structures. A template can contain multiple structure sets and image sets. Structure templates with multiple image sets and geometries are typically used for atlas-based segmentation which is covered in detail in *Atlas-based segmentation on page 228*.

Structure template management

The Structure Templates Management dialog lists all available structure templates in the system. Here, it is possible to create, delete, modify, import, and export structure templates. Select **New ROI geometry: Structure templates: Structure Template Management...** to open the Structure Template Management dialog.

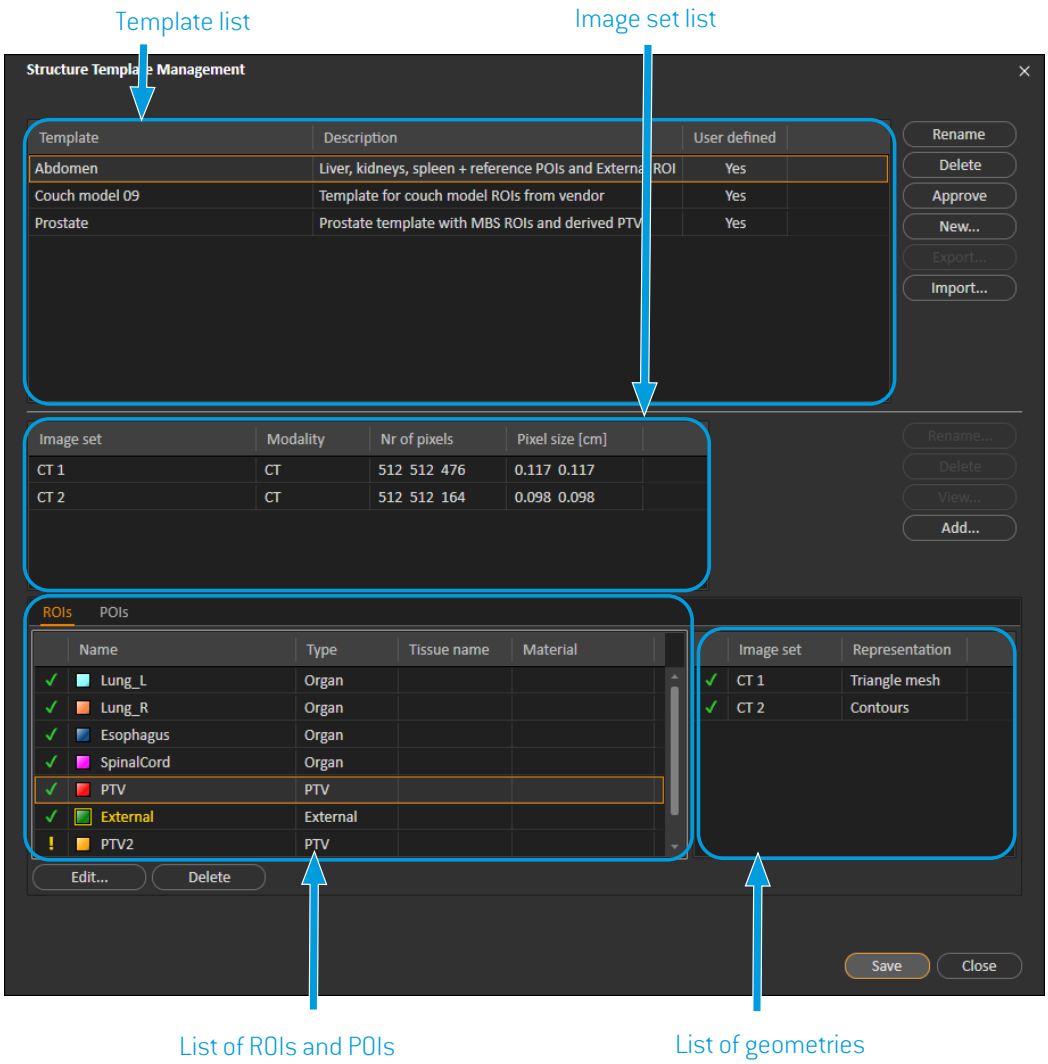


Figure 117. The Structure Template Management dialog.

The **Template** list displays the template name and description. The user defined property states if the template is user defined or not. Only user-defined templates may be modified or deleted. The list of templates can be sorted by clicking the desired column header. The selected template can be deleted by clicking **Delete**. In order to edit the name and/or description of the selected template, click **Rename...**. To approve a template, click **Approve**. Only admin users can approve or unapprove a template.

The **Image set** list displays the image set name, modality, number of pixels, and pixel size. The list of image sets can be sorted by clicking the name or modality column header. In the case of multiple image sets, the selected image set can be deleted by clicking **Delete**. In order to rename the selected image set, click **Rename...**.

The list of **ROIs** and **POIs** displays the available ROIs and POIs in the template. There is also a list of geometries that lists the ROI/POI geometries and whether they are defined on each image set. The lists support multi-selection. Editing the properties of an ROI or POI is performed by clicking **Edit...** or double clicking the desired ROI/POI. This will open the standard ROI/POI Properties dialog. In order to delete the selected ROI/POI, click **Delete**.

Add a new structure template to the database

To add a new structure template to the database:

1. Select **New ROI geometry: Structure templates: Structure Template Management...**. This opens the Structure Templates Management dialog.
2. Click the **New...** button. This opens the Create Structure Template dialog.

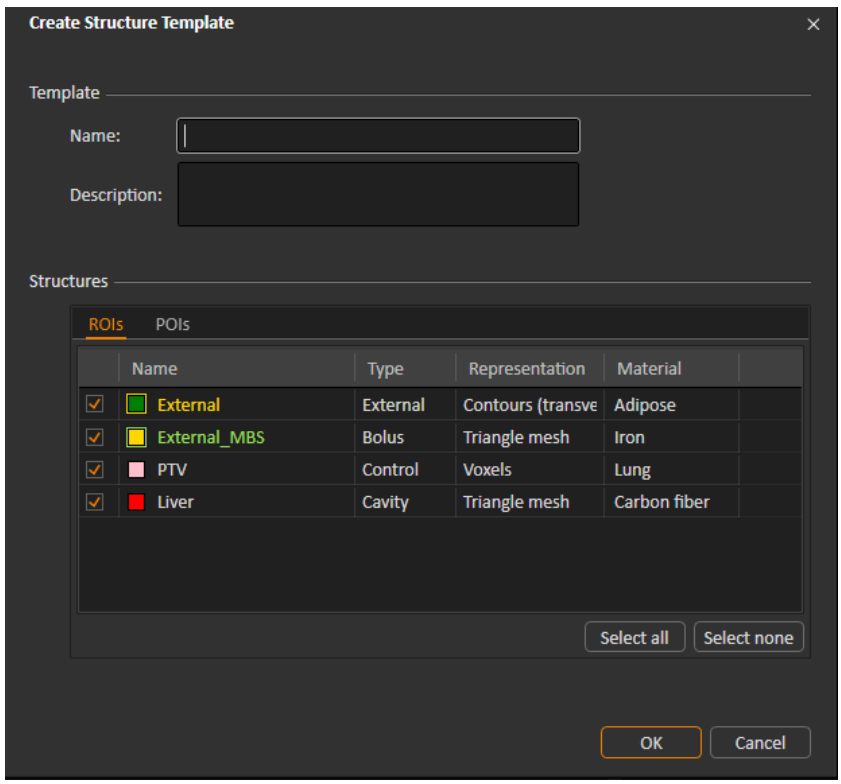


Figure 118. The Structure Template dialog.

3. Enter a **Name** and **Description** for the template.

4. Select which ROIs and POIs that should be included by checking the corresponding checkboxes.
5. Click **OK**. The new template will be displayed in the list.

Import / Export of structure templates

Import and export of templates is performed by clicking **Import…** or **Export…** in the Structure Templates Management dialog. The file formats is the same as for backup and restore (*.rsbak). Changes to the template must be saved before exporting.

Note: *The data is anonymized at export. Typically, no other patient data than ROI/POI names and image set names are presented in the GUI , but there is patient information in the exported file and this will be anonymized.*

Extend a structure template with new image set and structures

To add the active image set and structures from the currently selected case in RayStation 7:

1. Select **New ROI geometry: Structure templates: Structure Template Management…**. This opens the Structure Templates Management dialog.
2. Click the **Add…** button. This opens the Extend Structure Template dialog.

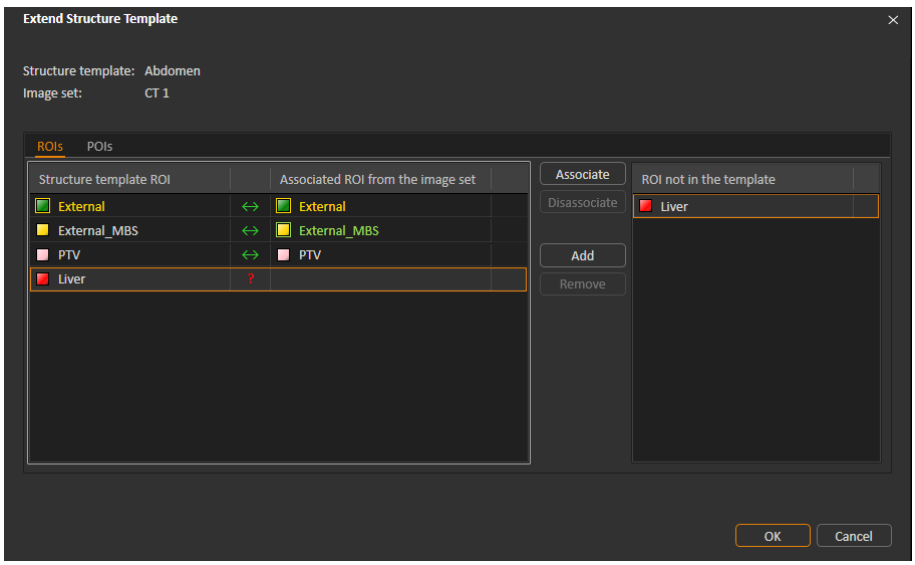


Figure 119. The Extend Structure Template dialog.

3. The ROIs and POIs from the active image set are associated to template ROIs and POIs by name. If there is a name mismatch, the structures can be manually associated by selecting the structures to associate and click **Associate**. Disassociation is performed by clicking **Disassociate**.
4. It is also possible to add new structures not currently in the template by selecting the new structure and click **Add**. An added structure can be removed by clicking **Remove**.

5. When finished with the associations of ROIs and POIs, click **OK**. The image set and structures are added to the template and are visible in the image set list and the ROI/POI list.

Viewing the structures

To view the content of a structure template:

1. Select **New ROI geometry: Structure templates: Structure Template Management…**. This opens the Structure Templates Management dialog.
2. Select the desired **Template** and **Image set**.
3. Click the **View…** button. This opens the Structure Template View that is showing the selected template and image set. This view supports scrolling, zooming, panning, and rotating (3D).

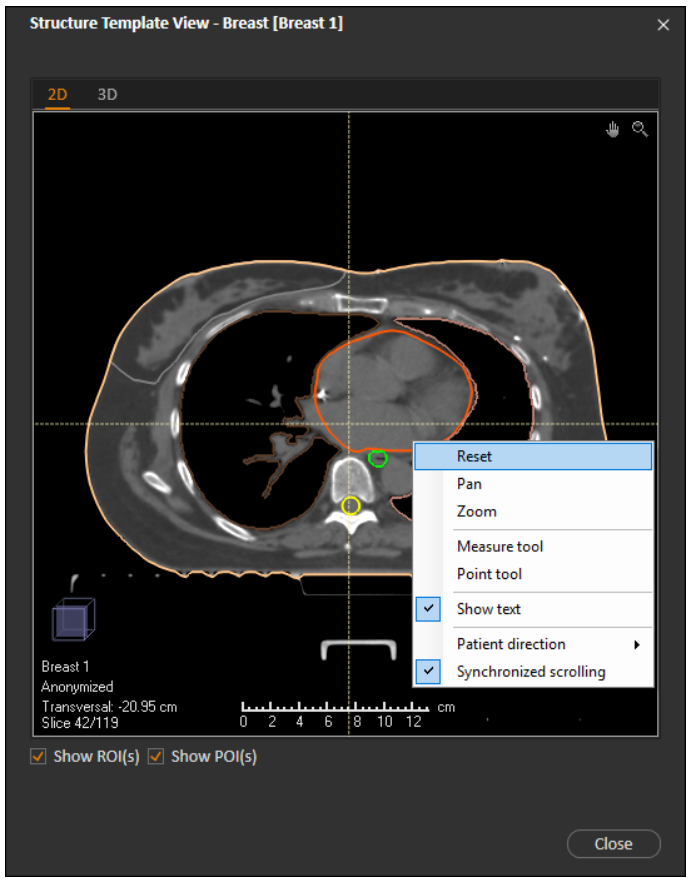


Figure 120. The Structure Template View dialog.

4. Visualization of ROIs/POIs can be toggled on or off by checking and unchecking **Show ROI(s)** and **Show POI(s)**.

5. Right click in the view for more options, i.e., changing **Patient direction**.
6. Click **Close** in order to close the viewer.

Create structures from template

To create structures from a template in the database:

1. Select **New ROI geometry: Structure templates: Create structures from template…**. This opens the Create Structures from Template dialog.

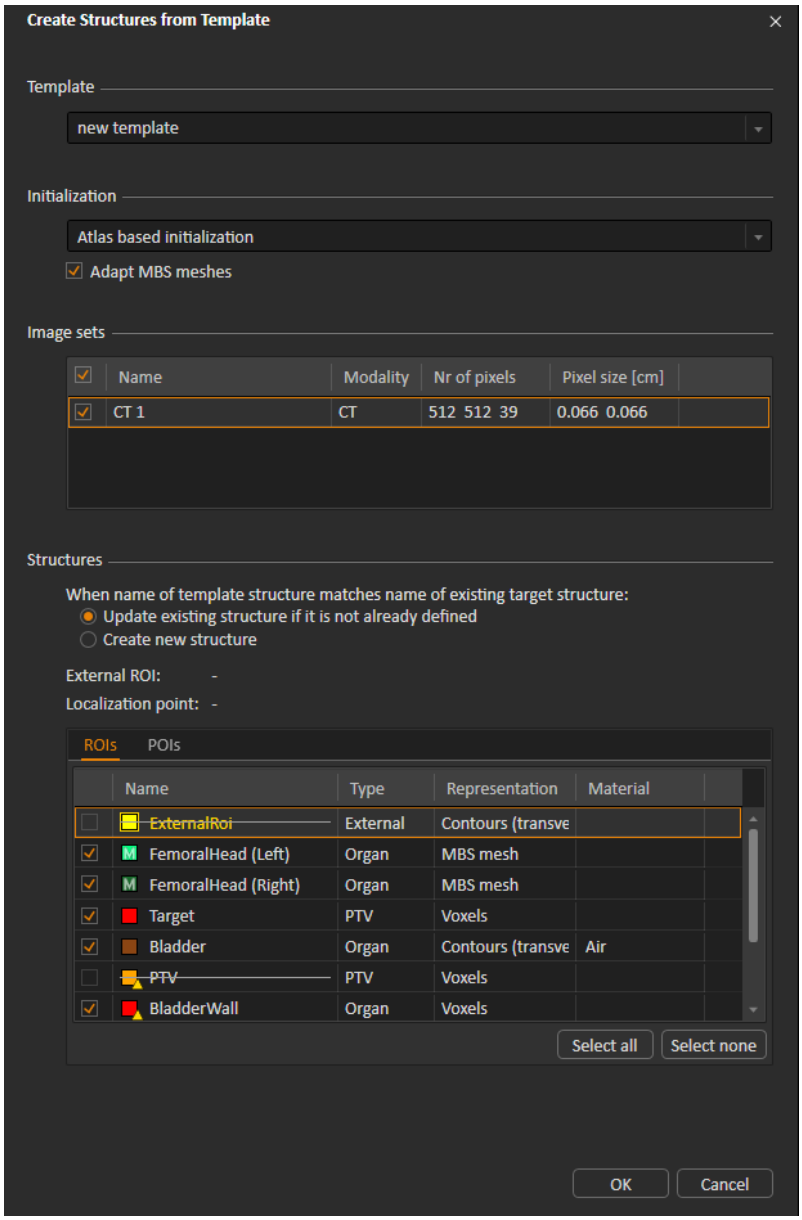


Figure 121. The Create Structures from Template dialog.

2. Select a **Template** from the drop-down list.

   Approved templates have a padlock next to the template name.

3. Select an **Initialization** option.

- **Empty geometries** – Create ROIs/POIs with empty geometries.
- **Align image centers** – Position geometries in center of image.
- **Rigid registration** – Perform a rigid gray-level based registration of the template image and the currently selected primary image set to position geometries.
- **Atlas-based initialization** – Combine rigid and deformable registration of the template images and the currently selected primary image set to initialize geometries. When selecting this option it is also possible to select whether MBS ROIs should be automatically adapter or not. Refer to *Atlas-based segmentation on page 228* for more about atlas-based initialization.

4. Review the selection of structures.
   - If existing non-empty structures have the same name as the template structures, they will be excluded by default. This behavior can be overridden by clicking **Create new structure** in order to create new ROIs and/or POIs with a name suffix.
   - If the template contains an ROI of type External, it will always be auto-generated independent of the selected initialization mode.
   - If the template contains a POI of type Localization point, its position will always be undefined independent of the selected initialization option and it must be manually defined after creation.
   - If the template contains derived ROIs, all dependencies from template must also be included in order to maintain its derived ROI expression.
5. Click **OK**.

   If a non-approved template is loaded, a warning will be displayed. These warnings can be disabled in Clinic Settings (*section D.2.2 The Preferences tab on page 922*).

Atlas-based segmentation

Atlas-based segmentation utilizes the structure template framework in order to create a versatile auto-segmentation tool. The idea is to take existing data from the clinic database to create templates with multiple image sets – atlases – and use these to segment new image data by locating the best matching atlases through rigid image registration and then apply deformable registration to deform the ROI and POI geometries onto the new image set.

The geometries contained in each atlas can be manually contoured or generated with MBS. If MBS ROIs are available in the template they may be automatically adapted after atlas-based initialization is finished. Derived ROIs created from a template will automatically be updated after initialization and MBS adaptation.

The only hard requirement on templates that are going to be used for atlas-based segmentation is that an external ROI must be defined for each image set. However, there are some things to consider when creating templates for atlas-based segmentation:

- *Structure consistency* – For best performance, it is preferred that the structures are defined in each atlas and are consistently contoured.
- *Atlas consistency* - The atlas image sets should cover the desired area of the patient and be applied to similar image sets.
- *Image modality* - The image to be segmented must be of the same modality as the images in the template. For MR-images, the same sequence should be used for all images.
- *Number of images* - When creating a template for atlas based segmentation, it is a good idea to start with 5-10 images and then iteratively evaluate it on new images using the atlas based segmentation functionality. If the segmentation result is not good enough on a particular image, then add the image to the template. Continue until a good compromise between segmentation results and computation speed is achieved.
- *Number of atlases* – One atlas is enough to run the algorithm, but the recommendation is at least 25 images.
- *Number of structures* – Include as many structures as possible. The cost of adding a single structure is low.
- *MBS structures* – Use MBS structures where it is has potential of improving the result, i.e., where the structure is well defined in the image data. For body sites with large anatomical variation, e.g., pelvis and abdomen, it is highly recommended to use MBS structures in order to improve the result.
- *Number of fusion atlases* - The atlas-based segmentation engine supports multi-atlas, which means that several atlases are selected for deformation and the final segmentation result is composed by fusing the individual segmentations. The number of fusion atlases will affect segmentation performance and computation times. The more fusion atlases, the longer the computation time. Experiments show that using more than about 15 fusion atlases does not improve segmentation results.

- Missing structures - Template structures that have no or little overlap in a majority of the fusion images are not included in the segmentation result.

Create structures with atlas-based segmentation

In addition to **Create structures from template...** there is also a dedicated menu option for atlas based segmentation:

1. Select **New ROI geometry: Atlas based segmentation...**. This opens the Atlas Based Segmentation dialog.

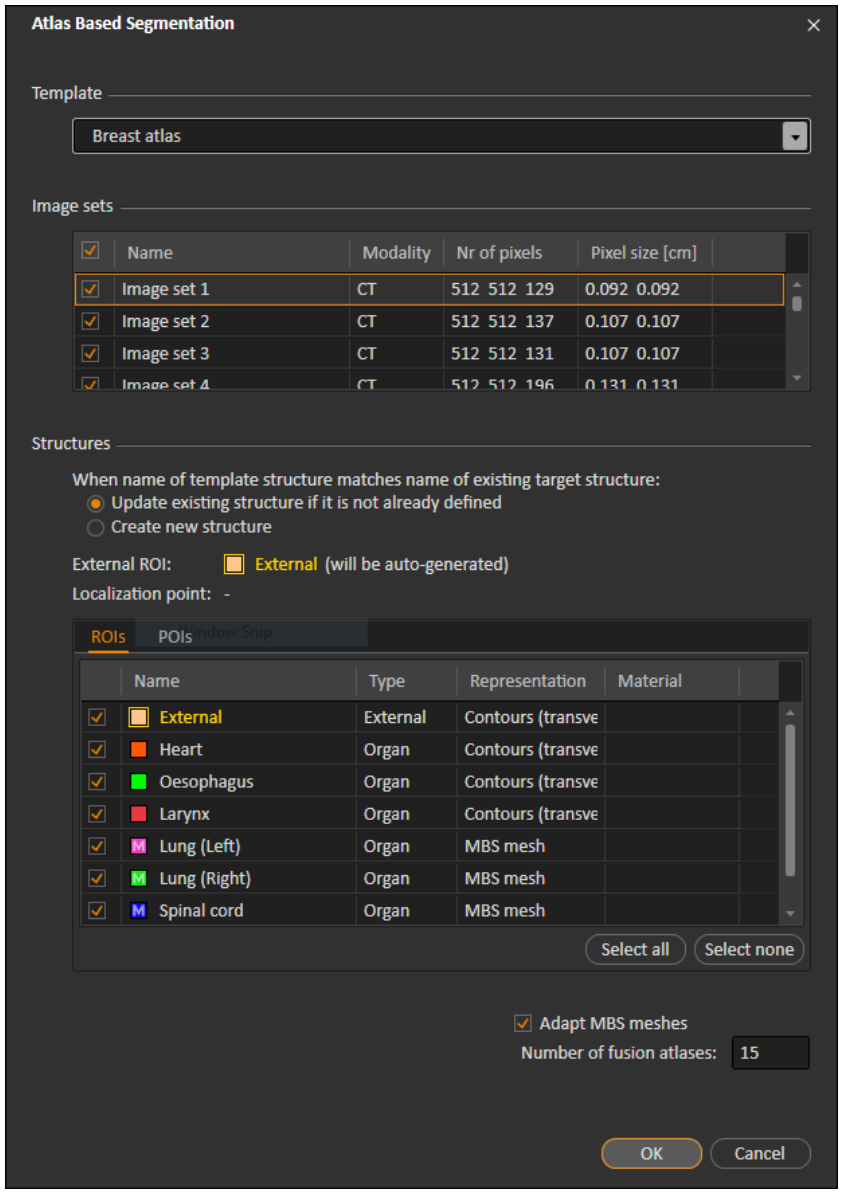


Figure 122. The Atlas Based Segmentation dialog.

2. Select the desired **Template**.
3. Select the **Image sets** to include by using the checkboxes (default is all).
4. Select the **Structures** to include.
5. If automatic adaptation of MBS meshes is desired, check **Adapt MBS meshes**.

6. Select **Number of fusion atlases** (default is 15).
7. Click **OK**.

Atlas-based segmentation starts. Follow the progress in the status bar. The operation can be cancelled as described in *section 3.11 Cancel procedure on page 106*.

5.3.8 Introduction to Model-Based Segmentation

The Model-Based Segmentation tool allows for semi-automatic delineation of structures in CT, CBCT and MR image sets. The idea of MBS is to match 3D shape models of the structures to new image data. Each shape model consists of an average model and a number of shape components that describe the most typical shape variations of the modeled structure.

Model construction

In order to build a shape model, a number of datasets have been collected where the structure to be modeled has been contoured by an expert. Contour sets that are consistent and of good quality have been chosen. The number of contour sets varies between models but is typically between 10 and 50. Each contour set has been transformed to a triangulated surface, each with the same number of triangles and vertices and with vertex-vertex correspondence. This set of triangulated surfaces constitutes the training set. From the training set, the average model has been computed and by statistical analysis the main components of shape variation have been extracted.

Model adaptation

To segment a structure in a new image set, the user starts by creating an ROI based on the shape model. The models are automatically initialized based on rigid and deformable registration. In order to make the model adapt to the image data, some grayscale information of the structure to be delineated is needed. Most models have default values, but in some cases the user needs to manually select an image region representing the desired structure and its surroundings. For CT and CBCT image sets, the models have default values, but in some cases the user needs to manually select an image region representing the desired structure and its surroundings. For MR image sets, no default values are set and the user always need to manually select an image region. Given the initial model and the grayscale information, image feature points are extracted for each vertex of the model by searching in the normal direction of the vertex. The adaptation algorithm then tries to match the model to the feature points without violating the shape constraints given by the underlying shape model. This matching is an iterative, non-linear optimization process where new feature points are extracted in each step.

User interaction

It is important to note that this is a semi-automatic method. There exist no methods that can segment any structure from any image set completely automatically. Therefore, some degree of user interaction is needed in almost all cases in order to fit the model to the structure in the image data set. Good image quality means less interaction and vice versa.

Hint contours

The user has the possibility to draw any number of transversal, sagittal, or coronal hint contours in order to guide the adaptation. If there are hint contours present, the adaptation algorithm tries to make the model "snap" to the contours. The hint contours provide a way for the user to give boundary information to the algorithm in low-contrast areas of the image set.

3D deformation tool

The user can also deform the model in 3D with a smooth deformation tool. At the point of interaction, the model deforms most and then the amount of deformation falls off with the distance from the point of interaction.

Interaction tools

The MBS module has several Interaction tools which allow the user to guide the model adaptation with better initial guesses and to manually improve the model. For all of the interaction tools, the user is advised to have the ROI of interest centered in all the patient planes and carefully watch the impact of the changes in all three dimensions. The ROI that has been chosen is highlighted in the image data. All interaction tools are deselected by pressing the same button again.

5.3.9 Creating and adapting MBS ROIs

As stated in *section 5.3.8 Introduction to Model-Based Segmentation on page 232*, there are several tools available to guide the model adaptation, using hint contours, and to adjust the resulting MBS ROI.

Tools for interaction and deformation

All 3D ROI tools can be used to interact with and modify MBS ROIs. (The 3D ROI tools – **Deform**, **Translate**, **Rotate**, **Scale**, and **Set to slice intersection** – are described in *section 5.3.3 The ROI modification tools on page 197*).

There is an additional 3D tool for MBS ROIs, **Convert to contours**. This tool will convert MBS meshes to contours which enable editing of the MBS meshes contour by contour. Note that the MBS status for the selected ROI will be lost.

Hint contours

Hint contours provide a way for the user to give boundary information to the algorithm in low contrast areas of the image set.

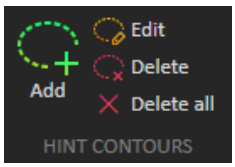


Figure 123. The Hint contour tools.

The **Add** hint contour tool allows the user to add hint contours for the currently selected ROI.

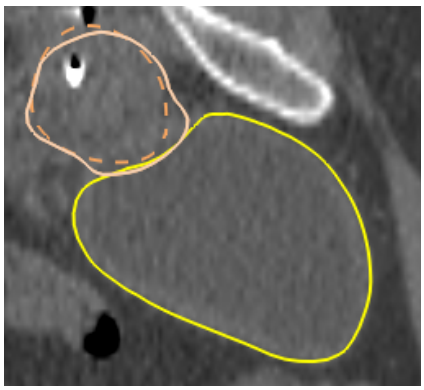
- Use the mouse button to start drawing in the image and continue to press the mouse button in order to add more points to the contour.
- Press the right mouse button to finish the contour. The contour does NOT close on finish and does not need to. The hint contours are represented by splines that are smooth and easy to work with. The hint contour is shown as a dashed line.
- Press the **Start** button and the model should "snap" to the added contour.

When a contour has been added in one of the patient planes, the intersection with the other planes is marked with a small cross. If contours are added in more than one patient plane, make sure that the added contours intersect these crosses.

The **Edit** hint contour tool allows the user to edit an already added hint contour. When pressing this button, all existing added contours will be shown with squares representing the spline control-points of the help contours. Put the mouse pointer on one of the control points, press the mouse button and move the mouse in order to change the contour.

This **Delete** hint contour tool allows the user to remove added hint contours one at the time. Put the mouse pointer on the added contour that is to be removed and press the mouse button.

The **Delete all** hint contours tool deletes all added hint contours for the current ROI.



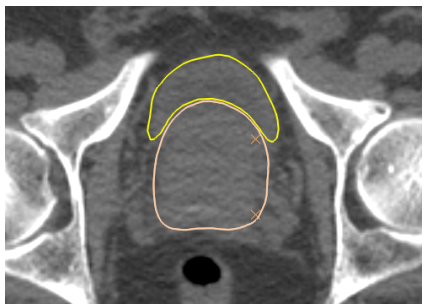


Figure 124. A) The Add contour interaction tool has been used to add a help contour to the prostate in the sagittal plane. B) The crosses indicate the intersection of the help contour with the transversal plane.

5.3.10 Creating MBS ROIs - workflow example

The MBS work flow here is demonstrated with a prostate case. Open the prostate patient and navigate to the Structure Definition module in the Patient Modeling planning activity.

Creating MBS ROI(s)

Start by placing initial ROI models in the image data:

1. Click the **New ROI geometry** button and select **MBS: Create MBS ROI(s)...**. This opens the Create MBS ROI(s) dialog.

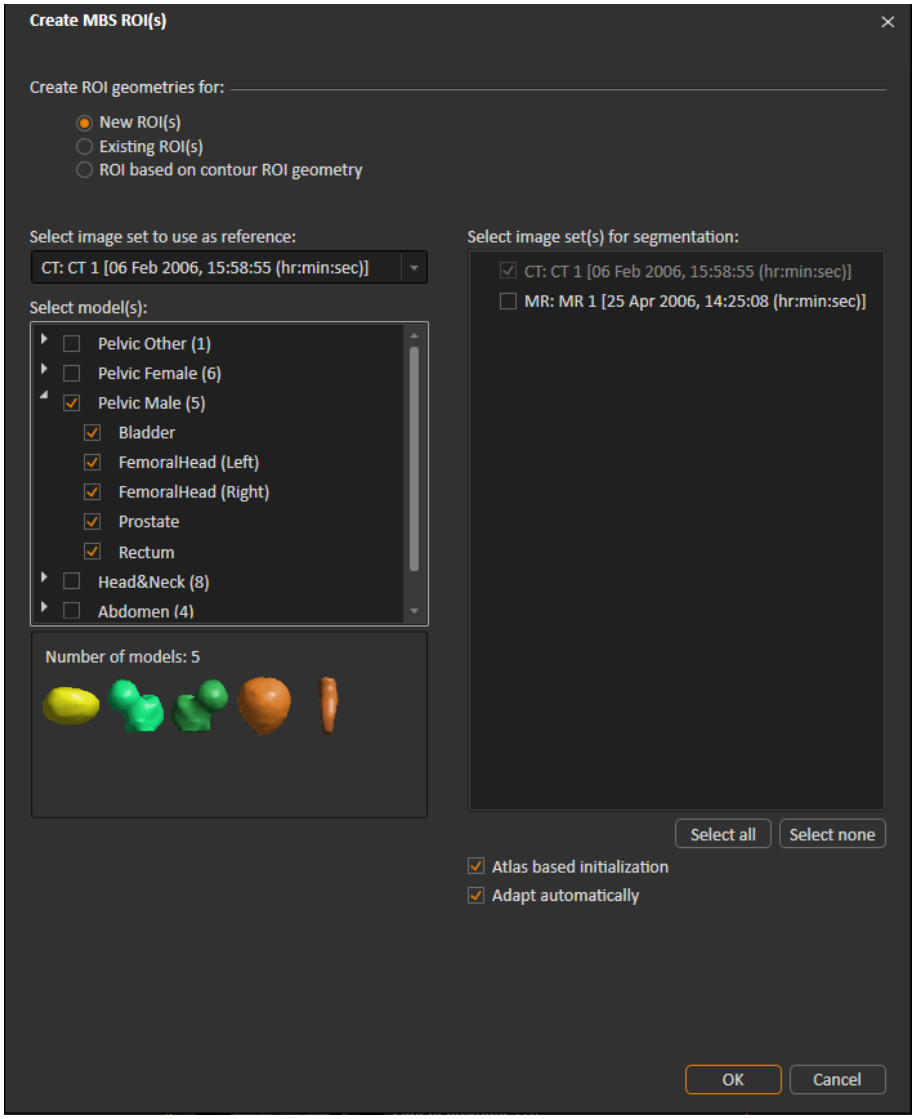


Figure 125. The Create MBS dialog where all pelvic male MBS models are selected.

2. Select to create a **New ROI**.
3. **Select model(s)**. The Models tree view presents different organ models, grouped by body site. It is possible to choose a complete group, for example Pelvic – Male, or individual organ models, for example Bladder. 3D images of the selected models are shown below the tree view. To get all possible models for the prostate patient, select the **Pelvic Male** node in the Models tree. It is also possible to select user-defined models. These are defined in the MBS Model Manager, see *section 5.3.11 The MBS Model Manager on page 242* for more information.

4. Select **Image set(s)** for segmentation.

   Note: *In the 4DCT case, it is possible to select a group of image sets or select a specific image set within the group.*

5. Click **OK**.

   The application now positions the Pelvic ROI models (Rectum, Prostate, Bladder, FemoralHead (Right), and FemoralHead (Left)) in the patient anatomy, and starts an automatic adaptation of the models to the current image data.

Review and manually adapt the created ROI(s)

The next step is to review the automatically adapded ROIs. Often some further adaptation of the new ROIs are needed. The best order to adapt the organs is Bladder, Prostate, Rectum and Femoral Heads. (The femoral heads are independent of the other organs and may be adapted at any point.)

1. Adapt the Bladder:

   a. Select the Bladder by choosing it in the **Current ROI** drop-down list in the toolbar. It is also possible to use the **Pick tool**.

   b. Click the **Localize ROI** button to get all patient views centered in the Bladder ROI. (By clicking the mouse wheel in one of the patient views, the other views will be updated to show this position.

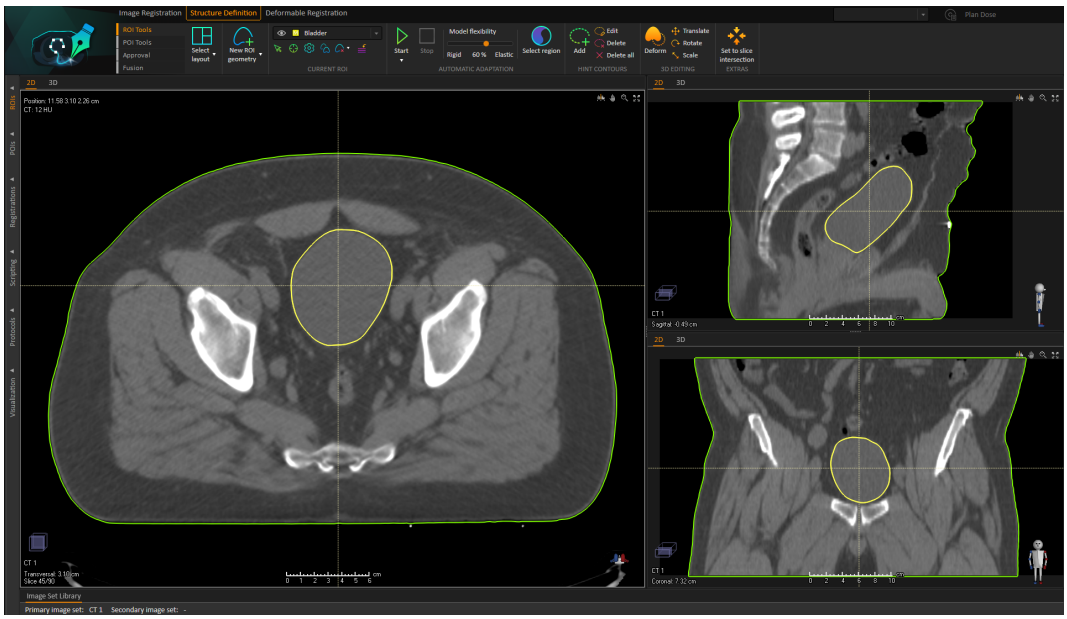
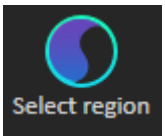


Figure 126. The bladder ROI has been chosen and the slice indicators mark the location in all planes.

c. If the automatic adaptation went wrong, and the model failed to locate the boundaries of the organ in the image it might be needed to adjust the gray level settings. Click the **Select region** button.



Now it is possible to draw a ring in the image data by clicking the mouse button and moving the mouse. The ring should cover an area containing the Bladder and an area outside the Bladder. Select a region of the image data containing a typical edge of the Bladder. The system will compute statistics describing inside and outside gray levels and display computed object intensities colored in the ROI's color. Be sure not to include, for example, bone when trying to adapt the Bladder. In the Image region box, a magnification of the selected region will be displayed.

d. In the Image region dialog, it is possible to define if the tissue of the desired organ is brighter or darker than the surrounding tissue using the **Bright** and **Dark** option buttons. The Bladder (as most organs) is brighter than the surrounding tissue and Bright is the correct setting. The part of the region that will be considered the organ to model is colored in the ROI's color.

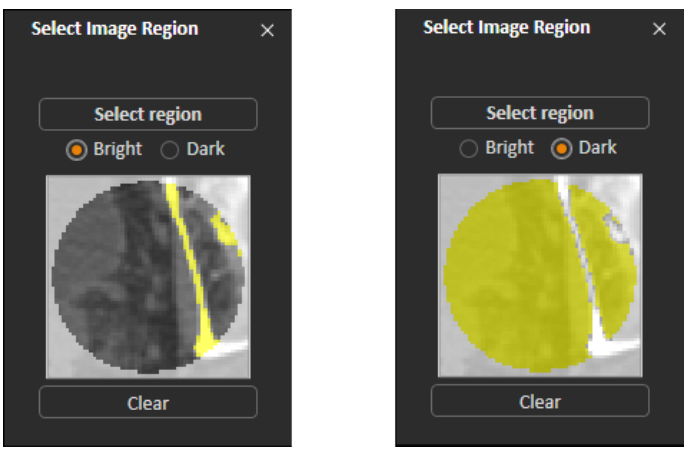


Figure 127. The correct setting for an organ which is brighter than the surrounding tissue (such as the Bladder) is shown to the left. The correct setting for an organ darker than the surrounding tissue is shown to the right.

e. If the contrast between the Bladder and the surrounding tissue was not good enough try to select another region in the image data slice or scroll to another image data slice.

f. If needed, it is possible to use the Interaction tools to give the Bladder a better initial position. Suitable Interaction tools at this initial state are Translate, Rotate and/or Scale.

g. Chose the level of flexibility of the model adaptation. This is done by moving the **Model flexibility** slider. With a more Rigid model adaptation, the model will stay closer to the typical model organ. With a more Elastic model adaptation, the model will be allowed to change more from the typical model organ based on the image data. Higher flexibility is recommended with high quality of the image data.

h. Click the **Start** button to start the model adaptation. This will start an adaptation of the Bladder contour to the current image data set. The algorithm uses a fixed number of iterations; the number can be changed by clicking the arrow below the **Start** button, and selecting the desired number from the menu.

   The model adaptation can be stopped by clicking the **Stop** button.

i. If the model is not good enough;

   I. Press the **Start** button again, several iterations may be needed.

   II. If pressing the **Play** button has no more effect, use the **Interaction tools**.

   III. The **Play** button may be pressed again after using the Interaction tools, for example in order to adapt the model to added hint contours.

j. When satisfied with the Bladder ROI, turn to the Prostate ROI.

2. Select the **Prostate**.

   a. Since the Bladder and Prostate are so close, the information of the Bladder ROI contour will be used to put the Prostate close to the already existing Bladder. This is only true if a Bladder ROI exists and has been adapted.

   b. Repeat the procedure from the Bladder adaptation.

   c. Next ROI to be adapted is the Rectum. The Rectum is difficult to adapt and needs more user interaction. It is also sensitive to the initial state.

3. Select the **Rectum**.

   a. Repeat the adaptation procedure from the former organs. When marking the Select ring under Image region, it is often wise to use the part of the Rectum towards the feet of the patient. In this area there is a sharper edge between Rectum and the surrounding tissue. In reality, not all of the tissue that is located inside the edge is actually part of the Rectum and the adaptation algorithm will take this into account but this edge can still be used.

   b. With the Rectum, some user interaction will usually be needed. In the part of the Rectum closest to the patient's feet, the model will not push the contour all the way out to the edge. This is correct (see previous step).

   c. The user will often have to model the Rectum somewhat manually at the end, using for example the Deform Interaction tool.

d. The last ROIs to be adapted are the Left and Right Femoral Heads. The following apply to both of them. Note that left and right refers to the patient's left and right.

4. Select the **Femoral Head Right/Left**.

   a. For Femoral Heads, **Select Image Region** is usually not needed.

   b. The Femoral Heads are sensitive to the initial conditions. It is often useful to use the **Translate**, **Rotate** and/or **Deform Interaction** tools to better match the contour with the current image data before clicking the **Play** button.

   c. Adapt the Femoral Heads model in the same way as the other organs.

5.3.11 The MBS Model Manager

The MBS Model manager lists all models in the database, both system default models and user-defined models.

Select **New ROI geometry: MBS: MBS model management** to open the MBS Model Management dialog.

The list displays the following model properties: **Color**, **Name**, **Case**, **Structure**, **Alignment**, **Gender**, **Shape stats** (Describes whether the model has shape statistics defined. A model without shape statistics will have limited adaptation possibilities.) The **User defined** property states if the model is user defined or not. Only user-defined models can be added, edited and deleted.

The list can be sorted by clicking the desired column header.

Filter the list by using the checkboxes **System** or **User defined**. It is also possible to enter text in the **Search** field.

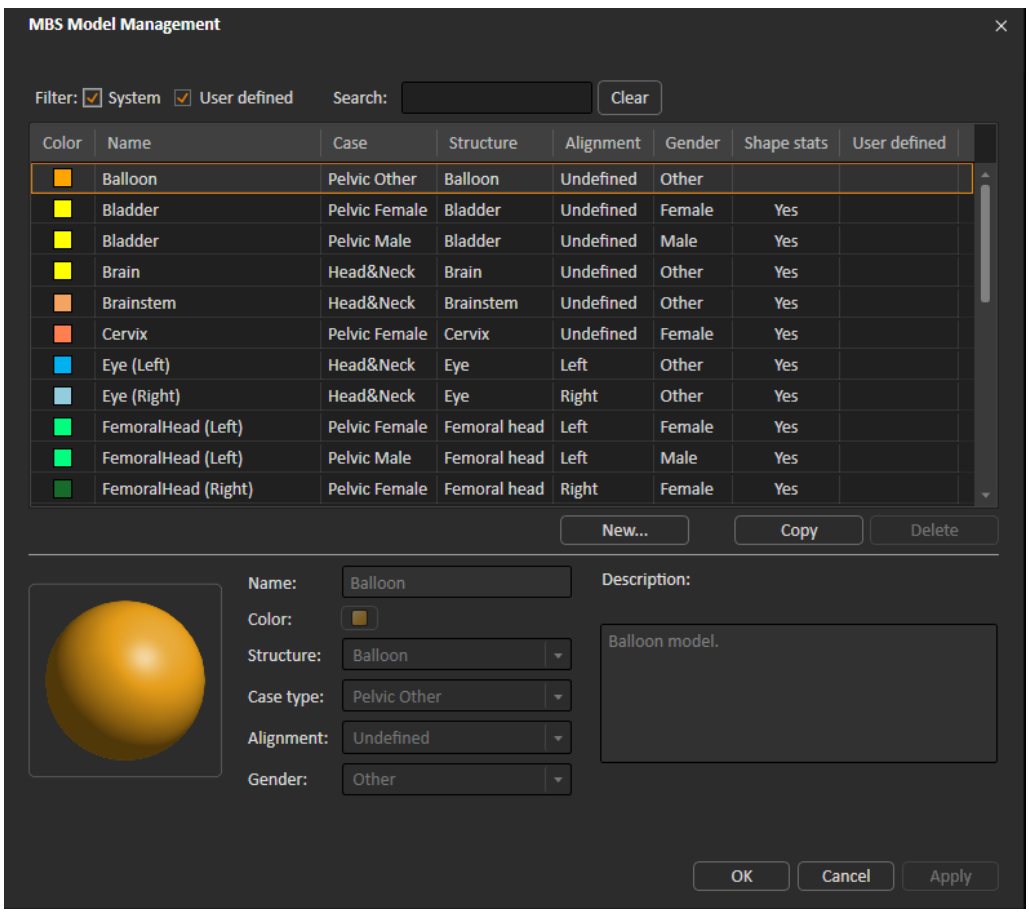
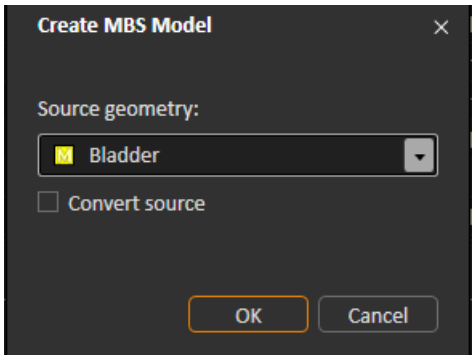


Figure 128. The MBS Model Management dialog.

Add a new MBS model to the database

To add a new model to the database:

1. Click the **New...** button. This opens the Create MBS Model dialog.



2. Select **Source geometry**.
3. Optionally, select to convert the source geometry to an MBS mesh representation by checking the **Convert source** checkbox.
4. Click **OK**. The new model will be displayed in the list and can be edited.
5. Edit the model parameters as desired.

Add a new MBS model based on an existing model

To create a new model based on an existing model:

1. Select a model in the list that the new model will be based on. (System default or user-defined).
2. Click the **Copy** button. The new model will be displayed in the list.
3. Edit the model parameters as desired.

Specify automatic adaptation settings for a user-defined model

When an ROI geometry based on a user-defined model has been created and adapted with manual adaptation settings (specified with the select image region tool), it is possible to save these settings to the model:

1. Select the model to update in the list.

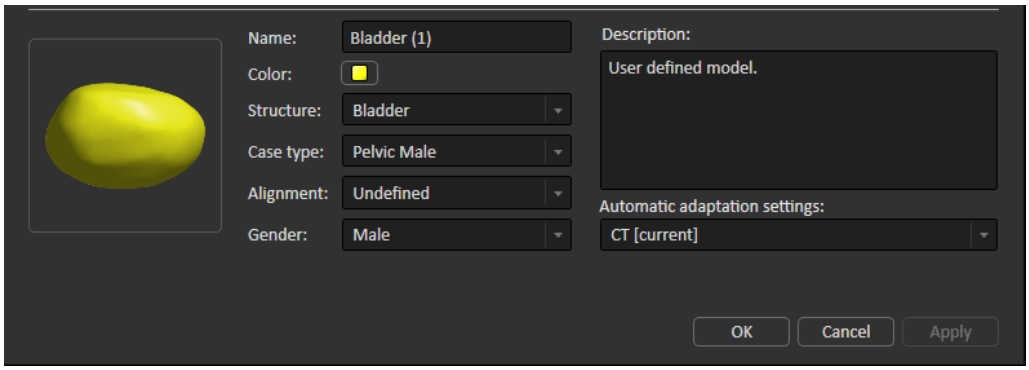


Figure 129. The MBS Model Management dialog for a user-defined model.

2. Select the desired **Automatic adaptation settings**.
3. Click **OK** and then **Save**.

Delete a user-defined model

To delete a user-defined MBS model, click the **Delete** button.

5.3.12 MBS - requirements, guidelines and facts

Image data

There are some basic requirements on the image scanning protocol:

- The selected organs must be partially included in the image set
- For automatic initialization, the femoral heads must be visible (for pelvic cases)

  Note: *Automatic initialization is not supported for all models and patient positions yet.*

- It is recommended that the slice distance is ≤ 3mm
- Imaging artifacts will decrease the performance of the automatic adaptation.

Using the deformation tool

Remember that the model adaptation is done in 3D. Sometimes it may look like there is a large error when looking at 2D-slices which is actually a very small discrepancy when considering the 3D-geometry. Consider this when using the deformation tool. Use the middle mouse button to navigate to the problem area and apply the tool in the most suitable view. Concrete example: In the transversal view, sometimes it looks like there is a large error at the boundary between bladder and prostate. If the Deformation tool is used in this view, it may be really hard to achieve what is desired. However, this is often due to the model intersecting the view plane at a very small angle. By pressing the middle mouse button at the problem area and then deforming from sagittal and coronal views a better understanding of the geometry is achieved and then often things look much better.

Using hint contours

If a hint contour is drawn far away from the model it will require much iteration before the model is attracted to the contour. If this is the case, use the deformation tool to bring the model closer to the contour before clicking the **Play** button.

Model information

All models have been generated from contour sets where the patient has been scanned Head First Supine (HFS). The pelvic male models are based on ~30 contour sets and the pelvic female models are based on ~100 contour sets. The model flexibility slider in the GUI can be used to make the model adaptation more rigid or more flexible. The more flexible, the more the adaptation relies on the extracted feature points in the image data. A flexibility of 0 will give a completely rigid adaptation.

5.3.13 Defining POIs

The POI tools are located under the **POI Tools** tab in the toolbar.

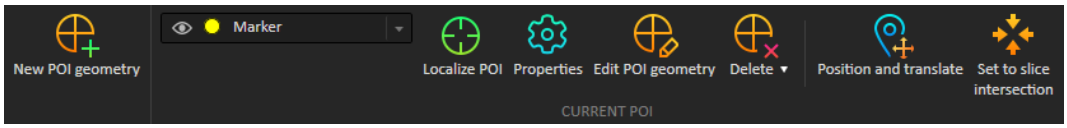
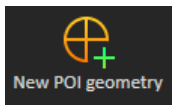


Figure 130. The POI tools.

Creating a POI

To create a POI:

1. Click the **New POI geometry** button.



This opens the New POI geometry dialog.

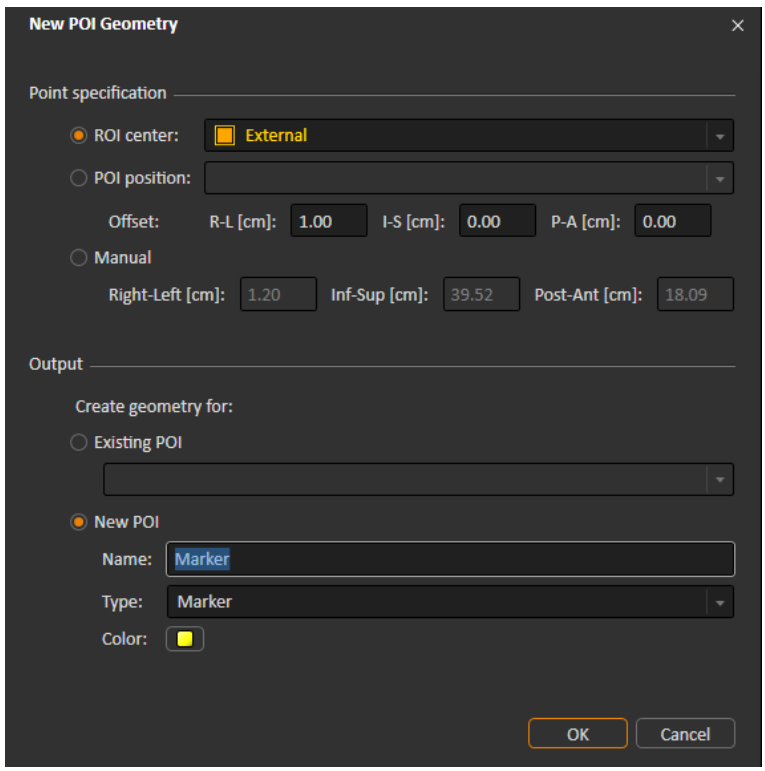


Figure 131. The New POI geometry dialog.

2. Select **Point specification**. The POI position can be defined either manually or by copying the center position of an ROI. The position defaults to the intersection of the transversal, sagittal, and coronal views.
3. Select to create geometry for an **Existing POI** or for a **New POI**.
4. Click **OK**. The new POI is created.
5. To create a POI geometry in a second, registered dataset, use the same dialog, but choose **Create geometry for existing POI**. A POI without geometry in the current structure set is indicated with a half-filled circle in the list.

Localization point for patient setup

To create a localization point for patient setup, create a point of type Localization point for example by placing the cross-hair so that it coincides with the markers visible in the CT and selecting **New POI**.

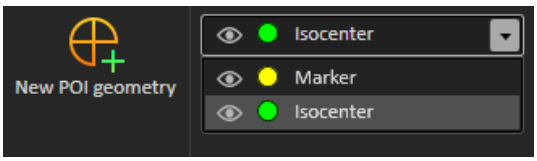


Figure 132. The POI list where two POIs are present. p1 is a localization point which is indicated with a golden frame and golden text.

As for other POIs, the localization point can have different positions in different image sets, but only one localization point can be created in each image set. When creating a localization point and more than one data set is present, keep in mind to create the localization point in the same data set as the plan should be created in.

Note: *To create a localization point in a phantom which has already been imported to RayStation is not possible. POIs in phantoms must be created in the image set prior to import.*

The POI tools

Below is a description of the POI tools.

The **Localize POI** button re-positions all patient views to the POI position.

The **Properties** button opens the POI properties dialog.

The **Delete POI** button holds options to delete either the entire POI or the current POI geometry.

The **Position and translate** button. Click anywhere in a 2D view to position the current POI, or click the current POI in the view and drag it to the desired position.

The **Set to slice intersection** button can be used to move the current POI to the intersection of the transversal, sagittal, and coronal views.

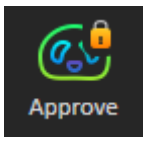
5.3.14 Approval of structures

The **Approval** tab in the toolbar displays approval information for the current structure set. For structure sets with approved structures, the approver's name as well as the date and time of approval are displayed.

Figure 133. The Structure set approval information and buttons toolbar.

To approve the structure set:

1. Click the **Approve** button.

   This opens the **Structure Set Approval Authentication** dialog.

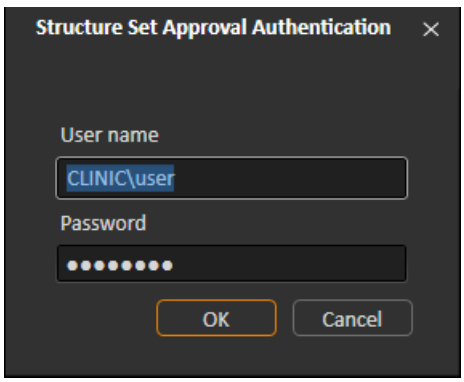
   

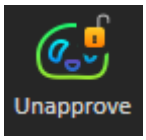
   Figure 134. The **Structure Set Approval Authentication** dialog.

2. Type **User name** and **Password**.

   Note: *The user has to be a member of the Plan approval user group to be able to approve the structure set.*

3. Click **OK**. All existing structures will be approved and become read-only.

To unapprove the structure set, click the **Unapprove** button.



If the patient case has multiple structure sets, it is possible to approve some of them and continue to work on the remaining structure sets that are not yet approved. It is for example possible to add new ROIs. It is not possible to change the external ROI or to edit or delete ROIs that have approved geometries.

5.3.15 Image fusion display options

The **Fusion** tab in the toolbar contains options for fusion display. The fusion settings can also be accessed from the **Visualization** tab (described in *section 3.4.5 The Visualization tab on page 62*).

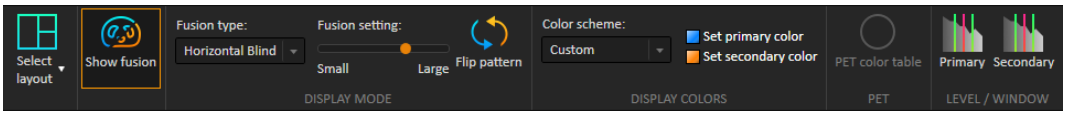


Figure 135. The Image fusion display options.

There are several display modes and color schemes to choose from; Additive Blend, Overlay, Checkers, Horizontal Blinds and Vertical Blinds. For example of fusion views, see *section 5.2.5 Image fusion on page 184*.

The fusion image set is selected in the Image set library at the bottom of the workspace.

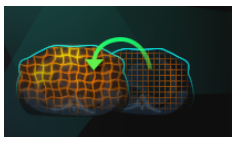
5.4 THE DEFORMABLE REGISTRATION MODULE

The Deformable Registration module consists of tools for creating, reviewing and evaluating deformable registrations between image sets. There are two deformable registration algorithms provided as described in *Deformable registration algorithms on page 254*. The result of a deformable registration algorithm is a displacement field from the reference image set to the target image set. The displacement field can be used to deform dose defined on the target image set to the reference image set geometry as well as mapping anatomical structures (ROIs and POIs) between the image sets.

The Deformable Registration module includes an approval mechanism for approval of deformable registrations. Only approved deformable registrations can be used in dose accumulation calculations in the Dose Tracking module and when creating an adapted plan in the Adaptive Replanning module. For each pair of reference and target image set, only one deformable registration can be set as approved.

In the Plan Evaluation module, it is possible to deform dose using any existing deformable registration but approved registrations are marked out and displayed as default choice.

Deformable registration can only be performed on image sets that already have a rigid registration.



In this section

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5.4.9	Tools for evaluating the result of a deformable registration	p. 271
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5.4.11	Controlling ROIs - Create meshes from contoured ROI(s)	p. 281
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5.4.1 Introduction to deformable registration

Deformable registration can be used in several planning situations in RayStation:

- For structure definition i.e., mapping structures from one image set to another
- For dose tracking purposes to perform dose deformation and dose accumulation
- For deforming dose for various purposes in the Plan Evaluation module

Deformable registration algorithms

There are two algorithms in RayStation that can be used to perform the deformable registration:

- **Hybrid intensity and structure based deformable registration**: Can be used to map structures and deform dose.
  - The algorithm is based on image intensity information and/or anatomical information.
  - Imaging modalities that can be used: CT-CT, CT-CBCT, CT-PET CT and CT-MRI.

  Reference

  O. Weistrand and S. Svensson, "The ANACONDA algorithm for deformable registration in radiotherapy", Medical Physics Vol. 42, No. 1, pp. 40-53, 2015.
- **Biomechanical model-based deformable registration**: Use cases include lung and cervix patients for deforming dose.
  - This approach uses a point-to-point correspondence of mesh ROIs. The biomechanical model can take the linear elastic material properties of an ROI and the sliding surfaces of organs into account.
  - No image intensity information is used and the algorithm can therefore be used with any imaging modality.

  References

  K. K. Brock et al., "Accuracy of Finite Element Model-Based Multi-Organ Deformable Image Registration", Medical Physics Vol. 32, No. 6, pp. 1647-1659, 2005.

  M. Velec et al., "Evaluation of Biomechanical Deformable Image Registration (DIR) in a Commercial Radiation Therapy Planning System", Int. J. Radiation Oncology Biol.Physics Vol. 93, No. 3, pp. 215-216, 2015.

Rigid registration

Prior to performing the deformable registration, a rigid registration must exist between the image sets. The image sets to be registered should have certain ROIs present in order to improve performance of the deformable registration.

Rigid registration requirements:

- For mapping ROIs or for deforming dose in the Plan Evaluation module, the rigid registration can be performed in the Image Registration module. For more information, see *section 5.2 The Image Registration module on page 173*.
- For dose tracking, a rigid registration via treatment position alignment and a rigid transform without focus on bone should be performed. For more information, see *section 11.2 Dose Tracking on page 868*.

ROIs to be included in the deformable registration

External ROI
An External ROI likely already exists from the rigid registration. If not, create the external ROI on both image sets.

ROIs for mapping of structures
Segment any relevant anatomy on at least one image set for mapping to the other image set after the deformation is completed.

Create External ROI for CBCT image sets intended for dose tracking
If the CBCT has a limited field-of-view, use the Limited FOV tools in the Structure Definition module to create an External ROI.

Controlling ROIs
In some hybrid deformable registration cases, preparation of other ROIs as controlling or focus structures should be made before creating the registration. Consider if this is a necessary step for your case. See *section 5.4.4 Hybrid deformable registration on page 261* for more information.

For biomechanical registrations, controlling ROIs must be created. Note that the controlling ROIs should be a mesh or MBS ROI. If it is of representation Contour, it should be converted to a mesh with the Create controlling ROIs function in Structure Definition or Deformable Registration (see section 5.4.3)

5.4.2 Workspace layouts

The Deformable Registration module has three different workspace layouts:

- Create and evaluate
- Side by side evaluation
- Image comparison

The workspace layout is selected via the buttons in the workspace layout toolbar.

The Create and evaluate workspace

The **Create and evaluate** workspace consists of three patient views showing the displacement field or the image fusion in various ways and an ROI/POI statistics component. The workspace also contains toolbars with buttons for creating, deleting, and approving a deformable registration as well as buttons for creating controlling ROIs and mapping structures.

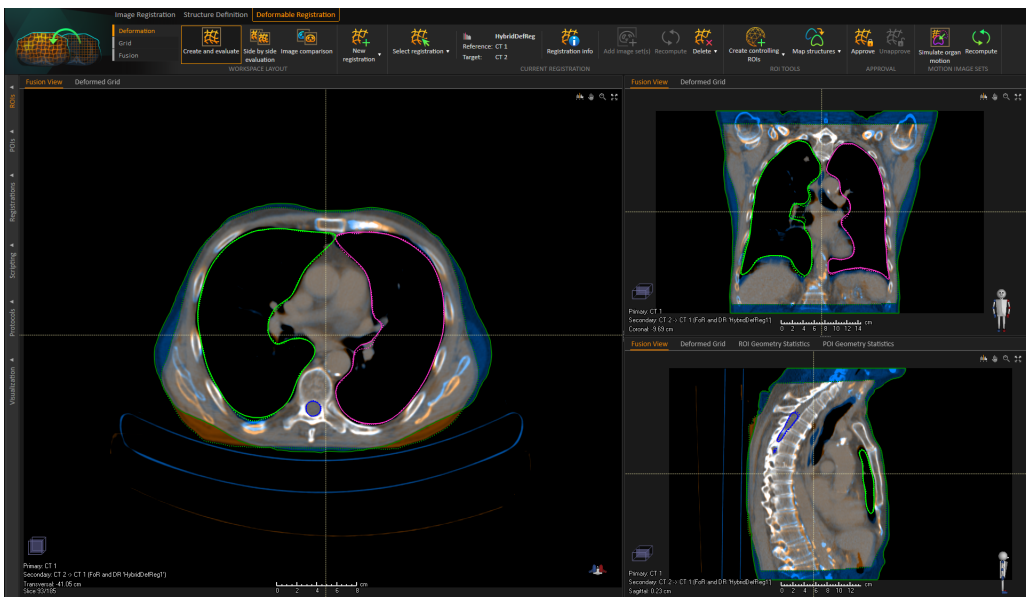


Figure 136. The Create and evaluate workspace layout of the Deformable Registration module.

The Side by side evaluation workspace

The **Side by side evaluation** workspace consists of six patient views showing the deformable registration either as deformed grid view or as fusion view for the current registration and for the secondary registration, which is the registration selected for comparison. The secondary registration can be any rigid or deformable registrations that have the same reference and target image sets as the current deformable registration. Note that for rigid registrations no deformed grid is displayed.

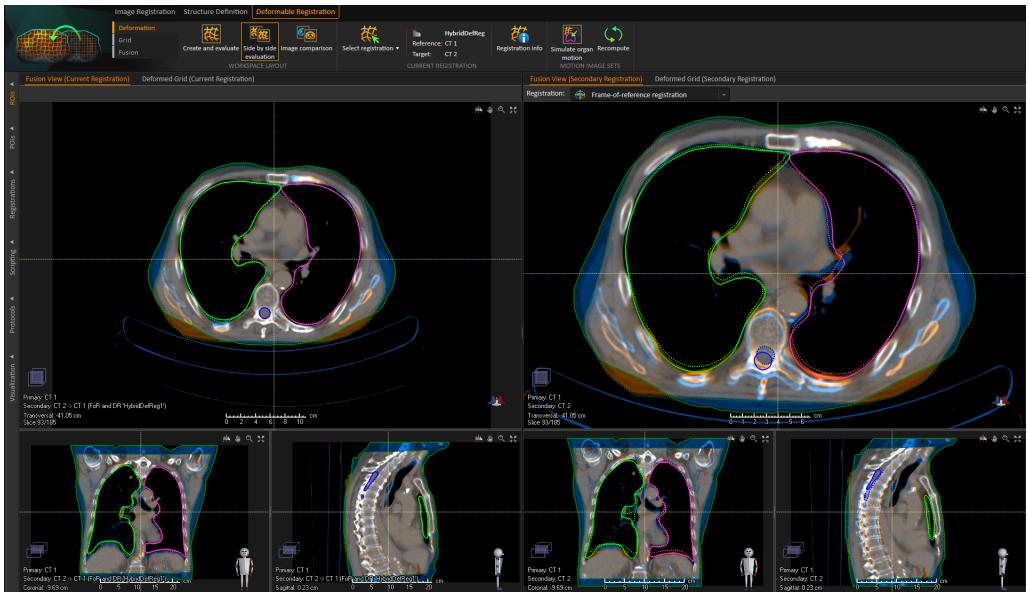


Figure 137. The Side by side evaluation workspace layout of the Deformable Registration module.

The Image comparison workspace

The Image comparison workspace consists of two 2D patient views, one view displaying the reference image set and the other view displaying the target image set (deformed and undeformed) and the corresponding evaluation points. The Reference view shows a color wash of the magnitude of the displacement field in the current slice. When an evaluation point is marked in the reference image set, the corresponding point will be displayed in the target image set according to the selected deformable registration. For more information about point evaluation, see *Point evaluation on page 272*.

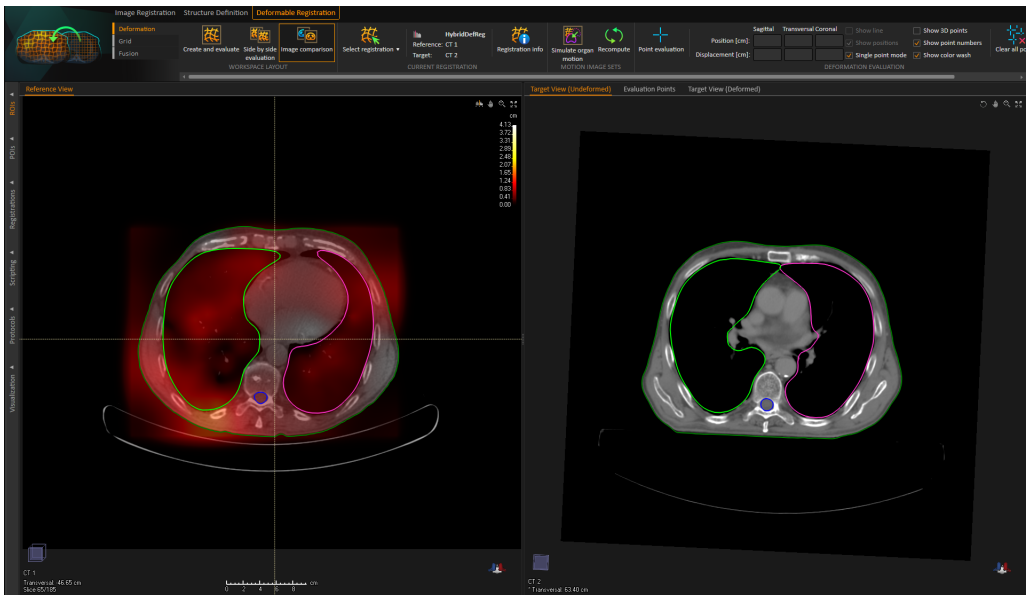


Figure 138. The Image comparison workspace layout of the Deformable Registration module.

5.4.3 Deformable registration workflows

This section contains two suggested workflows for deformable registrations, one for a hybrid intensity and structure based deformable registration and one for a biomechanical model-based deformable registration.

Hybrid intensity and structure based deformable registration workflow

This workflow can be used to map structures and deform dose for example for dose tracking purposes. This is a suggested workflow using the hybrid intensity and structure based deformable registration:

1. **Create a registration without controlling ROIs.** See *section 5.4.4 Hybrid deformable registration on page 261* for more information.
2. **Map ROIs/POIs to the image set without structures.** See *section 5.4.12 Map structures on page 283* for more information.
3. **Verify the mapped ROIs and edit as needed.** This should be done in the Structure Definition module. See *section 5.3.3 The ROI modification tools on page 197* for more information.
4. If dose deformation and dose tracking will be performed, the user should also:

   Validate the registration. There are several ways to validate the registration, including verification of the mapped structures. See *section 5.4.9 Tools for evaluating the result of a deformable registration on page 271* for more information.
5. **If the deformable registration is not satisfactory, another registration should be created.** Repeat step 1 to 4 and include ROIs as controlling or focus ROIs to improve the deformation.

   Validate the results of the second registration.
6. **Approve the registration.** This step is required for dose tracking cases. For more information, see *section 5.4.13 Approval of a deformable registration on page 287*.

Biomechanical model-based deformable registration workflow

This workflow can be used for deforming dose, use cases include lung and cervix patients for which the sliding interfaces can be useful. This is a suggested workflow using the biomechanical model-based deformable registration:

1. **Create controlling ROIs.** All biomechanical registrations must have controlling ROIs.

   To use an ROI as a controlling structure, it should be a mesh structure. The user can convert an ROI with contour shape to a new ROI with triangle mesh shape. The new ROI can then be used as a controlling ROI. An MBS ROI is already represented as a mesh shape (MBS mesh). For more information, see *section 5.4.11 Controlling ROIs - Create meshes from contoured ROI(s) on page 281*.

   If the External ROI is intended as a controlling ROI, an external MBS ROI has to be created. For more information, see *section 5.4.10 Controlling ROIs - Create External MBS ROIs on page 277*.
2. **Create the registration.** For more information, see *section 5.4.5 Biomechanical deformable registration on page 264*.

3. **Validate the registration.** There are several ways to validate the registration, including verification of the mapped structures. For more information, see *section 5.4.9 Tools for evaluating the result of a deformable registration on page 271*.

5.4.4 Hybrid deformable registration

Hybrid deformable registration uses a combination of image intensity information and anatomical information (ROIs and POIs). The problem is formulated as a non-linear optimization problem where the objective function is a combination of an image similarity term, grid regularization terms, and anatomical penalty terms.

Both ROIs and POIs can be used as controlling structures for driving the deformation. ROIs can also be used to define focus regions for the deformation. Controlling ROIs can be defined by contours or automatically generated using, e.g., MBS or atlas-based segmentation. The combination of image information and anatomical information provides a way to maintain the integrity of anatomical structures even in areas where the image information is less reliable.

When using controlling ROIs, it is important that they are well defined. Contours shall be consistent between slices and no ROIs shall overlap. Feeding the algorithm with conflicting constraints may result in a deformation field of low quality.

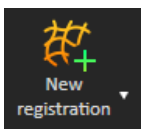
If the external ROI has the same extent in both the reference and target image set it can be used as controlling ROI, otherwise it is suggested to use an External MBS, see *section 5.4.10 Controlling ROIs - Create External MBS ROIs on page 277*.

Supported image modalities are currently CT, CBCT and MR.

The algorithm is developed to take advantage of GPU acceleration and multi-core processors. In order to configure GPU acceleration, see section *section D.4.2 Use GPU for accelerated computations on page 964*.

Perform hybrid deformable registration

1. Click the **New registration** button and select **Hybrid intensity and structure based...**.

   This opens the Create Hybrid Deformable Registrations dialog.

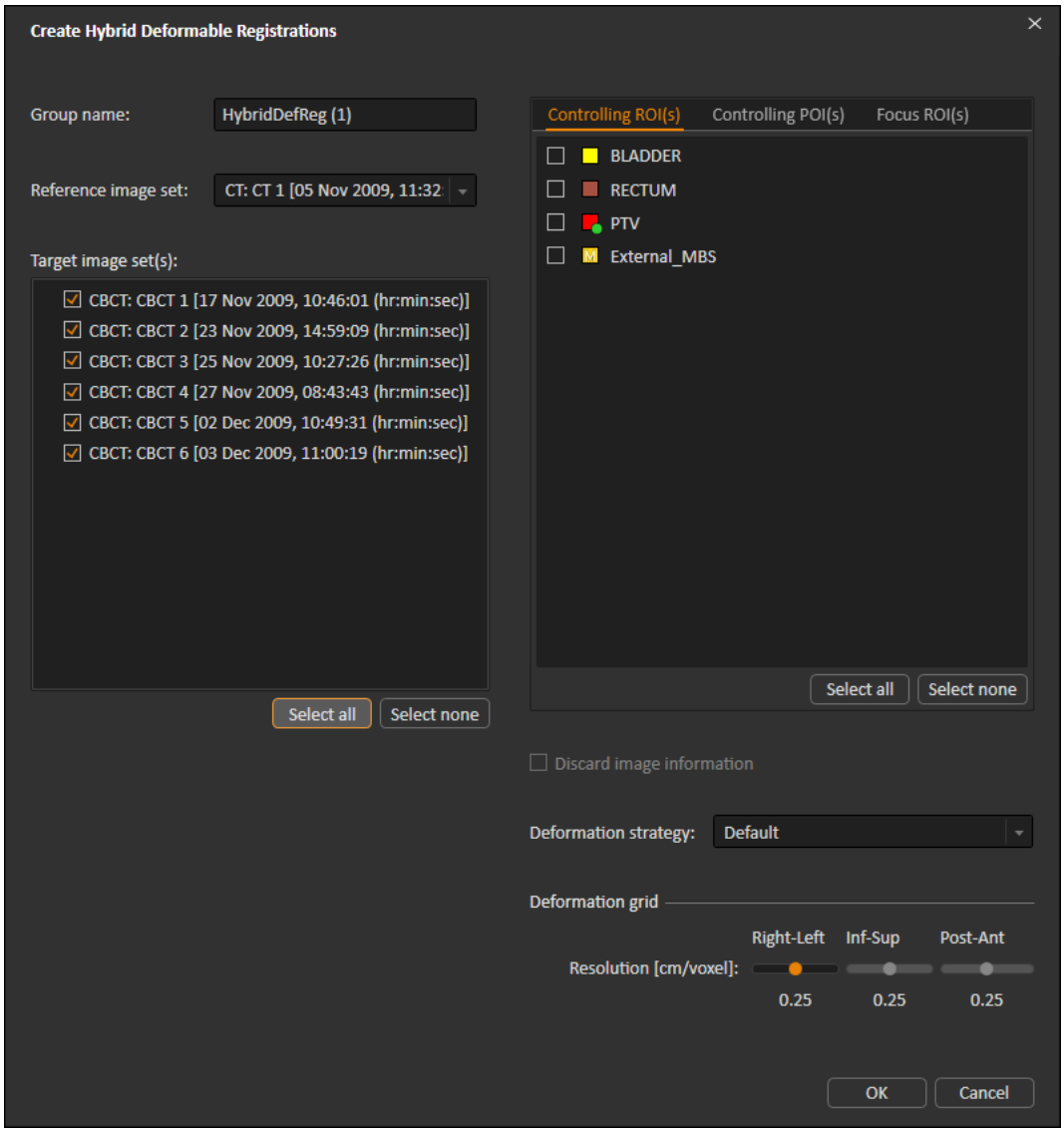
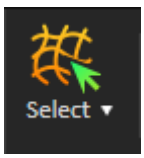


Figure 139. The Create Hybrid Deformable Registrations dialog.

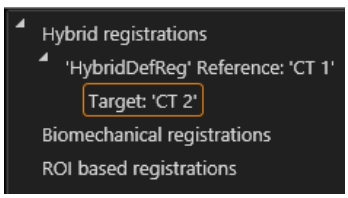
2. Select a **Reference image set**.
3. Select **Target image set(s)** by checking the corresponding checkbox. If several image sets are selected, they will belong to the same group of deformable registrations. The available image sets are the ones that are already registered to the reference image set via rigid registration or isocenter registration.

4. If necessary, select **Controlling ROI(s)**, **Controlling POI(s)** and/or **Focus ROIs** from the lists by checking the corresponding checkboxes or click the **Select all** button. The **Controlling ROIs** and **Controlling POIs** tabs list structures that are present on both image sets. The **Focus ROIs** tab will list all available ROIs on the reference image set.
5. If controlling ROIs or POIs are used, it is possible to check **Discard image information** in order to disregard image intensities during computation. This can be useful for multi-modality registrations.

   Note: *Discarding image information is highly recommended when performing a hybrid based deformable registration between a CT image set and an MR image set.*
6. If only the interior of the lungs should be deformed, select the **Deformation strategy** "Internal lung" and the lungs as controlling ROIs. Otherwise select "Default".
7. Select **Resolution**. It is recommended to use the default grid resolution of 0.25 cm/voxel.
8. Click **OK**. The deformation process starts. When the deformation is completed, the registration will be visible from **Select registration** and in the **Registration** tab of the tool panel.
9. Click the **Select registration** button and select the registration from the list.



The registration is displayed in the views and can be evaluated using the evaluation tools. See *section 5.4.9 Tools for evaluating the result of a deformable registration on page 271*.



10. Click the **Registration info** button to display the **Deformable Registration Info** dialog.

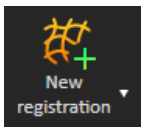
5.4.5 Biomechanical deformable registration

The biomechanical deformable registration computes the displacement field by solving a linear elasticity problem using the finite element method (FEM). The problem is set up by controlling ROIs represented by meshes with vertex-to-vertex correspondence in the reference and target image set. Note that the biomechanical deformable registration does not use image gray scale information. The meshes can be generated with model-based segmentation or with dedicated tools for constructing meshes from contours, see *section 5.4.11 Controlling ROIs - Create meshes from contoured ROI(s) on page 281*.

For controlling ROIs representing interior structures, the interface between the structure and the surrounding tissue can be modeled as either fixed or sliding, e.g., the sliding interface between the lungs and the chest wall.

Perform ROI based deformable registration

1. Click the **New registration** button and select **Biomechanical model based (MORFEUS)...** in order to open the Create Biomechanical Deformable Registrations dialog.



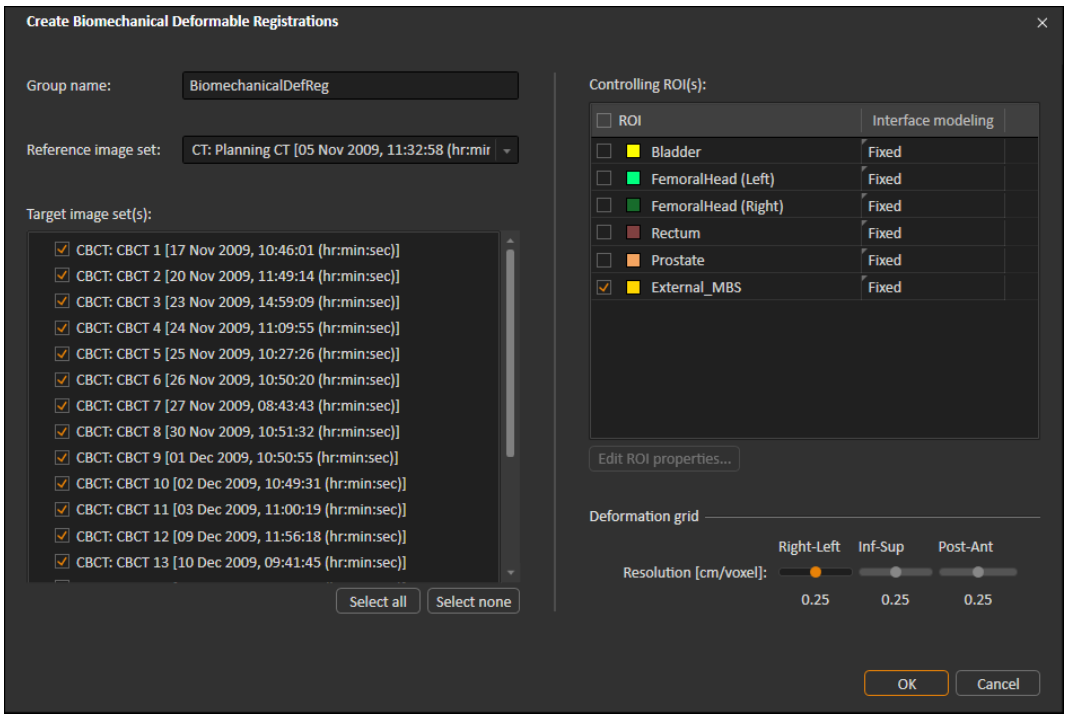


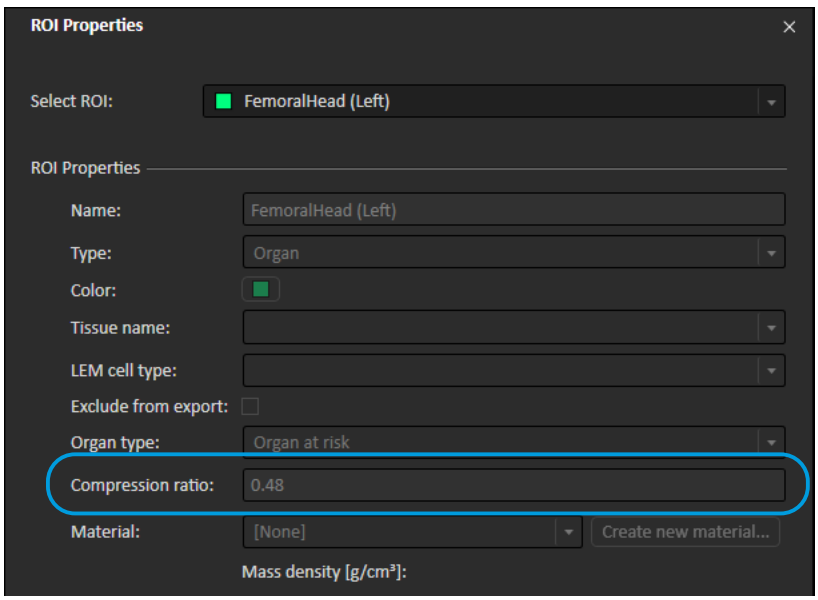
Figure 140. The Create Biomechanical Deformable Registrations dialog.

2. Select a **Reference image set**.
3. Enter a new name in the **Name** field or use the default name.
4. Select **Target image set(s)** by checking the corresponding checkbox. The available image sets are the ones that are already registered to the reference image set via rigid registration or isocenter registration.
5. Select **Controlling ROI(s)** from the lists by checking the corresponding checkboxes or click the **Select all** button.

   For each ROI, the modeling of the interface between the ROI and the surrounding tissue can be specified.

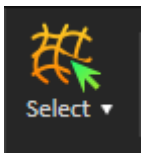
   "Fixed" means that the deformation will perform vertex-to-vertex mapping, i.e., the mesh vertices of the controlling ROI in the reference image set will be mapped to the corresponding mesh vertices in the target image set. The effect of fixed vertex mapping is that the deformation field will model a continuous deformation over the ROI surface.

   "Sliding" means that the reference mesh vertices will map to the mesh surface in the target image set without having to match the target vertices exactly. The effect of sliding vertex mapping is that the deformation field will model a discontinuous deformation over the ROI surface, such as that which occurs between the lung and the chest wall.
6. Optionally, click **Edit ROI properties...** in order to edit the **Compression ratio** for the controlling ROIs (the compression ratio is the Poisson's ratio in linear elasticity).



7. Specify **Deformation grid** resolution. The extent of the grid is automatically set to cover all controlling ROIs.

8. Click **OK**. The deformation process starts.
9. Click the **Select registration** button and select the registration from the list.



The registration opens and can be evaluated using the evaluation tools. See *section 5.4.9 Tools for evaluating the result of a deformable registration on page 271*.

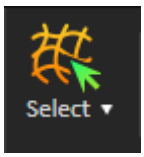
10. Click the **Registration info** button to display the deformable registration details.

5.4.6 Add image sets to a deformable registration group

Once a deformable registration has been calculated, the user can choose to create deformable registrations for other target image sets using the same settings and conditions (e.g., selection of controlling ROIs). This may be of interest for e.g., adding a new CBCT image set from a patient's course of treatment to a group containing the previous CBCT fractions for dose tracking.

To add image sets to a deformable registrations group:

1. Click the **Select registration** button.



2. Select a registration group from the list.

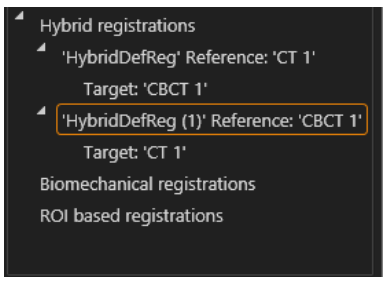
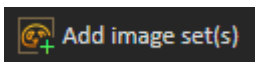


Figure 141. The list of selectable registrations, with a registration group marked.

3. Click the **Add image set(s)** button.



This opens the Add image set(s) to a deformable registration group dialog.

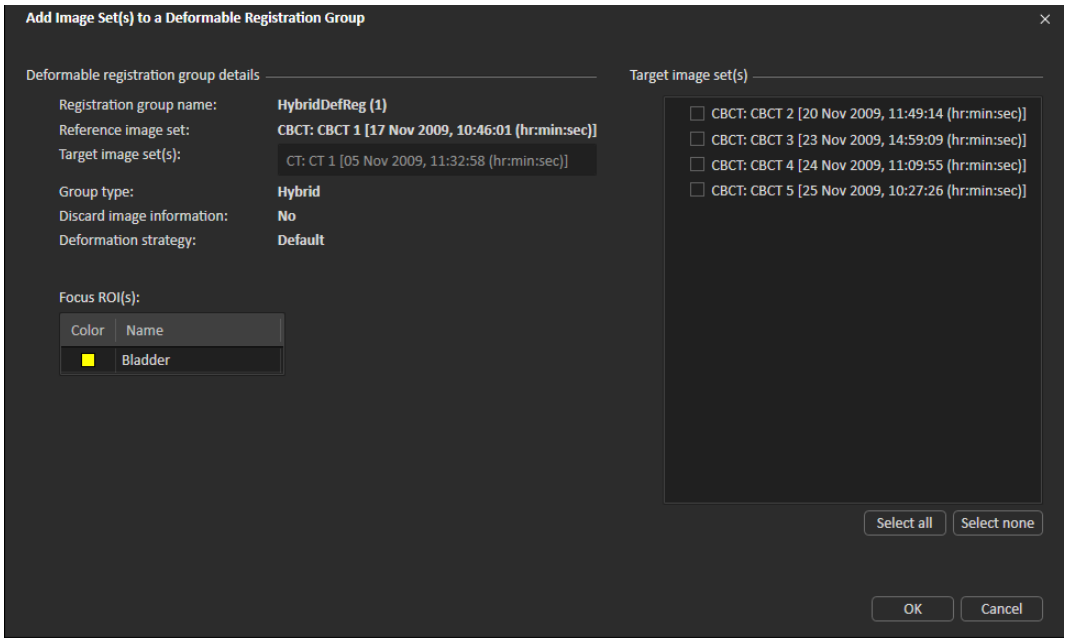


Figure 142. The Add image set(s) to a deformable registration group dialog.

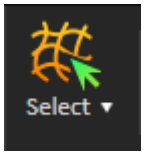
4. Click **OK**. The deformation process starts.

5.4.7 Recompute deformable registrations

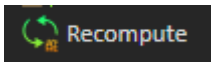
Deformable registrations will be invalidated if any of the controlling ROIs or POIs are modified. The registrations can be recomputed using the Recompute button in the tool panel.

To recompute a deformable registration or a group of registrations:

1. Click the **Select registration** button and select a registration or a group of registrations from the list.



2. Click the **Recompute** button.



This opens the Recompute Hybrid Deformable Registration(s) dialog.

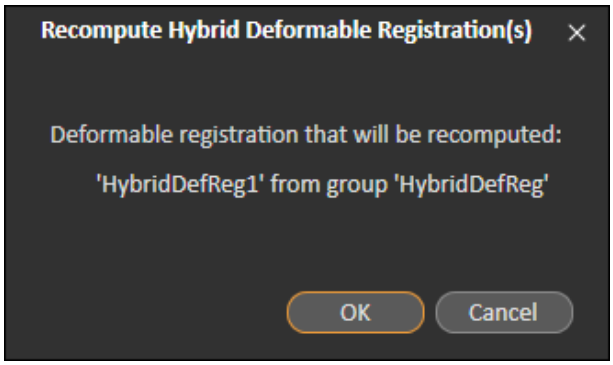


Figure 143. The Recompute Hybrid Deformable Registration(s) dialog.

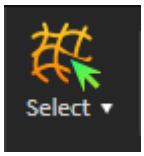
3. Click **OK**.

5.4.8 Delete registrations

Deformable registrations can be deleted from the system. It is possible to delete an individual registration as well as a group of registrations.

To delete a registration or a group of registrations:

1. Click the **Select registration** button.



2. Select a registration or a registration group from the list.

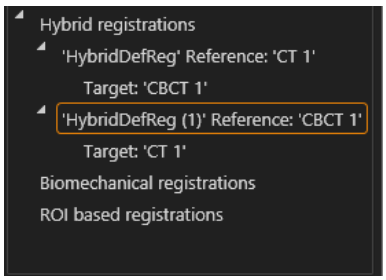
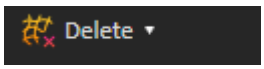


Figure 144. The list of selectable registrations, with a registration group marked.

3. Click the **Delete registration(s)** button and select **Delete current** (Delete all will delete all registrations in the list).



This opens the Delete Deformable Registration dialog.

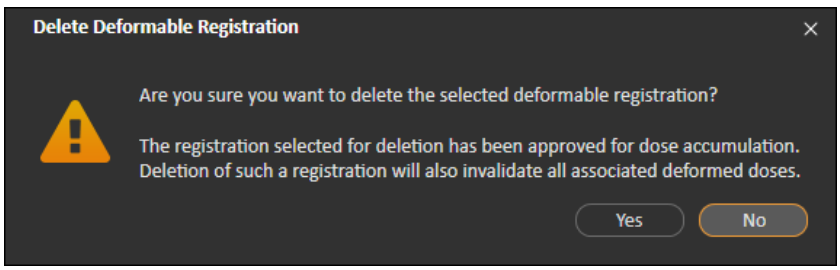

Delete Deformable Registration
Are you sure you want to delete the selected deformable registration?
The registration selected for deletion has been approved for dose accumulation.
Deletion of such a registration will also invalidate all associated deformed doses.
Yes
No

Figure 145. The Delete Deformable Registration dialog.

4. Click **Yes**. The selected registration or registration group will be deleted.

5.4.9 Tools for evaluating the result of a deformable registration

Once a deformable registration has been created, several tools are provided that can be used to evaluate the registration both visually and statistically.

ROI / POI geometry statistics tabs

The user can display ROI/POI geometry statistics for two image sets (reference and target). Part of the measurements are based on the geometries in the individual images (e.g., ROI volume and POI position) and part of how they are related based on the rigid registration (e.g., ROI translation and POI distance), where both frame-of-reference registration and, if such exists, added rigid transform are accounted for. In addition to that, if the deformable registration selected in the patient views has the same reference image set and a target image set as has been selected in the ROI/POI geometry statistics tabs, additional measurements based on the deformable registration are displayed (e.g., Dice similarity for mapped ROI geometries and target registration error for POIs). All measures are explained in detail below.

For the two selected images, the following information is listed:

ROI geometries

- **Volume:** Volume of geometry in reference image set and target image set.
- **Number of mesh points** (in geometry)
- **Centroid of mesh points** (in reference image set and target image set)
- **Translation**: Rigid registration translation between geometry in reference image set and target image set.
- **Rotation axis:** Rigid registration rotation axis between geometry in reference image set and target image set.
- **Rotation angle:** Rigid registration rotation angle between geometry in reference image set and target image set.
- **Mesh points distance:** average, standard deviation and max (Distance between a mesh point in the reference image set and corresponding mesh point in the target image set after rigid registration has been applied)
- **Mesh point difference**: Average, standard deviation and max (Difference between a mesh point in the reference image set and the corresponding mesh point in the target image set after the currently selected deformable registration has been applied.)
- **Dice similarity**: The overlap between:
  - the geometry in the reference image and the geometry in the target image after being deformed to the reference image (reference column) and

- the geometry in the target image and the geometry in the reference image after being deformed to the target image (target column) using the currently selected deformable registration. The value is between 0 to 1 with a higher value representing greater overlap.

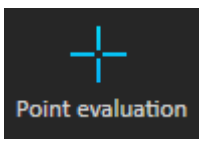
POI geometries

- **Position:** Two POI positions are shown. The first line is the POI position in the reference image set. The second line is the POI position in the target image set, rigidly transformed to the reference image set coordinate system. Note that the POI position in the target image set is transformed rigidly, as opposed to deformably.
- **Distance:** Distance between the two points in the Position column.
- **Displacement:** Deformable registration displacement at POI position in the reference image set.
- **Target registration error:** Absolute difference between distance and displacement.

Note: *The ROI columns "Mesh point difference" and "Dice similarity" and the POI columns "Displacement" and "Target registration error" are only shown if the reference image set and the target image set are the same as the currently selected deformable registration.*

Point evaluation

In the Image comparison workspace, the user can display the displacement in a single point of the reference image and also get the corresponding point in the target image (according to the selected deformable registration) marked out using the **Point evaluation** tool. The tool is enabled by selecting **Point evaluation** in the tool panel. Point evaluation can be run in single point mode or for multiple points.



In the tool panel, the position of the last marked evaluation point and the displacement for the corresponding position is shown.

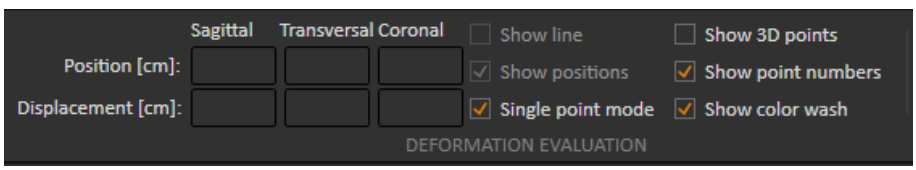


Figure 146. The deformation evaluation tool panel.

In the reference image and the target image, the points marked in the reference image are shown. The user can select to display their marking number by checking the **Show point number** checkbox in the tool panel.

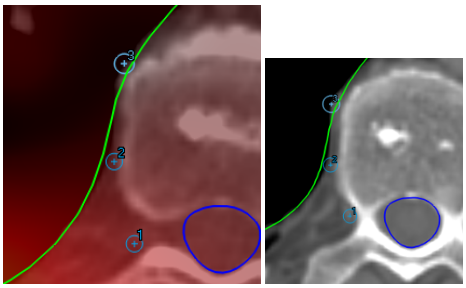


Figure 147. Point read out visualization displayed in A) the reference image and B) the target image.

Statistics for each point is displayed in the **Evaluation points** tab.

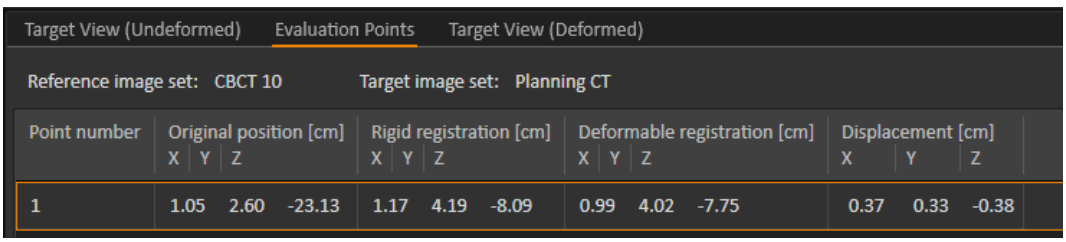
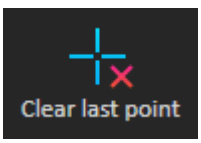


Figure 148. The **Evaluation Points** list.

The columns in the **Evaluation points** tab list the following information:

Column tab name	Description
Original position	Positions of evaluation points in the reference image set.
Rigid registration	Positions of evaluation points in the target image set with rigid registration applied.
Deformable registration	Positions of evaluation points in the target image set with deformable registration applied.
Displacement	Displacement field at evaluation point.

Clear the last point by clicking the **Clear last point** button.



Clear all points in the image by clicking the **Clear all points** button.

Visualization of the displacement field

The displacement field can be visualized as a grid, both deformed and undeformed. In the latter case, the color corresponds to the magnitude of the vector in each point. It can also be displayed as a vector field. The following visualization settings are provided for grid and vector fields:

- **Window size** controls the number of grid layers that are displayed
- **Visualization detail** controls the resolution of the grid
- **Line width** controls the width of the lines in the grid or the width of the vectors
- **Grid opacity** controls the opacity of the grid
- **Arrow size** controls the scaling factor for the vectors (if the vector field is displayed)
- The **Image set opacity** can be changed through the visualization settings

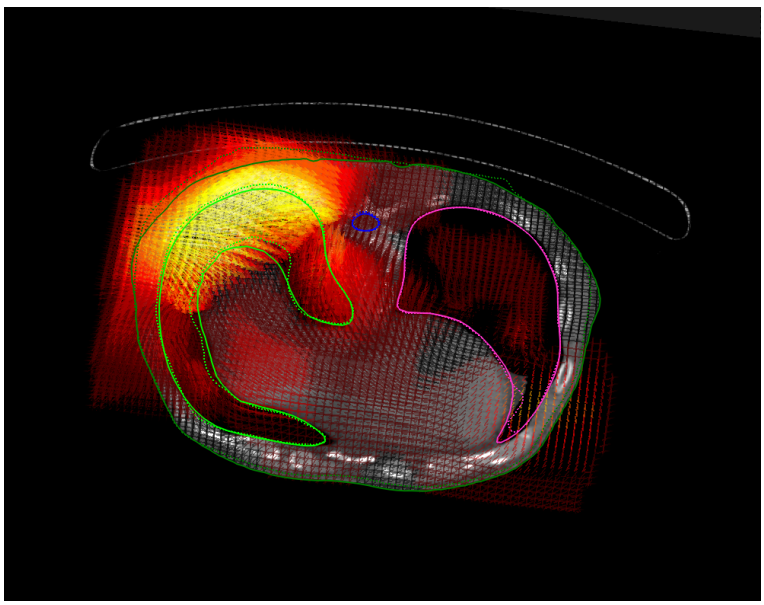


Figure 149. Visualization of the displacement field.

Displacement field color table

The color table for the displacement field can be changed through the displacement field color table available in the context menu (right mouse button click).

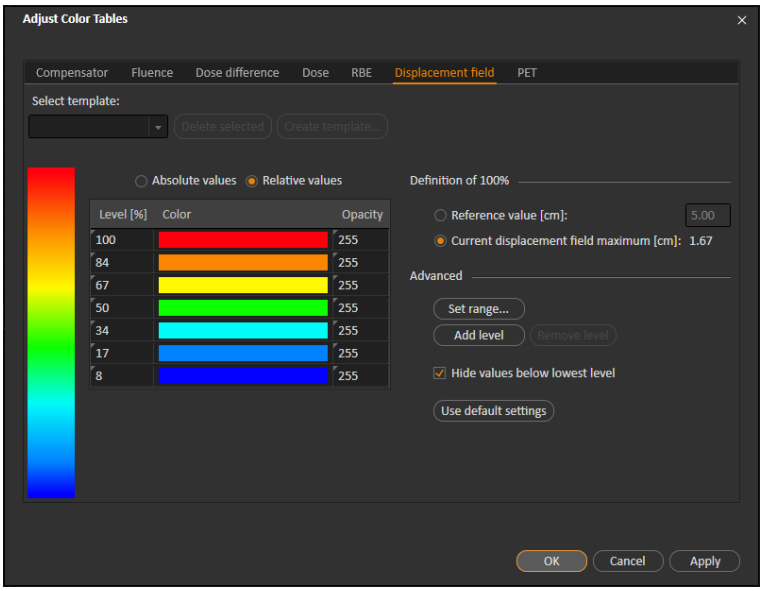
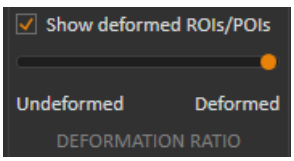


Figure 150. The displacement field color table.

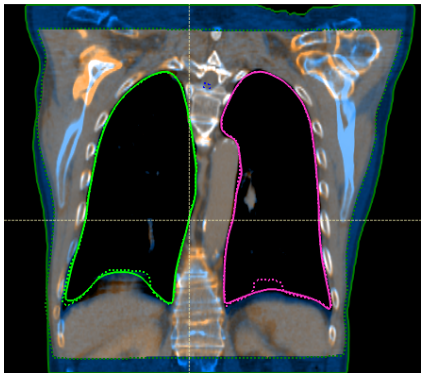
Visualization of deformed ROIs

The deformation of ROIs and POIs defined on the target image can be visualized in the fusion views and grid views. If the view mode **Show target 3D ROIs** is selected, the grid view will show deformed 3D meshes colored with the displacement field color map.

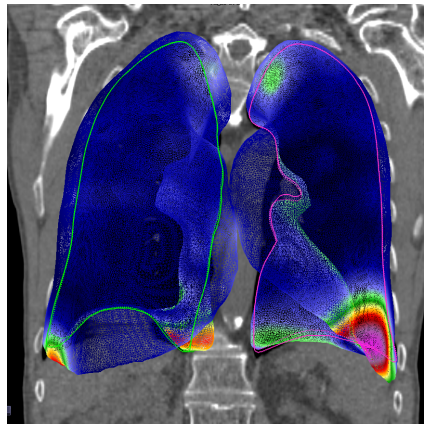
The degree of deformation can be controlled using the **Deformation ratio** slider.



Move the slider to adjust the degree of deformation.



A



B

Figure 151. Visualization of deformed structures in A) fusion views and B) grid views.

The user can select between different fusion modes in the tool panel. See *section 5.2.5 Image fusion on page 184* for more information.

Scripting

A number of scripts are available for validation of deformable registrations. They include export of the displacement field, number of inverted elements and the target registration error, among others. The scripts are available for download for all users. Ask your service representative for more information.

5.4.10 Controlling ROIs - Create External MBS ROIs

To use the external geometry as a controlling ROI in the biomechanical deformable registration, the External ROI needs to be converted to an MBS mesh. The user selects one image set which external geometry, for the selected sup-inf range, will be used as a model after converting it to an MBS mesh. The external MBS model is stored in the database and used when creating external MBS ROI geometries for other image sets. Note that this functionality is also a good option for creating a controlling ROI suitable for hybrid deformable registration as it ensures that the same sup-inf range is covered in all images. The model can also be used for the Generate external ROI on limited FOV data method, see *Generate external ROI on limited FOV data on page 219*.

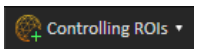
There are two possibilities:

- No external MBS model exists in the database.
- An external MBS model exists and has been used to create external MBS ROI with geometry in at least the model image set.

Create External MBS ROI when no external MBS model exists in the database

To create external MBS ROIs:

1. Click the **Create controlling ROIs** button and select **Create external MBS ROIs...**.

   This opens the Create External MBS ROIs dialog.

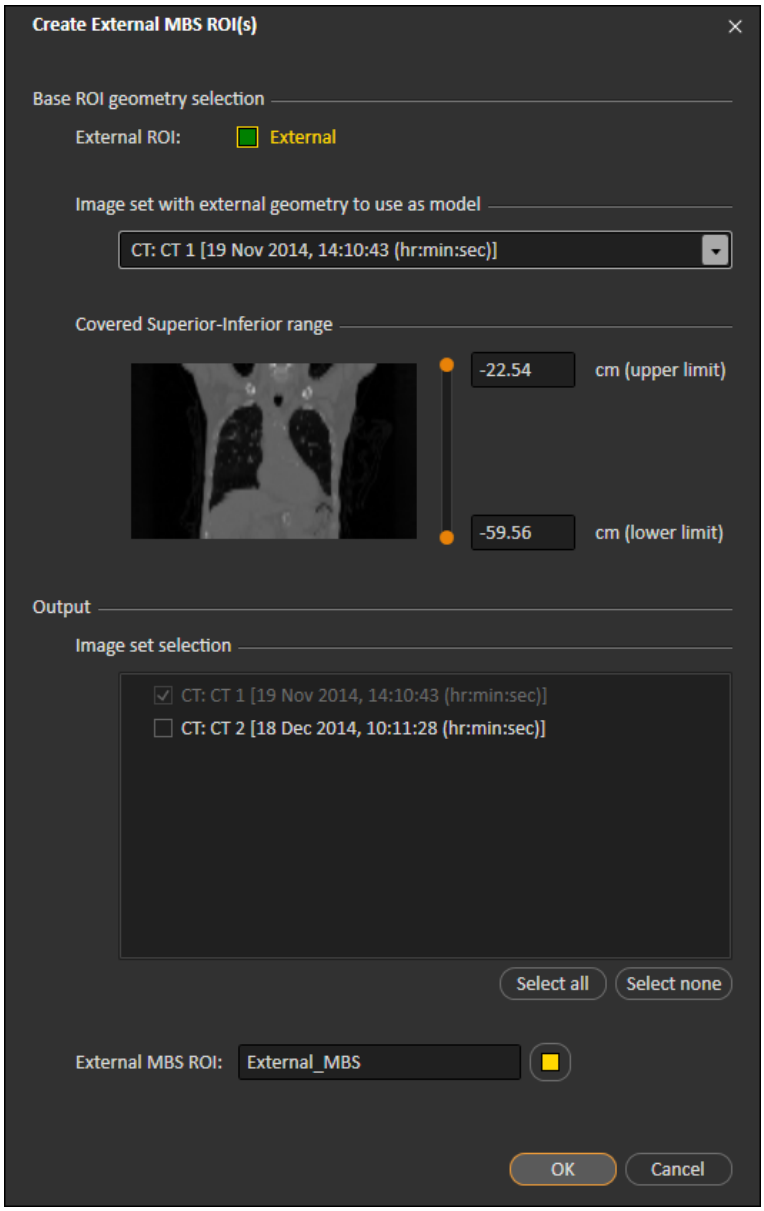


Figure 152. The Create External MBS ROIs dialog where it is possible to select an image set with external geometry to use as model.

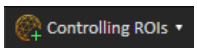
2. Select **Image set with external geometry to use as model** from the drop-down list.
3. Select **Covered superior-inferior range** with the sliders.
4. Select image set from the **Image set selection** list.

5. Click **OK**.

Create external MBS ROI when an external MBS model exists and has been used to create external MBS ROI with geometry in at least the model image set

To create external MBS ROIs:

1. Click the **Create controlling ROIs** button and select **Create external MBS ROIs…**.



This opens the Create External MBS ROIs dialog.

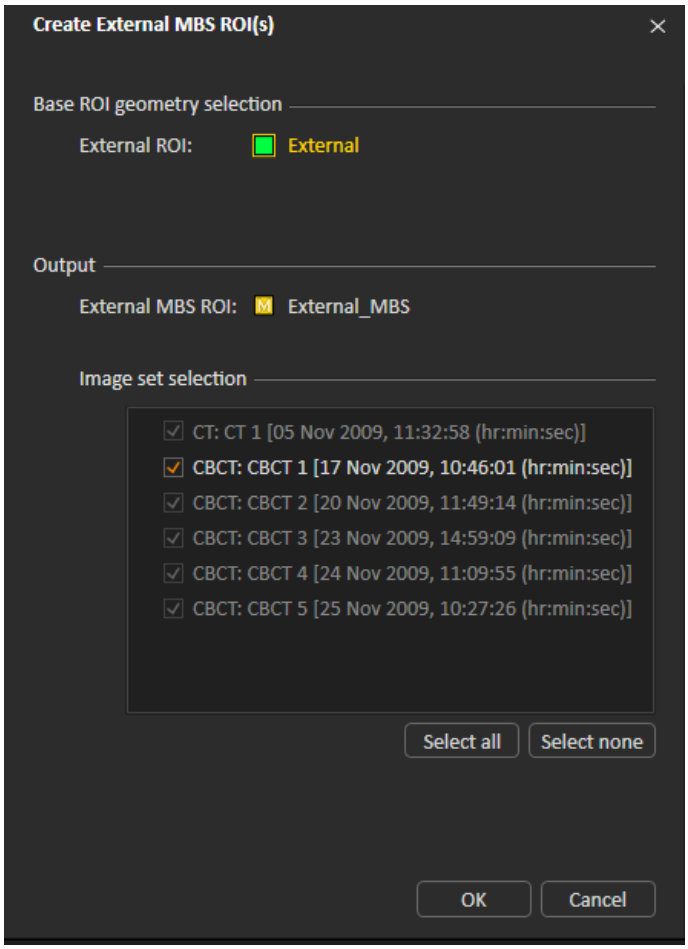

Create External MBS ROI(s)
Base ROI geometry selection
External ROI:
External
Output
External MBS ROI:
External_MBS
Image set selection
CT: CT 1 [05 Nov 2009, 11:32:58 (hr:min:sec)]
CBCT: CBCT 1 [17 Nov 2009, 10:46:01 (hr:min:sec)]
CBCT: CBCT 2 [20 Nov 2009, 11:49:14 (hr:min:sec)]
CBCT: CBCT 3 [23 Nov 2009, 14:59:09 (hr:min:sec)]
CBCT: CBCT 4 [24 Nov 2009, 11:09:55 (hr:min:sec)]
CBCT: CBCT 5 [25 Nov 2009, 10:27:26 (hr:min:sec)]
Select all
Select none
OK
Cancel

Figure 153. The Create External MBS ROIs dialog, where an existing model is used.

2. Select image set from the **Image set selection** list.

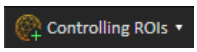
3. Click **OK**.

5.4.11 Controlling ROIs - Create meshes from contoured ROI(s)

The user can convert an ROI with contour shape to a new ROI with triangle mesh shape. The new ROI can be used as controlling ROI, which means that it has the same number of vertices in all image sets and that it has point-to-point correspondence for the vertices.

To create meshes from contoured ROIs:

1. Click the **Create controlling ROI(s)** button and select **Create controlling ROIs…**.

   This opens the Create Controlling ROI(s) dialog.

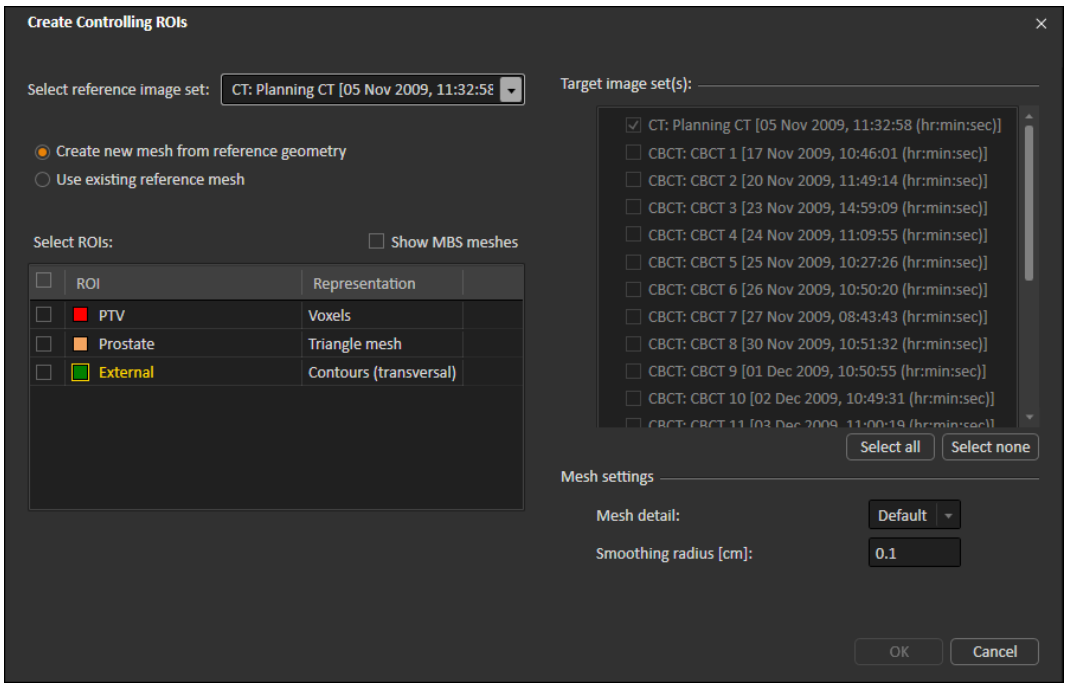

Create Controlling ROIs
Select reference image set:
CT: Planning CT [05 Nov 2009, 11:32:58
Create new mesh from reference geometry
Use existing reference mesh
Select ROIs:
Show MBS meshes
ROI
Representation
PTV
Voxels
Prostate
Triangle mesh
External
Contours (transversal)
Target image set(s):
CT: Planning CT [05 Nov 2009, 11:32:58 (hr:min:sec)]
CBCT: CBCT 1 [17 Nov 2009, 10:46:01 (hr:min:sec)]
CBCT: CBCT 2 [20 Nov 2009, 11:49:14 (hr:min:sec)]
CBCT: CBCT 3 [23 Nov 2009, 14:59:09 (hr:min:sec)]
CBCT: CBCT 4 [24 Nov 2009, 11:09:55 (hr:min:sec)]
CBCT: CBCT 5 [25 Nov 2009, 10:27:26 (hr:min:sec)]
CBCT: CBCT 6 [26 Nov 2009, 10:50:20 (hr:min:sec)]
CBCT: CBCT 7 [27 Nov 2009, 08:43:43 (hr:min:sec)]
CBCT: CBCT 8 [30 Nov 2009, 10:51:32 (hr:min:sec)]
CBCT: CBCT 9 [01 Dec 2009, 10:50:55 (hr:min:sec)]
CBCT: CBCT 10 [02 Dec 2009, 10:49:31 (hr:min:sec)]
Select all
Select none
Mesh settings
Mesh detail:
Default
Smoothing radius [cm]:
0.1
OK
Cancel

Figure 154. The Create Controlling ROIs dialog.

2. Select **Reference image set**.
3. Select to **Create new mesh from reference geometry** or to **Use existing reference mesh**.
   - Create new mesh from reference geometry:
     a. Select **ROIs**.
     b. Select **Target image set(s)**.
     c. Select **Mesh detail** and **Smoothing radius**.

- Use existing reference mesh:

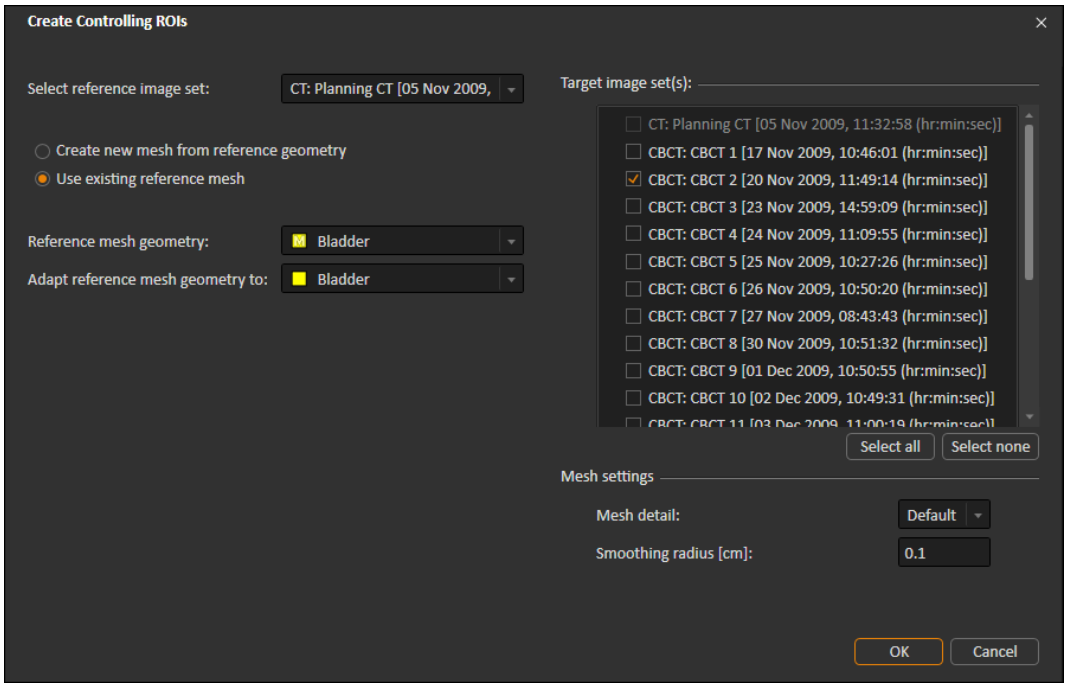

Create Controlling ROIs
Select reference image set:
CT: Planning CT [05 Nov 2009,
Create new mesh from reference geometry
Use existing reference mesh
Reference mesh geometry:
Bladder
Adapt reference mesh geometry to:
Bladder
Target image set(s):
CT: Planning CT [05 Nov 2009, 11:32:58 (hr:min:sec)]
CBCT: CBCT 1 [17 Nov 2009, 10:46:01 (hr:min:sec)]
CBCT: CBCT 2 [20 Nov 2009, 11:49:14 (hr:min:sec)]
CBCT: CBCT 3 [23 Nov 2009, 14:59:09 (hr:min:sec)]
CBCT: CBCT 4 [24 Nov 2009, 11:09:55 (hr:min:sec)]
CBCT: CBCT 5 [25 Nov 2009, 10:27:26 (hr:min:sec)]
CBCT: CBCT 6 [26 Nov 2009, 10:50:20 (hr:min:sec)]
CBCT: CBCT 7 [27 Nov 2009, 08:43:43 (hr:min:sec)]
CBCT: CBCT 8 [30 Nov 2009, 10:51:32 (hr:min:sec)]
CBCT: CBCT 9 [01 Dec 2009, 10:50:55 (hr:min:sec)]
CBCT: CBCT 10 [02 Dec 2009, 10:49:31 (hr:min:sec)]
Select all
Select none
Mesh settings
Mesh detail:
Default
Smoothing radius [cm]:
0.1
OK
Cancel

Figure 155. The Create Controlling ROIs dialog, where the option Use existing reference mesh is selected.

a. Select **Reference mesh geometry**, i.e., the ROI that should have a mesh representation on the reference image set.

b. Select what target geometry to **Adapt reference mesh geometry to**, i.e., the target geometry that the reference mesh should be adapted to.

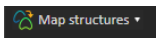
4. Click **OK**.

5.4.12 Map structures

A deformable registration can be used to map ROI and POI geometries between images. It is possible to map in the direction of the displacement field or in the reverse direction as well as to create a new geometry for an existing ROI/POI or to create a new ROI/POI geometry. In the latter case, geometries will be created in both images. Structures can also be mapped directly from the ROI list, see *section 3.4 The tool panel tabs - ROI list, POI list, Visualization, etc. on page 53* for more information. If any of the selected structures are not fully covered by the deformation grid, the grid will be automatically expanded. The expansion will be smoothly extended from the boundary and finally padded by zero deformation vectors to cover the structure.

Map ROI(s)

1. Click the **Map structures** button and select **Map ROI(s)**.

   This opens the Map ROI(s) dialog.

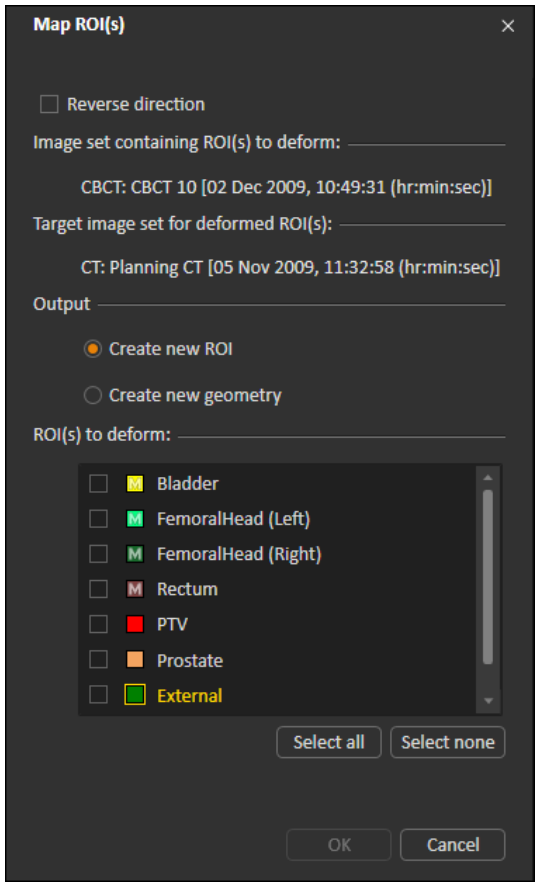
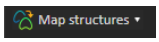


Figure 156. The Map ROI(s) dialog.

2. Select the direction of the mapping. If the **Reverse direction** checkbox is unchecked, the ROI(s) will be mapped in the direction of the displacement field. If it is checked, the ROI(s) will be mapped in the reversed direction.
3. Select **Output**. The options are **Create New ROI** and **Create new geometry**.
   - **Create new ROI**: This option creates a new ROI based on the ROI being deformed. The name will have the ending _Def.
   - **Create new geometry**: This option will create a new geometry for an existing ROI.
4. Click **OK**.

Map POI(s)

1. Click the **Map structures** button and select **Map POI(s)**.

   This opens the Map POI(s) dialog.

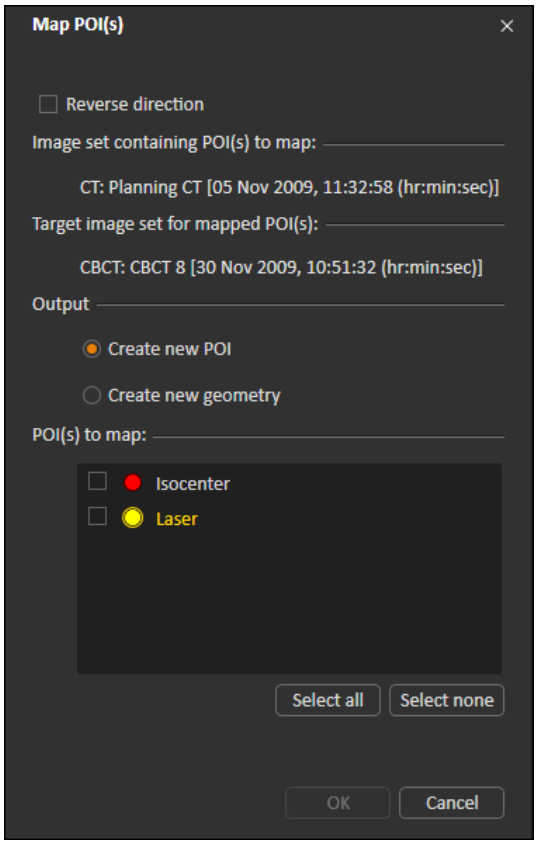


Figure 157. The Map POI(s) dialog.

2. Select the direction of the mapping. If the **Reverse direction** checkbox is unchecked, the POI(s) will be mapped in the direction of the displacement field. If it is checked, the POI(s) will be mapped in the reversed direction.
3. Select **Output**. The options are **Create New POI** and **Create new geometry**.
   - **Create new ROI**: This option creates a new ROI based on the ROI being deformed. The name will have the ending _Mapped.
   - **Create new geometry**: This option will create a new geometry for an existing POI.

4. Click **OK**.

5.4.13 Approval of a deformable registration

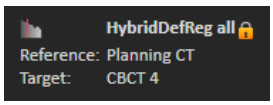
When an acceptable deformable registration is achieved, it can be approved for dose accumulation. The deformable registration can then be used for deforming dose and in dose accumulation calculations in the Dose Tracking module and when creating an adapted plan in the Adaptive Replanning module. For more information, see *chapter 11 Treatment Adaptation*.

To approve a deformable registration for dose accumulation:

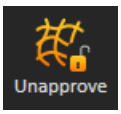
1. Click the **Approve** button.

2. The approved registration will be marked * in the list of registrations (located under the **Select registration** button).

   The approved registration will also be marked with a padlock in the Current registration toolbar.



To unapprove an approved registration, click the **Unapprove** button.



5.4.14 Simulated organ motion

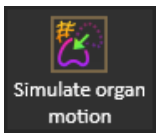
In RayStation, it is possible to generate deformed image sets to simulate organ motion without taking multiple CT/CBCT/MR scans of the patient. One ROI is defined as the motion ROI, and this ROI will drive the deformation of the patient anatomy. Structures that are not considered to move can also be used as input to the deformation by being specified as fixed. When the new anatomy has been defined, all other structures will be mapped deformably to the generated deformed image sets and they will be perceived to move with the motion ROI.

The generated motion image sets may be used both for evaluation and as input when planning robustly against intra-fractional or inter-fractional organ motion.

The simulated organ motion functionality is available in the Deformable Registration module and in the Plan Evaluation module.

Generate image sets based on simulated organ motion

1. Click the **Simulate organ motion** button.

   This opens the **Generate Image Sets Based on Simulated Organ Motion** dialog.

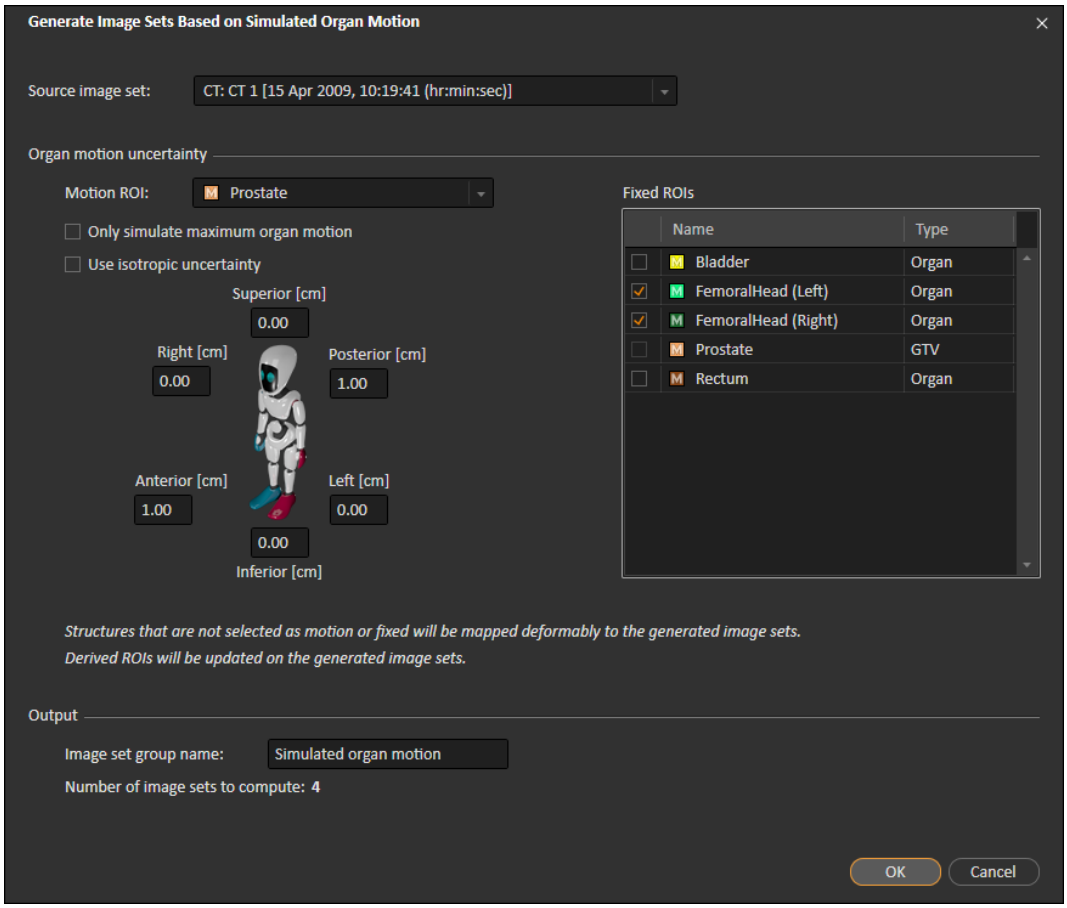


Figure 158. The **Generate Image Sets Based on Simulated Organ Motion** dialog.

2. Select **Source image set**. This is the image set that will be deformed. ROIs in this image set will drive the deformation, and the image set needs to have the motion ROI and any ROIs to be fixed, contoured. The deformation image set will be based on the source image set.
3. Specify **Organ motion uncertainty** settings:
    a. Select **Motion ROI**. This is the ROI that will be simulated to move according to the specified uncertainty parameters.
    b. If desired, check the **Only simulate maximum organ motion** checkbox to reduce the number of generated image sets. When this option is selected, only the image sets that take the maximum movement scenarios into account will be generated.
    c. Enter the **Motion uncertainty** for the expected motion in every direction.

To specify the same motion uncertainty in all directions, check the **Use isotropic uncertainty** checkbox.

d. Set any ROIs that are considered not to move as **Fixed**.

Structures that are not selected as **Motion ROI** or **Fixed** will be mapped deformably to the generated image sets. Derived ROIs will be updated in the generated image sets.

In the **Output** section of the dialog, the **Number of image sets to compute** is stated. This value is based on the **Organ motion uncertainty** settings. The larger the maximum organ motion will be, the more image sets will be generated to appropriately cover the possible anatomical changes that can occur. To increase/decrease the number, change the **Organ motion uncertainty** settings or check the **Only simulate maximum organ motion** checkbox.

4. If desired, enter an **Image set group name**.
5. Click **OK**.

Result: Image sets that simulate different patient anatomies, given the **Organ motion uncertainty** settings specified in the dialog, will be generated. The images will be collected in an image set group with the given name.

View deformed motion image sets

The generated image sets will be available in the image set library. The name of the image set group will be as specified in the **Generate Image Sets Based on Simulated Organ Motion** dialog (Figure 158).

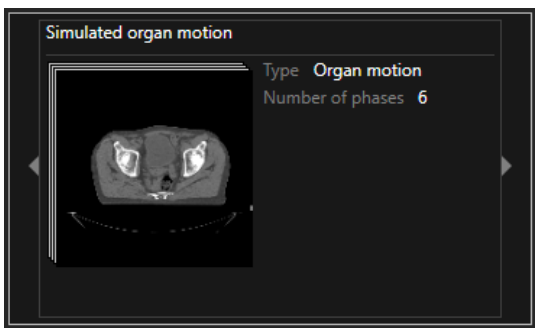


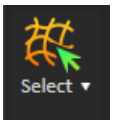
Figure 159. The simulated organ motion image sets will be grouped together and available in the image set library.

In the Structure Definition module, the play button in the views can be used to view the simulated organ motion. Click the pie chart to view the organ motion with visualized ROIs.

View organ motion deformable registration fields

The organ motion deformation fields used to compute the deformed image sets are listed and viewable in the Deformable Registration module.

Click the **Select** button in the **Deformation** tab to view and select the registration from the list.



The registration is displayed in the views and can be evaluated using the evaluation tools. See *section 5.4.9 Tools for evaluating the result of a deformable registration on page 271*.

Invalidation of deformable registration and deformed organ motion image sets

Editing any ROIs included in the deformable registration used to compute a deformed image set will invalidate the deformable registration and the deformed image set.

Note: *Editing a ROI geometry in the source image set will invalidate all registrations and all dependent deformed image sets. Editing a ROI geometry on any of the deformed image sets will only invalidate that image set and the registration used to compute it.*

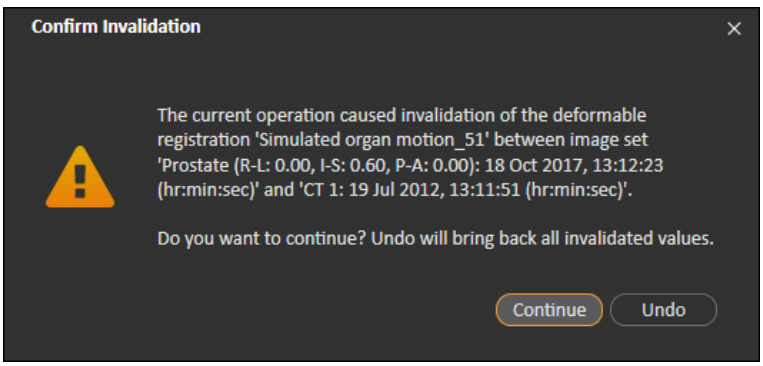

Confirm Invalidation
The current operation caused invalidation of the deformable registration 'Simulated organ motion_51' between image set 'Prostate (R-L: 0.00, I-S: 0.60, P-A: 0.00): 18 Oct 2017, 13:12:23 (hr:min:sec)' and 'CT 1: 19 Jul 2012, 13:11:51 (hr:min:sec)'.
Do you want to continue? Undo will bring back all invalidated values.
Continue
Undo

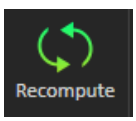
Figure 160. The **Confirm Invalidation** warning when invalidating the deformable registration and the image set. Click **Continue** to confirm the invalidation or **Undo** to undo the invalidation and bring back all invalidated states.

An invalidated image set will be shown as black in the graphical patient views. If the motion ROI or the fixed ROIs in the invalidated image set are to be edited as new input when recomputing the image set, the invalidated image set can be fused with the original image set as a guide.

Recomputation of deformable registration and deformed organ motion image sets

Recomputation of deformable registrations and deformed organ motion image sets can be done in the Deformable Registration module:

1. Click the **Recompute** button.

   This opens the **Recompute Motion Image Sets** dialog.

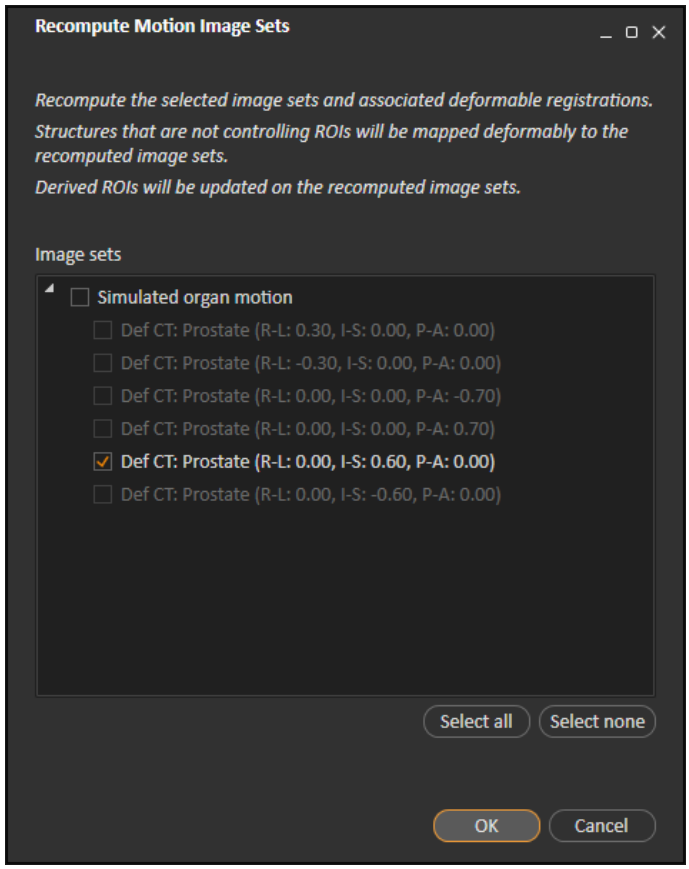

Recompute Motion Image Sets
Recompute the selected image sets and associated deformable registrations.
Structures that are not controlling ROIs will be mapped deformably to the recomputed image sets.
Derived ROIs will be updated on the recomputed image sets.
Image sets
Simulated organ motion
Def CT: Prostate (R-L: 0.30, I-S: 0.00, P-A: 0.00)
Def CT: Prostate (R-L: -0.30, I-S: 0.00, P-A: 0.00)
Def CT: Prostate (R-L: 0.00, I-S: 0.00, P-A: -0.70)
Def CT: Prostate (R-L: 0.00, I-S: 0.00, P-A: 0.70)
Def CT: Prostate (R-L: 0.00, I-S: 0.60, P-A: 0.00)
Def CT: Prostate (R-L: 0.00, I-S: -0.60, P-A: 0.00)
Select all
Select none
OK
Cancel

Figure 161. The **Recompute Motion Image Sets** dialog.

2. Select the image sets to be recomputed.
3. Click **OK**.

   Result: The selected image sets and the associated deformable registrations will be recomputed and the structures will be remapped using the recomputed deformation field. Derived ROIs will be updated in the recomputed image sets.

Use organ motion image sets for evaluation

Evaluate a plan with respect to organ motion by computing dose on additional data sets. For more information, see *section 8.1.8 Compute dose on additional image sets on page 736*.

Use organ motion image sets as input when planning robustly with respect to organ motion

Motion image sets can be used as input when planning robustly with respect to organ motion. For more information, see *section 7.6 Robust optimization on page 711*.

6 PLAN DESIGN

The Plan Design planning activity contains the Virtual Simulation module, the Plan Setup module, the 3D-CRT Beam Design module, the Electron Beam Design module and the Proton Beam Design module.

The Plan Setup module is where the basis for the treatment plan is specified such as treatment modality, treatment technique, treatment orientation, number of beams and isocenter positioning.

In the 3D-CRT Beam Design module, the Electron Beam Design module and the Proton Beam Design module beam orientations, apertures and various beam modifiers are designed by the user in order to manually create the optimal plan.

In this chapter

This chapter contains the following sections:

6.1	The Plan Setup module	p. 295
6.2	The Virtual Simulation module	p. 386
6.3	The 3D-CRT Beam Design module	p. 421
6.4	The Electron Beam Design module	p. 460
6.5	The Proton Beam Design module	p. 478

6.1 THE PLAN SETUP MODULE

The Plan Setup module is where the basis for the treatment plan is specified such as treatment modality, treatment technique, treatment orientation, number of beams and isocenter positioning.

Treatment plans can also be automatically generated using plan generation protocols. See *section 6.1.2 Plan generation protocols on page 300* for more information.

In this section

This section contains the following sub-sections:

6.1.1	The Plan Setup user interface	p. 298
6.1.2	Plan generation protocols	p. 300
6.1.3	Create a new plan	p. 306
6.1.4	Define and edit the dose grid	p. 312
6.1.5	Edit isocenter position	p. 314
6.1.6	Add, edit, copy or delete beams	p. 316
6.1.7	Beam list templates	p. 328
6.1.8	The DRR views and settings	p. 330
6.1.9	Beam dose specification point	p. 337
6.1.10	Create POI from plan point	p. 340
6.1.11	Create bolus	p. 341
6.1.12	Define or modify prescription	p. 343
6.1.13	Beam entry validation	p. 349
6.1.14	Compute dose	p. 354
6.1.15	Scale dose	p. 356
6.1.16	Auto scale to prescription	p. 358
6.1.17	Setup beams	p. 359
6.1.18	Patient setup	p. 360
6.1.19	Volume Rendering settings	p. 364
6.1.20	Multiple beam set planning	p. 372
6.1.21	Create new adapted plan	p. 379
6.1.22	Create template plans for fallback planning	p. 382
6.1.23	Define views for plan report	p. 385

Precautions

WARNING!

Computing dose for small structures. It is important to choose dose grid resolution based on the smallest structures that need to be reconstructed. When structures are reconstructed for visualization in patient views, a structure specific high-resolution grid is used in order to represent the structure accurately. However, for plan optimization, dose computation and dose statistics, the structures are reconstructed on the dose grid. If the dose grid voxels are too large, the reconstruction may represent the structures inaccurately. Furthermore, there will be a discrepancy between the visualized structures and what is actually used for dose computations. It is therefore highly recommended to use a dose grid resolution such that the size of one dose grid voxel does not exceed half the size of the smallest structure to be reconstructed. (254767)

WARNING!

Density visualization. Note that if selecting to visualize density, this does not include ROIs of type bolus, support and fixation. (259822)

6.1.1 The Plan Setup user interface

Workspace

The upper left part of the workspace shows the **Plan information**; plan name, beam set name, number of fractions, plan modality and treatment technique.

The workspace also contains three sub-windows showing 2D image data in a specific patient plane, making it possible to simultaneously work in three dimensions. It is possible to change the patient direction using shortcuts. Click in a patient view and type T (Transversal), C (Coronal) or S (Sagittal). The two sub-windows to the right show image data in **3D**, **Room View**, **Setup DRR**, the Beam's Eye View (**BEV**), and **DRR**.

The lower part of the workspace contains the beam list, which contains the tabs **Beams**, **Control points/MLC**, **Jaw Assignment** (applicable for LINACs only), **Setup beams** and **Beam dose specification points**.

For TomoHelical plans there is a **Leaf Open Times** view that displays a histogram for the leaf open time of all leaves and of all projections.

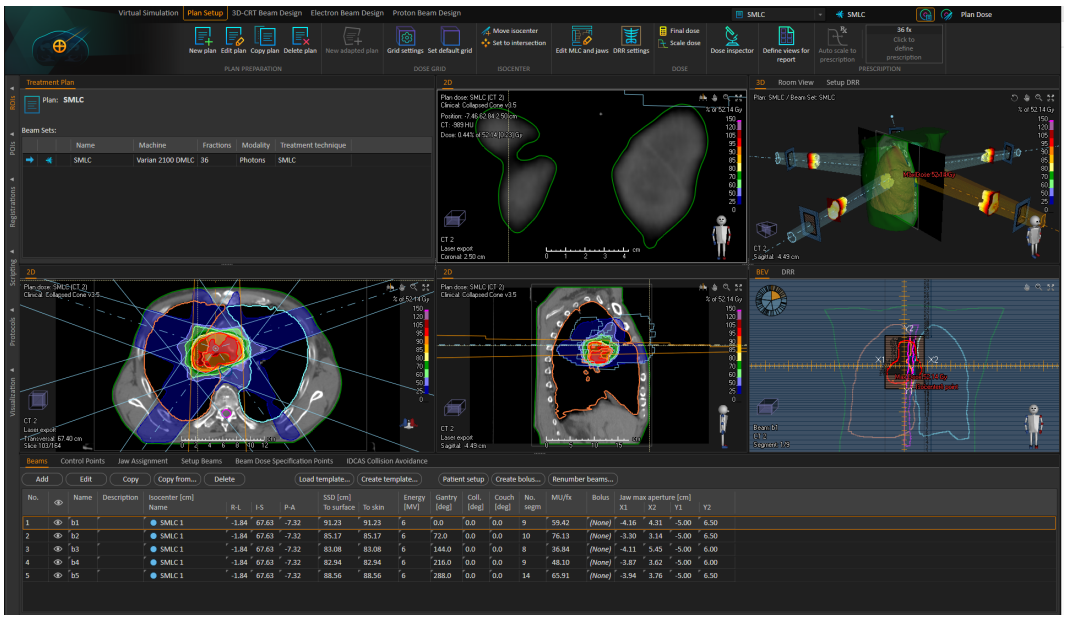


Figure 162. The Plan Setup workspace.

Graphical User Interface

For more information about the tools, operations and various view types in the Graphical User Interface, see *chapter 3 The Graphical User Interface*.

Context menus

Each view has a context menu which is opened by right-clicking in the view. Several of the view functions are common for all views (pan, zoom, and measure etc.) while others are dependent on the view type. For a description of the general context menu options, see *section 3.9 The context menu on page 102*.

The 2D patient view context menu contains a Plan Setup module specific option; **Edit dose grid**. This option allows for visual editing of the dose grid position and size. Click and drag the handles of the top, bottom, sides or corners of the grid displayed in the view. For more information, see *View manipulation tools on page 102*. Make sure to exit editing mode by deselecting **Edit dose grid** from the 2D view context menu.

Selecting the **Edit color table** option in the 2D patient view opens a dialog where the visual appearance of the dose can be edited. In the BEV, the color table option opens a dialog where the fluence display can be defined. For more information, see *section 3.8.2 Color tables on page 96*.

Dose presentation

The dose can be displayed as plan dose or as separate beam doses using the buttons in the toolbar. The selected dose presentation will influence all dose views, dose statistics, DVHs etc. in all modules presenting doses (except the Plan Evaluation module, the QA Preparation module and the Dose Tracking module).

The dose presentation buttons are described below:

The **Plan dose** button.

The **Beam dose** button (not applicable for carbon ion beams).

For multiple beam sets, the beam set dose can be displayed, see *Dose presentation for multiple beam sets on page 374*.

6.1.2 Plan generation protocols

Treatment plans can be generated automatically using pre-defined protocols. Supported treatment techniques are 3D-CRT, SMLC, DMLC, VMAT, Conformal Arc, Static Arc and TomoHelical. The following plan generation steps can be automated:

- Create structures from template
- Create plan
- Create beam set
- Add prescription
- Set default dose grid
- Load beam list template
- Load clinical goal list template
- Load optimization function list template
- Beam optimization settings
- Generate pareto plans
- Run optimization
- Reduce OAR dose
- Compute dose

The plan generation protocols are located in the **Protocols** tab in the tool panel at the left border of each workspace.

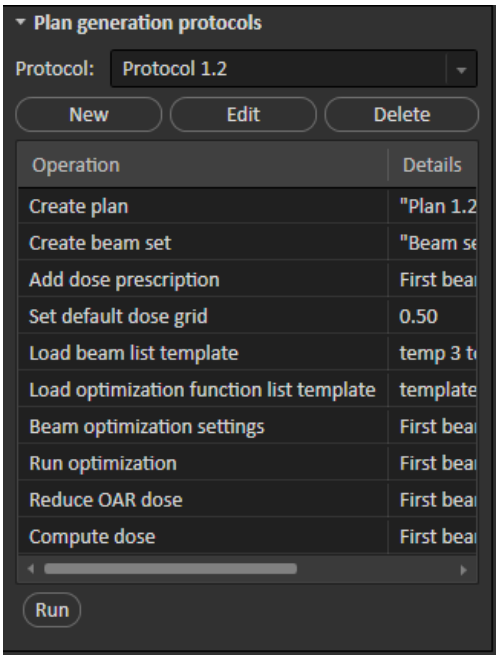


Figure 163. The Plan generation protocols area.

WARNING!

Plan Generation Protocols. Be aware that any user may edit plan generation protocols. These changes affect all other users at the clinic. (97456)

Create new protocol

To create a new protocol:

1. Click the **New** button. This opens the New Protocol dialog.

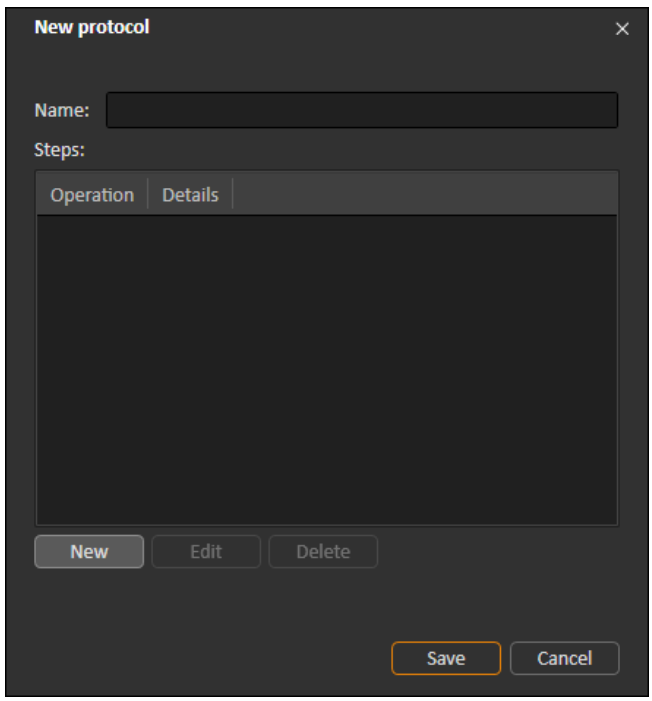


Figure 164. The New protocol dialog.

2. Enter a protocol **Name**.
3. Add protocol steps.

   Click the **New** button. This opens the New Protocol Step dialog.

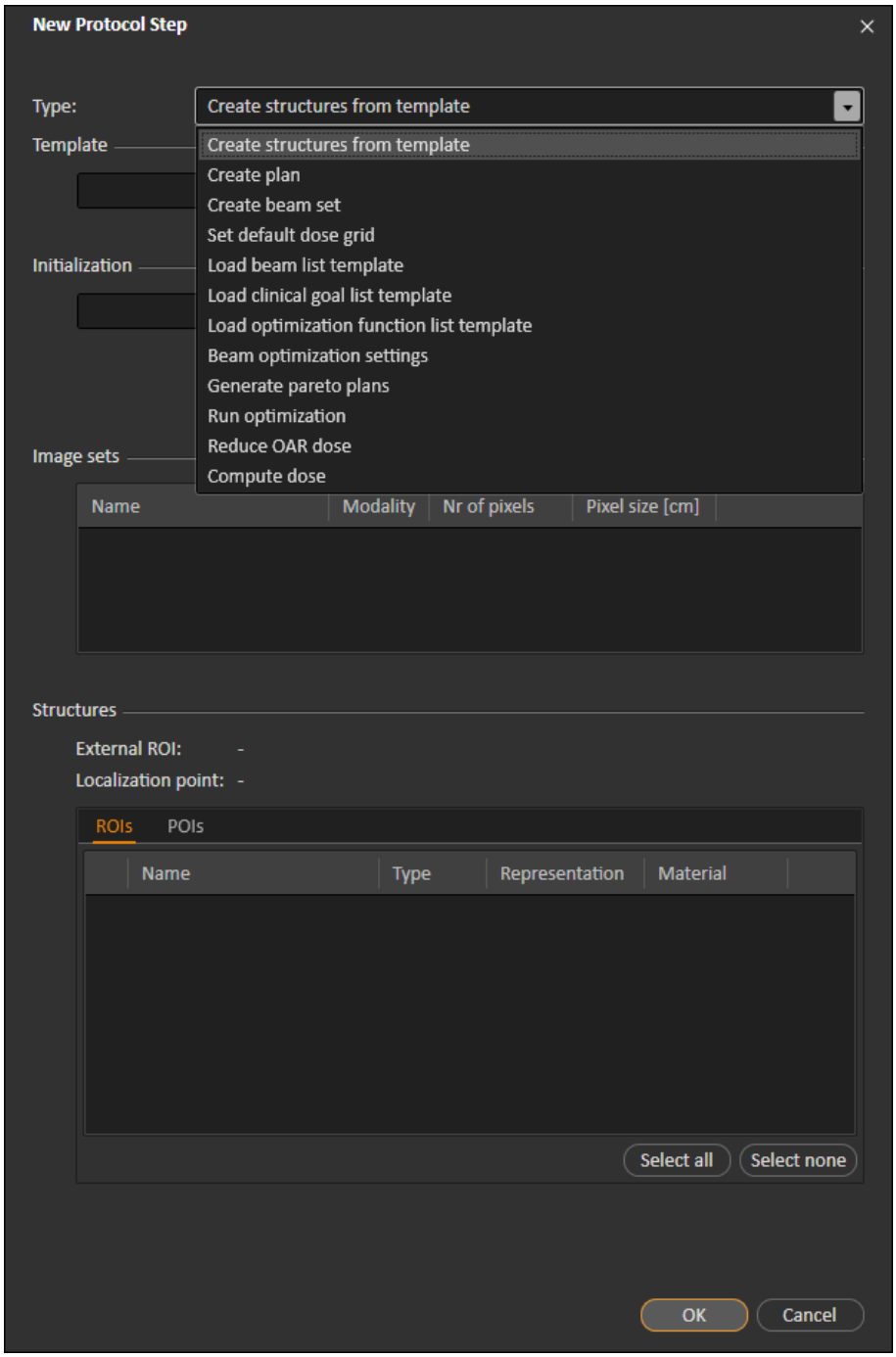


Figure 165. The New Protocol Step dialog.

4. Select a protocol **Type** from the drop-down list. The following options are available:
   - **Create structures from template** - described in *section 5.3.7 Structure templates on page 220*
   - **Create plan** - described in *section 6.1.3 Create a new plan on page 306*
   - **Create beam set** - described in *Add beam set information on page 308*
   - **Add dose prescription** - described in *section 6.1.12 Define or modify prescription on page 343*
   - **Set default dose grid** - described in *section 6.1.4 Define and edit the dose grid on page 312*
   - **Load beam list template** - described in *section 6.1.7 Beam list templates on page 328*
   - **Load clinical goal list template** - described in *section 3.7.3 Clinical goals on page 81*
   - **Load optimization function list template** - described in *section 7.1.4 Optimization function list templates on page 529*
   - **Beam optimization settings** - described in *section 7.1.9 Beam optimization settings on page 542*
   - **Generate pareto plans** - described in *section 7.4.5 Create and add function list templates on page 663* and *section 7.4.6 Pareto plans on page 664*
   - **Run optimization** - described in *section 7.1.12 Running the optimization on page 549*
   - **Reduce OAR dose** - described in *section 7.1.12 Running the optimization on page 549*
   - **Compute dose** - described in *section 7.1.15 Compute dose on page 553*

   Note: *For the protocol types Load beam list template, Load optimization function list template, Beam optimization settings, Run optimization, Reduce OAR dose and Compute dose it is possible to either select a beam set created by the protocol by name or by the beam set number in the plan the protocol is applied to. If selecting a beam set in the plan, the number refers to the beam set number in the plan and not the number in the protocol. For example, for a protocol where two beam sets are added to an existing plan that already has a beam set, and beams are added to the beam set 'Second', the beams will actually be added to the first beam set that was created by the protocol.*

   Note: *A protocol cannot contain a Generate pareto plans step in combination with any of the following: Run Optimization, Function list template, Compute final dose or Reduce OAR dose.*

   Note: *For Conformal Arc, it is not possible to select gantry spacing in the Beam optimization settings.*
5. Enter the information required for the selected protocol type.
6. Click **OK**.

7. Click **Save**.

Edit protocol

1. Select the desired protocol from the **Protocol** drop-down list.
2. Click the **Edit** button. This opens the Edit protocol dialog.
3. Edit the protocol steps as desired.
4. Click **Save**.

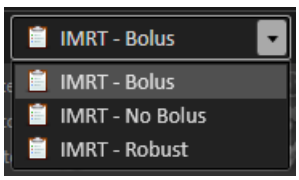
Delete a protocol

1. Select the desired protocol from the **Protocol** drop-down list.
2. Click the **Delete** button.

Run protocol

To run a plan generation protocol:

1. Select the desired protocol from the **Protocol** drop-down list.
2. Click the **Run** button. A new treatment plan will be created based on the settings specified in the protocol.
3. Click **Save**. The new plan can be selected in the plan and dose selection bar at the top of the workspace.



4. Select the plan and review all automatically generated settings.

6.1.3 Create a new plan

Treatment plans can also be automatically generated using plan generation protocols. See *section 6.1.2 Plan generation protocols on page 300* for more information.

To create a new plan:

1. Click the **New plan** button to open the **New plan** dialog.

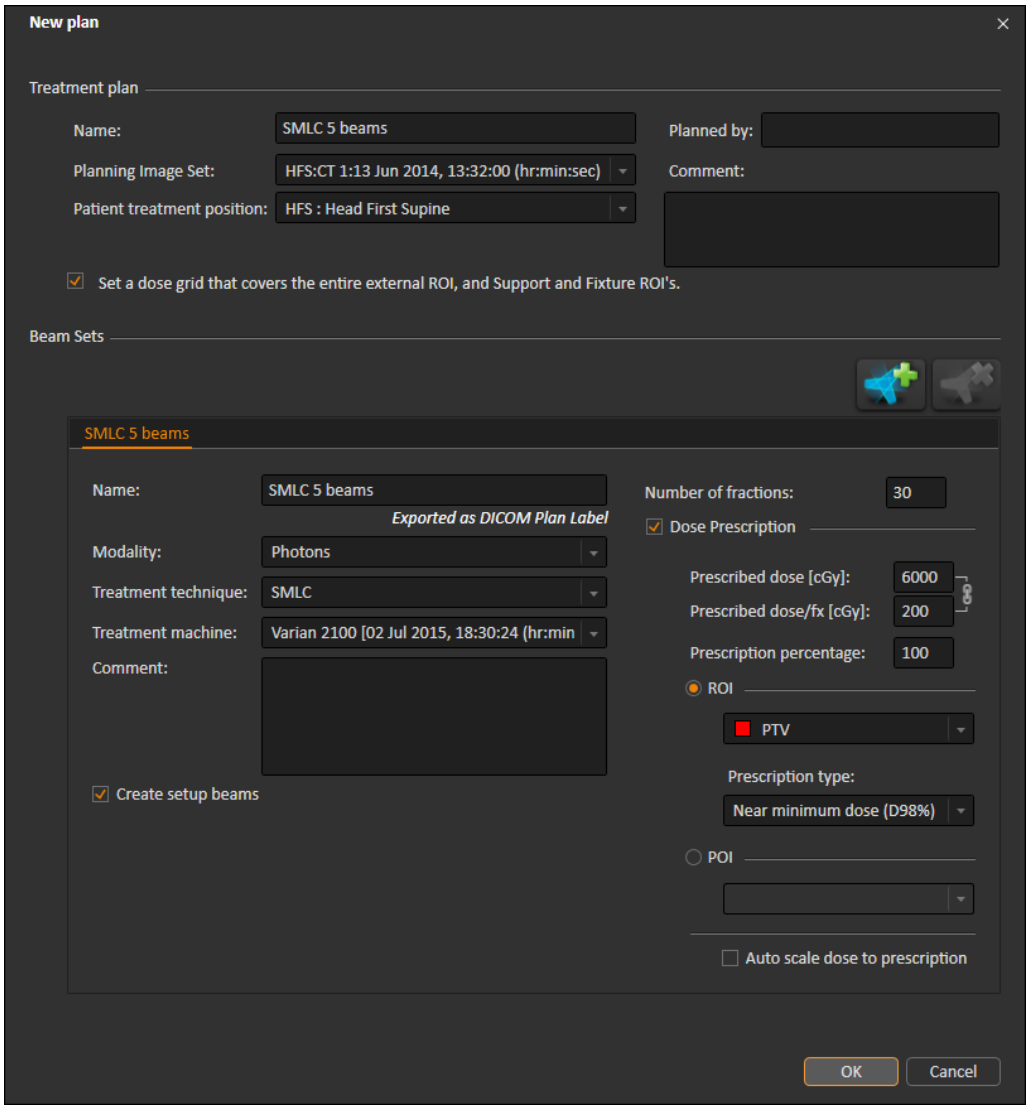


Figure 166. The **New plan** dialog for photons.

Add treatment plan information

Enter information about the treatment plan:

1. Enter a plan **Name**.

   Note: *The plan name is exported as DICOM RT Plan Name [300A,0003].*

2. Select **Planning image set** from the drop-down list to use as a basis for the treatment plan.

3. Select **Patient treatment position**.

   Note: *For treatment technique TomoHelical, the patient treatment position must be the same as the CT scanning position.*

4. Enter information in the **Planned by** field (optional).
5. Enter a **Comment** in free text (optional).
6. Select to **Set a dose grid that covers the entire external ROI and Support and Fixture ROIs** by checking the corresponding checkbox (this is checked by default if an External ROI has been assigned to the patient).

   Note: *If a bolus will be added at a later stage, the dose grid has to be regenerated to cover it.*

Add beam set information

Enter beam set information. This information is dependent on the treatment technique.

1. Enter a beam set **Name**.

   Note: *The beam set name is exported as DICOM RT Plan Label [300A, 0002].*

2. Select **Modality**. The options are photons, protons, electrons or carbon.
3. Select **Treatment technique**. The following options are available:

   - Photons: 3D-CRT, SMLC, VMAT, Conformal Arc, Static arc, DMLC (Sliding window) and TomoHelical
   - Protons: Pencil Beam Scanning, Double Scattering, Uniform Scanning, Wobbling and Line Scanning
   - Electrons: Applicator and cutout
   - Carbon ions: Pencil Beam Scanning

4. Select **RBE model** (applicable for carbon ions only).

   The RBE model is created in the RayBiology application. Note that the checkbox **Allow for clinical use** in the RBE model settings needs to be checked in order to calculate a final clinical dose.

   For more information about the RayBiology application, see *Appendix E RayBiology*.

   Note: *An RBE model needs to be selected in order to be able to define optimization functions that relates to the RBE dose.*

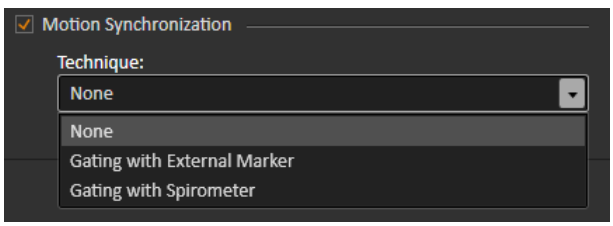
   Note: *If no RBE model is selected, no RBE dose will be displayed in RayStation.*

5. Select **Treatment machine**. The list contains treatment machines that are commissioned for the selected treatment technique. Beam Commissioning is described in *RSL-D-RS-7.0-RPHY, RayStation 7 RayPhysics Manual*.

Note: *If treatment technique VMAT is selected and the treatment machine is commissioned for burst mode, then the plan will be delivered in burst mode (also known as mArc) which is a type of rotational delivery where the leaves are not allowed to move while the beam is on.*

Note: *When changing treatment machine for an existing plan with modality electrons, jaw and MLC positions will be updated to the positions defined in Beam Commissioning for the selected applicator of the new machine.*

6. Enter a **Comment** in free text (optional).
7. Select to **Create Setup beams** (for ion treatment machines, only applicable with defined imaging system) by checking the corresponding checkbox. See *section 6.1.17 Setup beams on page 359* for more information about setup beams.
8. Select **Enable dynamic tracking for Vero** (applicable for Vero LINACs only). This activates the dynamic tracking functionality on Vero during treatment. Note that the dose calculation in RayStation is not affected by this flag.
9. Select **Motion Synchronization Technique** (applicable if enabled only). This allows export of motion synchronization parameters for beam sets. See *section D.2.2 The Preferences tab on page 922* for more information on how to enable this.



- The option **Gating with External Marker** is translated into DICOM equivalent Respiratory Motion Compensation Technique 'GATING' and Respiratory Signal Source 'EXTERNAL_MARKER'.
- The option **Gating with Spirometer** is translated into DICOM equivalent Respiratory Motion Compensation Technique 'GATING' and Respiratory Signal Source 'SPIROMETER'.

10. Enter **Number of fractions**.
11. Check the **Dose Prescription** checkbox to add a **Prescription** for an ROI, POI or SITE.

12. Enter either the **Prescribed dose** or the prescribed dose per fraction (**Prescribed dose/fx**).

    When changing the prescribed dose, the prescribed dose per fraction is updated based on the number of fractions. If instead the prescribed dose per fraction is changed, the prescribed dose will be updated based on the number of fractions.

    If the number of fractions is changed, only the prescribed dose will be updated based on the current prescribed dose per fraction.

    Note: *The dose color table by default uses the prescribed dose level as reference.*

    Note: *For carbon ions, prescription always relates to RBE dose.*

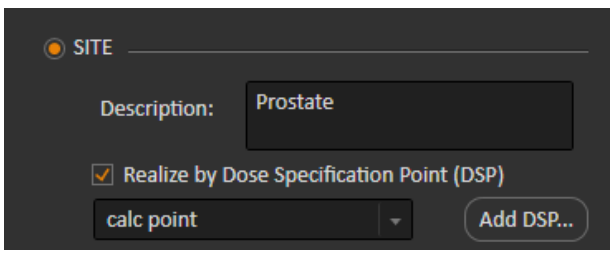
13. Enter **Prescription percentage**.

14. For a selected ROI there are several options in the **Prescription type** drop down list:

    - **Average dose** is defined as the average dose in the specified ROI.
    - **Near maximum dose (D2%)** is defined as the desired dose at 2% volume of the specified ROI.
    - **Median dose (D50%)** is defined as the desired dose at 50% volume of the specified ROI.
    - **Near minimum dose (D98%)** is defined as the desired dose at 98% volume of the specified ROI.
    - **Dose at volume** is defined as the desired dose at the entered volume [%] of the specified ROI.

    It is possible to add a prescription, or to modify an existing prescription after the plan has been created. For more information, see *section 6.1.12 Define or modify prescription on page 343*.

15. For a SITE prescription, a description of the prescribed site is required. A SITE prescription with only description will not be evaluated on if it is fulfilled or not.



    Optionally, the site prescription can be set to be realized by a selected dose specification point. The prescription will then be evaluated on the dose to the plan specific dose specification point.

    It is possible to click **Add DSP...** to add a dose specification point from the prescription dialogue. See *SITE prescription on page 347* for details.

16. If desired, select to **Auto scale dose to prescription** by checking the corresponding checkbox. For more information, see *section 6.1.16 Auto scale to prescription on page 358*.

    Note: *Auto scale dose to prescription cannot be used for carbon ions, nor for SITE prescriptions with description only.*

17. If desired, add an additional beam set to the plan by clicking the add beam set button.

    Repeat step 1-7 for the new beam set. See *section 6.1.20 Multiple beam set planning on page 372* for more information.

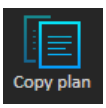
18. Click **OK**. The plan (without beams) is opened. The image set selected for the plan is displayed in the patient views.

Edit plan settings

To edit plan settings click the **Edit plan** button. This opens the Edit Plan dialog.

Copy plan

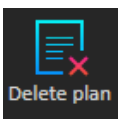
To make a copy of the current plan, click the **Copy plan** button.



In the Copy Plan dialog, enter a name for the new plan and click **OK**. The new plan will be opened as the selected current plan, i.e. the plan that is displayed in Plan Setup workspace.

Delete plan

To delete a plan, click the **Delete plan** button. This will delete the plan from the plan list.

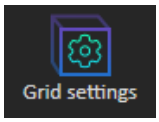


6.1.4 Define and edit the dose grid

Defining the dose grid

The dose grid is the 3D grid in which the dose distribution is calculated. To edit the dose grid:

1. Click the **Grid settings** button.



This opens the Edit Dose Grid Settings dialog.

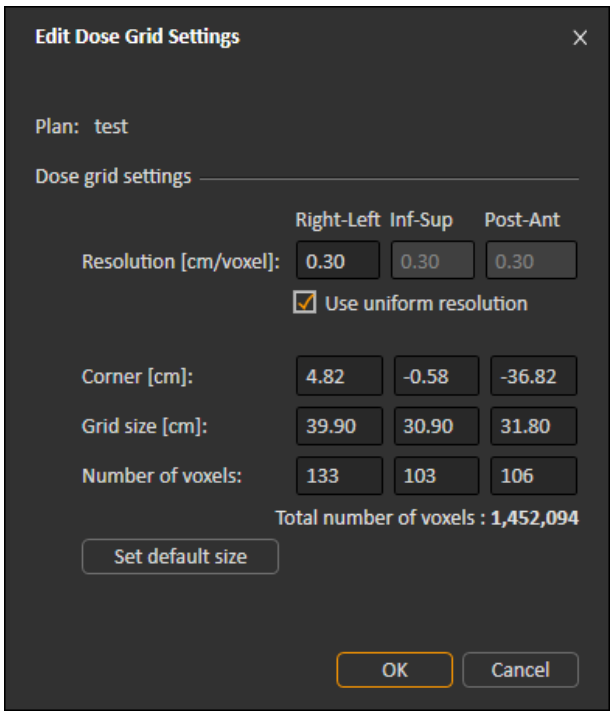


Figure 167. The Edit Dose Grid Settings dialog.

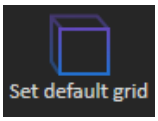
2. Enter **Resolution** values. This is the size of the voxels in the dose grid. Uncheck the **Use uniform resolution** checkbox to define individual values per direction. The default resolution is specified in the Clinic Settings application. See *Appendix D System administration* for more information.

Note: *For proton, carbon and electron plans only: The dose grid resolution must be smaller than or equal to 0.3 cm per voxel or in order to get a clinical dose. Otherwise, the plan cannot be approved or exported.*

3. Click the **Set default size** button to create a grid that covers the entire External geometry, support and fixture ROIs or select to enter **Corner** value, **Grid size** and/or **Number of voxels**.
4. Click **OK**.

Set default grid

Clicking the **Set default grid** button in the toolbar sets a grid, of the current resolution, that covers the entire External geometry, patient support, fixation and bolus referenced from the plan.



Note: *The exact size of the grid is dependent on the resolution, since the grid is always divided into whole pixels.*

Visual editing of the dose grid

To visually edit the grid position and size, select **Edit dose grid** from the 2D view context menu. Click and drag the handles at the top, bottom, sides or corners of the grid displayed in the view.

Make sure to exit editing mode by deselecting **Edit dose grid** from the 2D view context menu.

Make sure that the dose grid visualization is turned on by checking the **Show dose grid** checkbox in the **Visualization** tab. See *section 3.4 The tool panel tabs - ROI list, POI list, Visualization, etc. on page 53* for more information.

6.1.5 Edit isocenter position

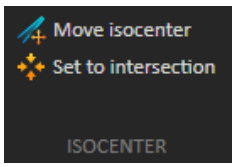
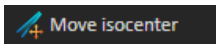
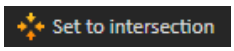


Figure 168. The Isocenter tools.

There are several options for editing the isocenter using the the **Isocenter** tools.



Move isocenter: Move the isocenter to the desired position by click and drag in the BEV.



Set to intersection: Move the isocenter to the slice intersection.

As a help when editing the isocenter, the intersection point of the beam center with the patient is displayed as a cross on the External ROI surface.

FOV and Bore visualization

The 2D and 3D views includes machine specific FOV and Bore visualization that can be used to verify that no collisions will occur. The FOV (blue) and Bore (orange) is visualized in the 2D and 3D views, together with a cross marking the isocenter position for the beam. These can be disabled in the **Visualization Settings** tab. For more information, see *chapter 3 The Graphical User Interface*.

WARNING!

Collision avoidance for TomoHelical. After isocenter adjustments, always make sure that the patient will fit comfortably on the couch in the gantry bore. The 2D and 3D views include machine specific FOV and Bore visualization that can be used to verify that no collisions will occur. Do not use the Room view to verify collision avoidance. (254787)

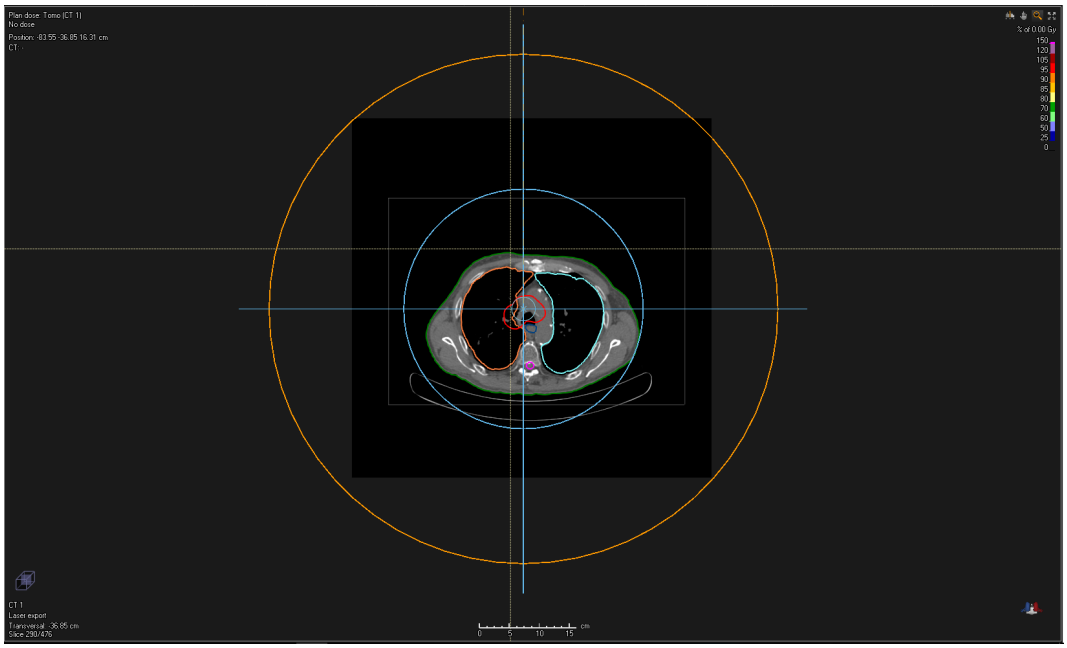


Figure 169. The FOV and Bore visualization in the 2D view.

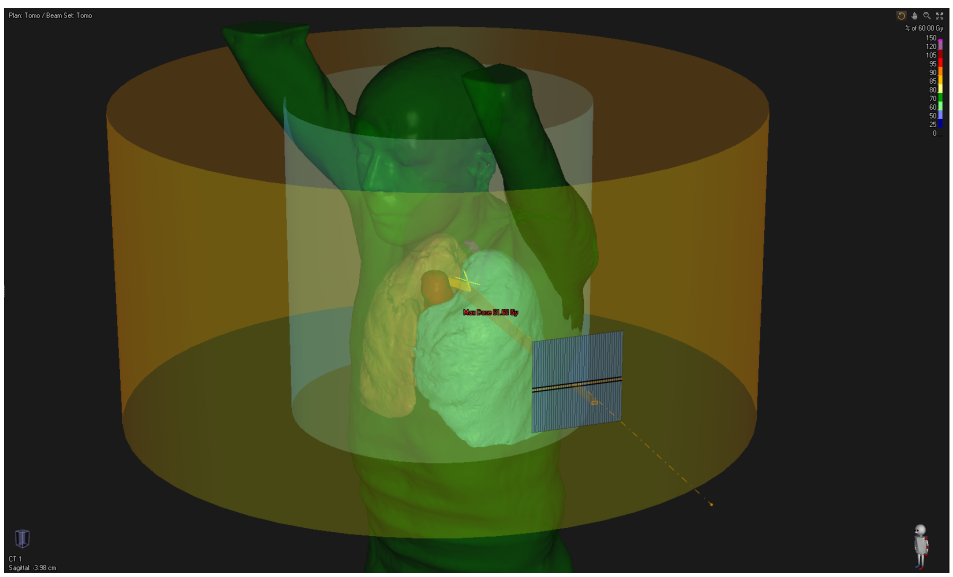


Figure 170. The FOV and Bore visualization in the 3D view.

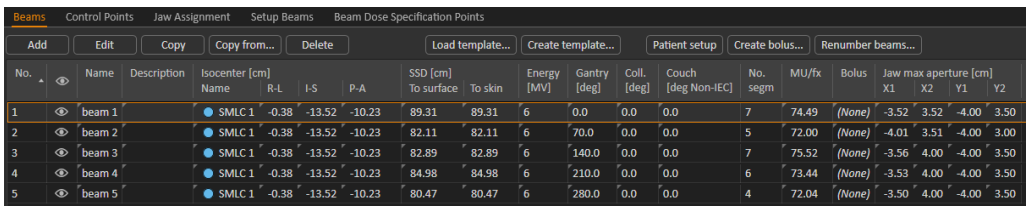
6.1.6 Add, edit, copy or delete beams

Beams can be added to a plan in several ways;

- adding a new beam by specifying beam properties
- copying an already existing beam, from the current beam set or another beam set
- adding a set of pre-defined beams from a template. See *section 6.1.7 Beam list templates on page 328* for more information.
- create opposed beam (only available for 3D-CRT planning)

The beam properties vary depending on the selected treatment modality, but the steps to create, copy, and delete beams are common.

Note: *Copying a VMAT, Conformal Arc or Static arc beam does not result in a new beam with MU=0. Instead the new beam will get the same MU as the original beam.*



No.		Name	Description	Isocenter [cm] Name	R-L	I-S	P-A	SSD [cm] To surface	To skin	Energy [MV]	Gantry [deg]	Coll. [deg]	Couch [deg Non-IEC]	No. segm	MU/fx	Bolus	Jaw max aperture [cm] X1	X2	Y1	Y2
1		beam 1		SMLC 1	-0.38	-13.52	-10.23	89.31	89.31	6	0.0	0.0	0.0	7	74.49	(None)	-3.52	3.52	-4.00	3.50
2		beam 2		SMLC 1	-0.38	-13.52	-10.23	82.11	82.11	6	70.0	0.0	0.0	5	72.00	(None)	-4.01	3.51	-4.00	3.00
3		beam 3		SMLC 1	-0.38	-13.52	-10.23	82.89	82.89	6	140.0	0.0	0.0	7	75.52	(None)	-3.56	4.00	-4.00	3.50
4		beam 4		SMLC 1	-0.38	-13.52	-10.23	84.98	84.98	6	210.0	0.0	0.0	6	73.44	(None)	-3.53	4.00	-4.00	3.50
5		beam 5		SMLC 1	-0.38	-13.52	-10.23	80.47	80.47	6	280.0	0.0	0.0	4	72.04	(None)	-3.50	4.00	-4.00	3.50

Figure 171. The **Beams** tab for a photon plan. To edit a beam, select it and click the **Edit** button, or edit the beam by clicking the desired property field.

Add photon beams

1. Click the **Add** button in the beam list. This opens the Add beam dialog.

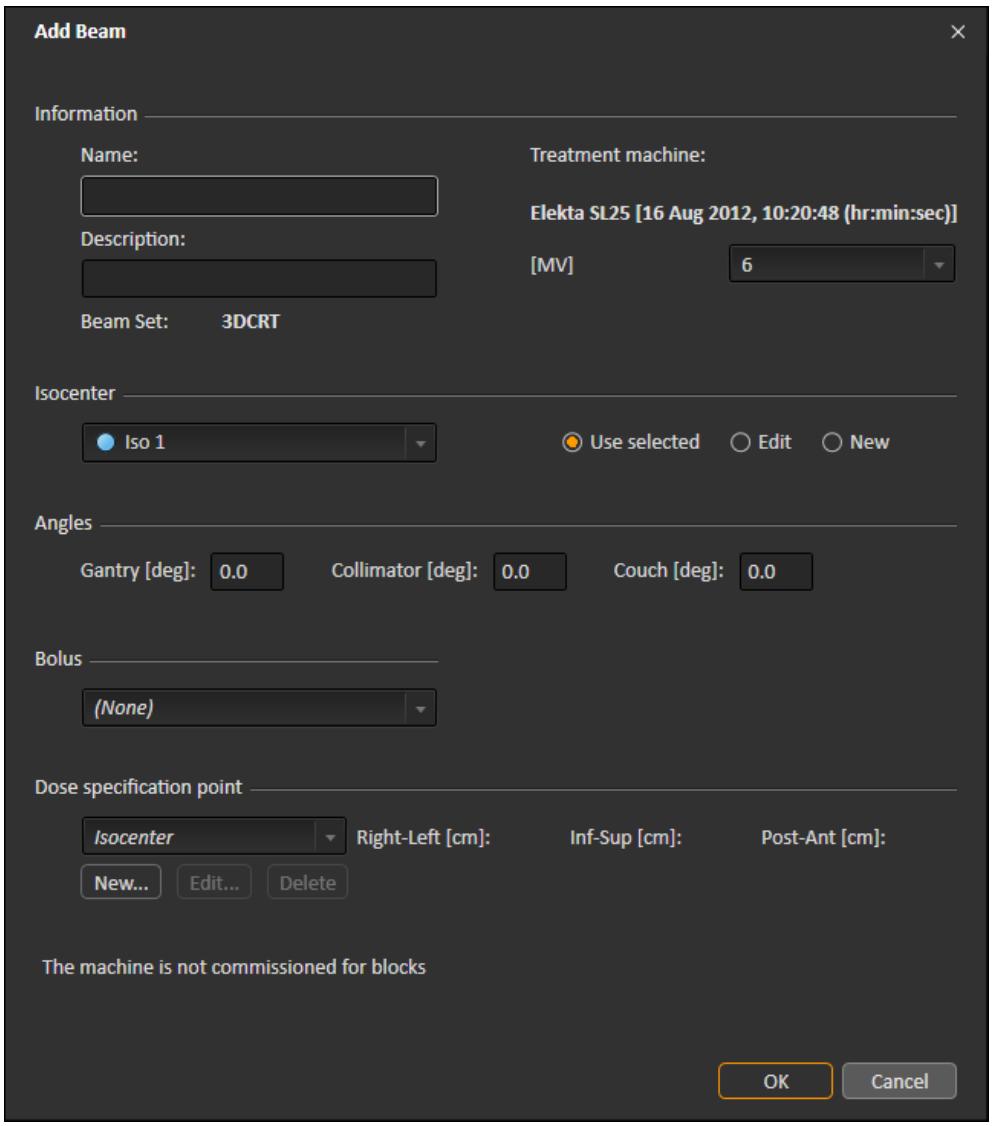


Figure 172. The Add beam dialog for photons.

2. Enter a **Name** for the beam.
3. Enter a **Description** of the beam (optional).
4. Select **Energy**.

5. Select **Isocenter**. Select to use an existing isocenter (**Use selected**), edit the existing isocenter (**Edit**) or define a new isocenter manually (**New**) or by copying the bounding box center positions of an ROI or a POI.

   - **Use selected**: If an isocenter already exists it will linked to this beam by default. The isocenter of the selected beam in the beam list will be the default selection. If there are no beams but an isocenter exists, this isocenter will be used by default when adding beams.
   - **Edit**: Edit the selected isocenter. Name and color is assigned by default but can be changed.
     - If the isocenter shall be in the center of an ROI, select an ROI from the **Center of ROI** drop-down list.
     - If the isocenter shall be in the same position as a POI position, select a POI from the **POI** drop-down list.
     - If the isocenter shall be in the center of the image set, select the **Center of image set** checkbox.
     - Multiple beam sets only: If the isocenter shall be in the same position as an isocenter in another beam set, select the isocenter from the drop-down list and click the **Copy position** button.

     Note: *Any edits will affect all beams sharing this isocenter.*
   - **New**: Create a new isocenter for this beam by defining it manually or by copying the bounding box center positions of an ROI or a POI. Name and color is assigned by default but can be changed. When creating a new isocenter it is possible to copy positions in the same way as when editing an isocenter (described in the previous bullet point). If the isocenter shall be in the center of the image set, click the **Center of image set** button. For TomoHelical beams, the isocenter position will default to the center of the image set.

WARNING!

Collision avoidance for TomoHelical. After isocenter adjustments, always make sure that the patient will fit comfortably on the couch in the gantry bore. The 2D and 3D views include machine specific FOV and Bore visualization that can be used to verify that no collisions will occur. Do not use the Room view to verify collision avoidance. (254787)

It is also possible to assign a separate isocenter to the beam by right-clicking the isocenter in the beam list and select "Duplicate isocenter".

Note: *Isocenter names must be unique within the plan. If multiple plans uses the same isocenter names, but the isocenters have different coordinates at the time of approval, export or plan report printout, the isocenters need to be renamed to prevent misinterpretation.*

6. Enter **Gantry angle**, **Collimator angle** and **Couch angle**.

   For a VMAT beam, Conformal Arc beam or Static Arc beam, the user does not enter gantry angle, but instead Gantry start angle, Gantry stop angle and Rotational direction. For a Conformal Arc beam, the user also selects the gantry spacing.

   For a machine set up to support variable couch angles (dynamic wave arcs) in RayPhysics, a **Wave arcs** checkbox is available if VMAT has been selected as treatment technique. For more information about this option, see *section 7.1.20 Wave arc on page 563*.

7. If desired, select a **Bolus** from the list. If there is no bolus in the list this has to be created, see *section 6.1.11 Create bolus on page 341* for more information.

8. A **Dose Specification Point** can be selected or created. (This point and its dose value are exported and may be used as reference for independent verification of the dose calculation. See *section 6.1.9 Beam dose specification point on page 337* for more information.)

9. Click **OK**. The created beam will be visible in the beam list.

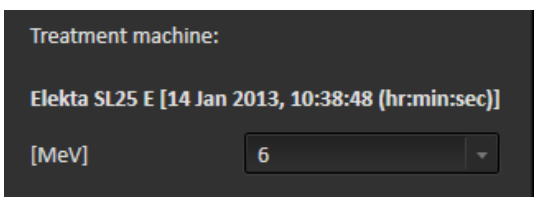
   To add additional beams, repeat step 1 to 8 above, or copy the created beam by clicking the **Copy** button (see *Copy a beam in the current beam list on page 326*) or the **Copy from...** button (See *Copy beams from another plan or another beam set on page 326*).

   Beams can also be added from a template by clicking the **Load template** button (see *Add beams from template on page 328*).

Note: *All 3D-CRT beams will be created with virtual jaws.*

Add electron beams

1. Perform steps 1 to 5 in *Add photon beams on page 317*. Note that the beam energy is selected in MeV for electrons.



2. Enter **Gantry angle**, **Collimator angle** and **Couch angle**.

3. If desired, select a **Bolus** from the list. If there is no bolus in the list this has to be created, see *section 6.1.11 Create bolus on page 341* for more information.

4. A **Dose Specification Point** can be selected or created. (This point and its dose value are exported and may be used as reference for independent verification of the dose calculation. See *section 6.1.9 Beam dose specification point on page 337* for more information.)
5. Select an **Applicator**. The available applicators are defined during Beam Commissioning.

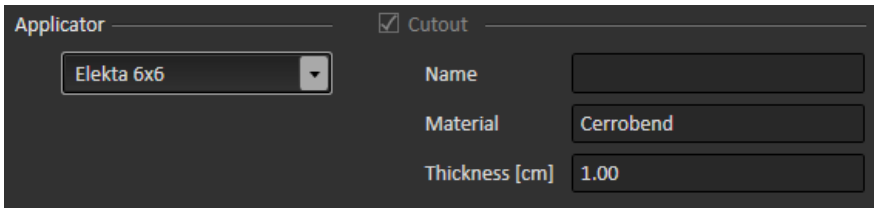


Figure 173. The electron specific properties of the **Add Beam** dialog.

6. Enter a **Name** for the cutout.

   The cutout **Material** and **Thickness** are defined for the selected applicator during Beam Commissioning.
7. Click **OK**. The created beam will be visible in the beam list.

   To add additional beams, repeat step 1-9 above, or copy the created beam by clicking the **Copy** button (see *Copy a beam in the current beam list on page 326*).

   Beams can also be added from a template by clicking the **Load template** button (see *Add beams from template on page 328*).

Add proton beams for Uniform Scanning/Double Scattering/Wobbling

1. Click the **Add** button in the beam list. This opens the Add beam dialog.
2. Enter a **Name** for the beam.
3. Enter a **Description** of the beam (optional).
4. Select **Isocenter**. Select to use an existing isocenter (**Use selected**), edit the existing isocenter (**Edit**) or define a new isocenter manually (**New**) or by copying the bounding box center positions of an ROI or a POI. For more information, see the Select isocenter step in *Add photon beams on page 317*.

   Note: *Isocenter names must be unique within the plan. If multiple plans uses the same isocenter names, but the isocenters have different coordinates at the time of approval, export or plan report printout, the isocenters need to be renamed to prevent misinterpretation.*
5. Enter **Gantry angle**, **Collimator angle** and **Couch angle**.
6. A **Dose Specification Point** can be selected or created. (This point and its dose value are exported and may be used as reference for independent verification of the dose calculation. See *section 6.1.9 Beam dose specification point on page 337* for more information.

7. Select a **Snout**. The available snouts are defined during Beam Commissioning.

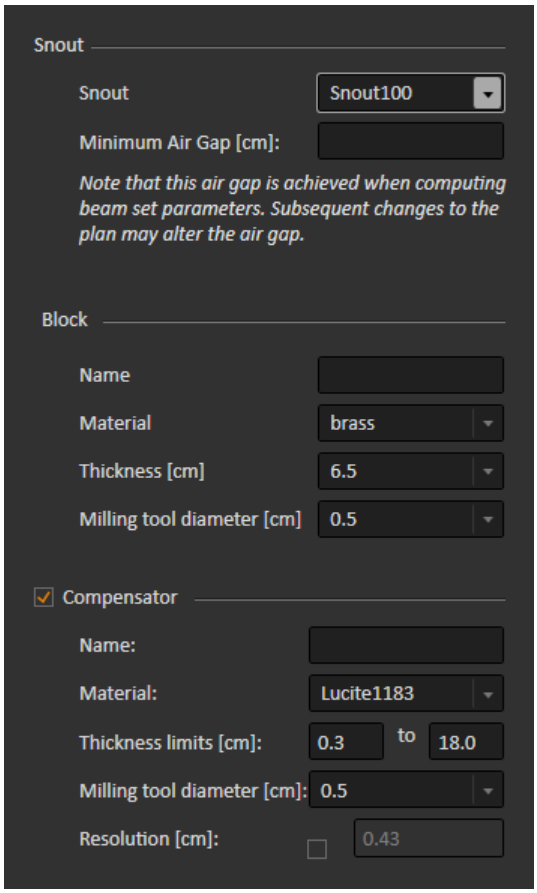


Figure 174. The Uniform Scanning/Double Scattering/Wobbling specific properties of the **Add Beam** dialog.

8. Enter **Minimum Air gap**. For more information, see *Air gap for proton beams on page 325*.

   Note: *This air gap is achieved when computing beam set parameters. Subsequent changes to the plan may alter the air gap.*

9. If applicable, select a **Meterset Rate Setting**. The available meterset rate settings are defined during Beam Commissioning.
10. Select if a **Block** shall be used by checking the corresponding checkbox (applicable if the machine has MLC).
11. Enter **Block** information. The block parameters are defined during Beam Commissioning.
    a. Enter a **Name** for the block.

b. Select a **Material** for the block.

c. Select a **Thickness** for the block.

d. Select **Milling tool diameter** for the block.

The block contour is edited in the Proton Beam Design module. Refer to the *section 6.5.11 Edit block aperture on page 506* for more information.

12. Select if a **Compensator** shall be used by checking the corresponding checkbox. If this is unchecked, the beam will be created without a compensator. The compensator settings are defined during Beam Commissioning.

    a. Enter a **Name** for the compensator.

    b. Select a **Material** for the compensator.

    c. Enter **Thickness limits** for the compensator. The minimum and maximum compensator thickness have to be entered in centimeter.

    d. Select **Milling tool diameter** for the compensator.

    e. Enter compensator **Resolution**. This defines the proximity of the drill positions. By default this value is calculated based on selected milling tool diameter. To enable editing of this value, check the **Resolution** checkbox.

    f. The comensator shape is edited in the Proton Beam Design module. Refer to the *section 6.5.13 Edit Compensator on page 513* for more information.

WARNING!

Always verify that the compensators created in the Proton Beam Design module can be manufactured. It is not possible to define all compensator manufacturing constraints in RayStation. It is the responsibility of the user to ensure that the compensator can be manufactured with respect to any limits on the drilling depths, since this is not explicitly handled in RayStation. However, any maximum drilling depth can be implicitly accounted for by the minimum and maximum compensator thickness limits that are defined when adding or editing a beam. (93369)

13. Click **OK**. The created beam will be visible in the beam list.

    To add additional beams, repeat step 1-8 above, or copy the created beam by clicking the **Copy** button (see *Copy a beam in the current beam list on page 326*).

Add proton beams for Pencil Beam Scanning/Line Scanning or add carbon ion beams for Pencil Beam Scanning

1. Click the **Add** button in the beam list. This opens the Add beam dialog.
2. Enter a **Name** for the beam.
3. Enter a **Description** of the beam (optional).
4. Select **Isocenter**. Select to use an existing isocenter (**Use selected**), edit the existing isocenter (**Edit**) or define a new isocenter manually (**New**) or by copying the bounding box center positions of an ROI or a POI. For more information, see the Select isocenter step in *Add photon beams on page 317*.

   Note: *Isocenter names must be unique within the plan. If multiple plans uses the same isocenter names, but the isocenters have different coordinates at the time of approval, export or plan report printout, the isocenters need to be renamed to prevent misinterpretation.*

5. Enter **Gantry angle**, **Collimator angle** (not for carbon ion beams) and **Couch angle**.
6. A **Dose Specification Point** can be selected or created. (This point and its dose value are exported and may be used as reference for independent verification of the dose calculation. See *section 6.1.9 Beam dose specification point on page 337* for more information.
7. Note the **Spot Tune ID**. The spot tune id is defined during Beam Commissioning. Only one spot tune id is supported in RayStation 7.

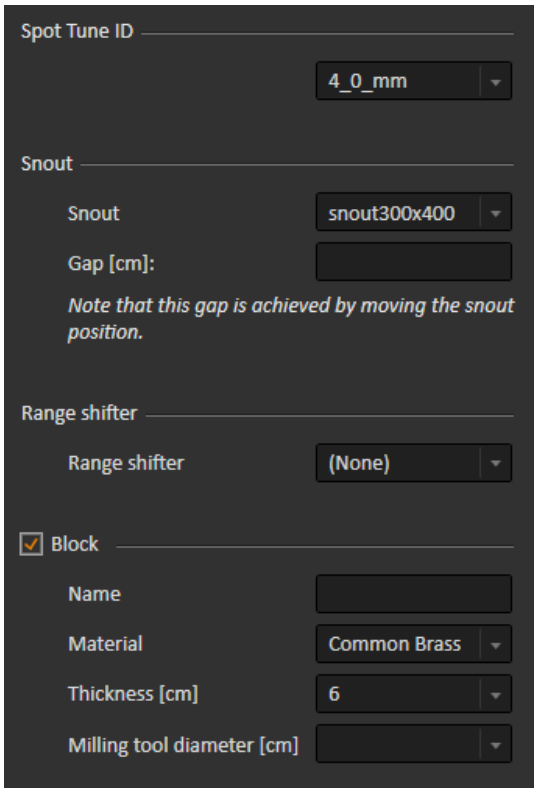


Figure 175. The Pencil Beam Scanning/Line Scanning specific properties of the **Add Beam** dialog.

8. Select a **Snout**. The available snouts are defined during Beam Commissioning.
9. A **Gap** can be entered. See *Air gap for proton beams on page 325* for more information.

   Note: *The gap value will adjust the snout position for moveable snouts. For fixed snouts, the patient position will be adjusted along the beam centerline.*

   Leaving the **Gap** edit box empty will set the snout to the most retracted position. The snout position and the gap can also be edited manually in the beam list. When editing the gap in the beam list, the snout position (moveable snouts) or the patient position (fixed snouts) is adjusted to achieve the desired gap.
10. If applicable, select a **Meterset Rate Setting**. The available meterset rate settings are defined during Beam Commissioning.
11. Select a **Range Shifter**. The available range shifters are defined during Beam Commissioning.

    Note: *For Mevion Hyperscan, range shifters are not selected manually for the beam. The only option available is (None), Range shifter settings are selected automatically for each energy layer during optimization.*

12. Select if a **Block** shall be used by checking the corresponding checkbox (applicable if the machine supports block).
13. Enter **Block** information. The block parameters are defined during Beam Commissioning.
    a. Enter a **Name** for the block.
    b. Select a **Material** for the block.
    c. Select a **Thickness** for the block.
    d. Select **Milling tool diameter** for the block.

    The block contour is edited in the Proton Beam Design module. Refer to the *section 6.5.11 Edit block aperture on page 506* for more information.

    Note: *The Mevion Hyperscan adaptive aperture is handled as a block and must be actively added by the user in order to get collimated fields.*

    For more information about Mevion Hyperscan adaptive aperture representation in RayStation 7, refer to RSL-D-RS-7.0-REF, RayStation 7 Reference Manual.
14. Click **OK**. The created beam will be visible in the beam list.

    To add additional beams, repeat step 1-8 above, or copy the created beam by clicking the **Copy** button (see *Copy a beam in the current beam list on page 326*).

Air gap for proton beams

The air gap is the distance along the nominal beam direction between the patient surface and the downstream plane of the most downstream snout mounted object for the selected snout in the beam. This can either be the snout tip, the compensator downstream surface or the range shifter downstream surface, depending on how the machine is commissioned. It is not allowed to commission machines so that the MLC or block is downstream of the snout tip plane, so they will thus not affect the air gap calculation.

Snout mounted objects will inherit lateral shape and outer dimensions from the selected snout for the beam, with the exception of range shifter that can optionally be assigned individual lateral shapes and dimensions during beam commissioning. The gap calculation is performed within these lateral shapes and dimensions.

The patient surface includes any fixation and support ROI(s).

WARNING!

Gap value for fixed snouts. The gap value for fixed snouts should only be given a value or be changed if the user plans for non-isocentric treatments. For fixed snouts, the patient position will be adjusted along the beam center line to achieve the desired gap. (125586)

Add or copy beams after dose computation

Adding a new photon beam or electron beam after dose computation will invalidate the dose since the new beam will automatically get the MU value 1 when the first control point is added. In order to add a new beam and modify the shape without losing the dose, make a copy of an existing beam. The result is a beam with the MU value 0 and the beam can then be shaped on top of an existing dose distribution. The MU value must however be changed prior to dose computation to avoid a beam with the MU value 0.

Copy a beam in the current beam list

To copy a beam in the current beam list, select the beam and click the **Copy** button. The name of the new beam will be the name of the old beam with a number at the end (where the number is 1 for the first copy, 2 for the second copy etc.).

Note: *The beam set dose is not invalidated when copying an existing beam. The copied beam will get the value MU=0.*

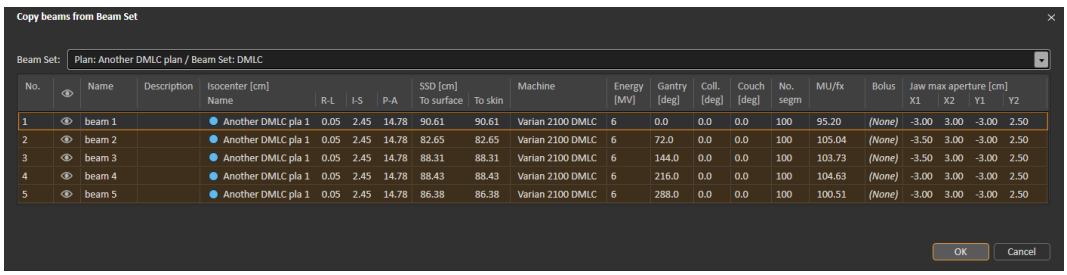
Note: *New or copied ion beams will get the value MU=0.*

Note: *For VMAT plans, Conformal Arc plans and Static Arc plans the copied beam will get the same MU as the original beam and therefore the beam set dose is invalidated when a beam is copied. For other treatment techniques, the beam set dose is not invalidated when a beam is copied since the copied beam will get the value MU=0.*

Copy beams from another plan or another beam set

To copy beams from another plan or from another beam set to the current plan:

1. Click the **Copy from...** button in the beam list. This opens the **Copy beams from Beam Set** dialog.



No.		Name	Description	Isocenter [cm] Name	R-L	I-S	P-A	SSD [cm] To surface	To skin	Machine	Energy [MV]	Gantry [deg]	Coll. [deg]	Couch [deg]	No. segm	MU/fx	Bolus	Jaw max aperture [cm] X1	X2	Y1	Y2
1		beam 1		Another DMLC pla 1	0.05	2.45	14.78	90.61	90.61	Varian 2100 DMLC	6	0.0	0.0	0.0	100	95.20	*(None)*	-3.00	3.00	-3.00	2.50
2		beam 2		Another DMLC pla 1	0.05	2.45	14.78	82.65	82.65	Varian 2100 DMLC	6	72.0	0.0	0.0	100	105.04	*(None)*	-3.50	3.00	-3.00	2.50
3		beam 3		Another DMLC pla 1	0.05	2.45	14.78	88.31	88.31	Varian 2100 DMLC	6	144.0	0.0	0.0	100	103.73	*(None)*	-3.50	3.00	-3.00	2.50
4		beam 4		Another DMLC pla 1	0.05	2.45	14.78	88.43	88.43	Varian 2100 DMLC	6	216.0	0.0	0.0	100	104.63	*(None)*	-3.00	3.00	-3.00	2.50
5		beam 5		Another DMLC pla 1	0.05	2.45	14.78	86.38	86.38	Varian 2100 DMLC	6	288.0	0.0	0.0	100	100.51	*(None)*	-3.00	3.00	-3.00	2.50

Figure 176. The **Copy beams from Beam Set** dialog.

2. Select the beam set to copy beams from in the drop-down list. Only beam sets that have the same treatment technique and machine are available for selection.
3. Select one or several beams to copy and click **OK**.

Create opposed beam

For 3D-CRT plans, an opposed beam can be created. Select a beam in the list and click the **Create opposed** button. This creates a new beam with an opposed gantry angle.

Edit beam

To edit a beam, select it in the **Beam** list and click the **Edit** button. The beam properties can also be edited directly in the **Beam** list by clicking the desired property field.

Delete beam

To delete a beam, select it in the **Beam** list and click the **Delete** button.

Renumber beams

The beams will be delivered in ascending order. To renumber the beams, click the **Renumber beams** button.

Edit beam angles in patient views

The gantry angle, for the current beam, can be edited visually from 2D patient views and from the Beam's Eye View (BEV). The couch and collimator angles can also be edited visually from the BEV.

The angle edit tools are activated from the view's context menu, by selecting the angle to modify in the **Edit Beam Angles** sub menu. Click in the view, keep the mouse button down and move the mouse to alter the angle. The result shows in all image windows, as well as in the beam list. Deselect the tool in the context menu, to switch it off.

To edit angles numerically, in the Edit Beam dialog or directly in the beam list, see *section 6.2.6 Edit beam properties on page 402*.

6.1.7 Beam list templates

A set of beams can be stored as a beam list template. The beam list templates can simplify the planning process, since standard beam setups can be re-used as a starting point when creating new plans. Beam list templates are applicable for all photon treatment techniques, for protons with treatment technique PBS and Line Scanning, and for carbon ions with treatment technique PBS.

Create beam list template

A beam list template is created from a plan's existing set of beams. To store the beams of the current plan as a template, click the **Create template...** button and enter a name for the new template. (The template can later be renamed or deleted from the Load template dialog).

For PBS/Line Scanning beams, the user will be asked if the gap values shall be stored in the template. When loading a template with the gap values stored, the snout (moveable snouts) or patient (fixed snout) will be moved to achieve this gap. If the gap values are not stored, the snout will be placed in the most retracted position and the patient will not move. Note that the blocks will not be saved in the template.

Add beams from template

To add beams from a template:

1. Click the **Load template...** button. This opens the Load Template dialog.

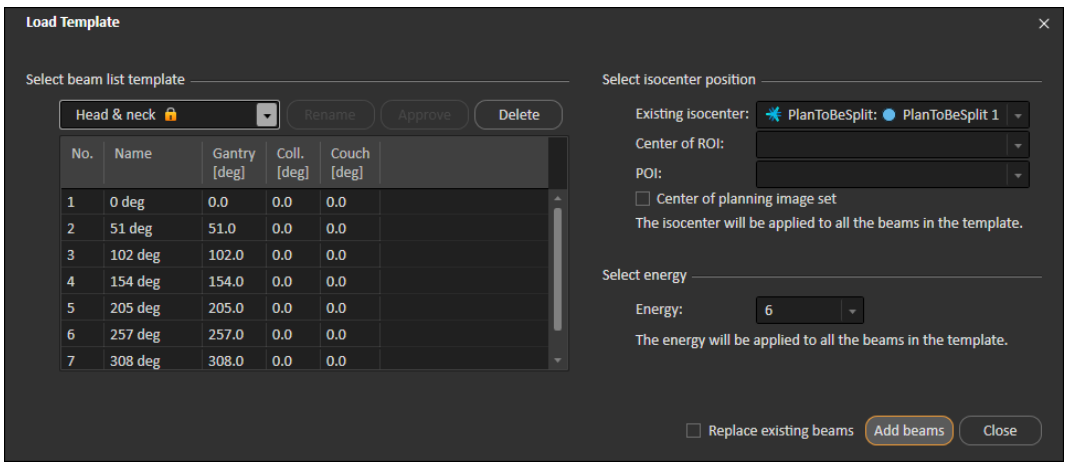


Figure 177. The Load Template dialog for treatment technique SMLC.

2. Select a **Beam list template** in the drop-down list. The beams for the selected template are listed in the beam list of the Load Template dialog.

   Note: *Only PBS/Line Scanning beam list templates with a snout id supported by the selected machine will be available in the drop-down list.*

3. The beam's isocenter position can be set by selecting the position of the existing isocenter, the center of an ROI, a POI or the center of the planning image set. If the isocenter shall be in

the center of the image set, check the Center of image set checkbox. The isocenter will be applied to all the beams in the template.

Multiple beam sets: It is also possible to select an isocenter from another beam set. Note that the coordinates will be copied to a new isocenter. Isocenters cannot be shared between beam sets. Editing the isocenter will hence not affect any beams in another beam set.

4. Select **Energy**. The energy will be applied to all the beams in the template. (Energy selection is not applicable for PBS/Line Scanning beam list templates.)
5. Select to **Replace existing beams** by checking the corresponding checkbox.
6. Click the **Add beams** button. This will add the template's beams to the plan.

To rename the selected template, click **Rename** and enter a new name for the template. To delete the selected template, click **Delete**.

To approve a template, click **Approve**. Only admin users can approve a template. Approved templates have a padlock next to the template name. If a non-approved template is loaded, a warning will be displayed. These warnings can be disabled in Clinic Settings. For more information on template approval, see *Approval of templates on page 43*.

6.1.8 The DRR views and settings

A DRR (Digitally Reconstructed Radiograph) is a 2D radiograph reconstructed from the CT data set slices (or densities based on CT to density conversion and material overrides, if selected). A DCR (Digitally Composited Radiograph) is a type of DRR, generated in a way that makes it possible to selectively suppress or enhance tissue types in the image. For DCRs, portions of the patient anatomy can be removed entirely, to further enhance specific areas, organs, or parts of organs. The term "DRR" is used in RayStation and in the user documentation when referring to DRR/DCR.

RayStation 7 supports multiple DRR types per beam set. Each DRR type has its own settings, which makes it possible to have various DRR images per beam, e.g., to visualize or highlight different aspects of the patient anatomy. Each DRR type generates an image for each beam, including possible setup beams. When a DRR is shown in a view, the **Current type** of the DRR type settings is also displayed.

It is possible to view a DRR generated from the densities based on CT to density conversion and material overrides, defined on the dose grid, by changing the patient data to "Material vis." by clicking the image set identification name in the view. For more information, see *Lower left corner on page 69*.

Note: *For VMAT, Conformal Arc and Static Arc plans, DRRs will be generated from the beam angle of the first segment of each beam.*

The DRR view and the Setup DRR view

The **DRR** view and the **Setup DRR** view are found in the Plan Setup workspace. The **DRR** view is visualized in any chosen angle belonging to a treatment plan. There is also a corresponding view for the setup beams, the **Setup DRR** view.

Selecting a beam in the **Beams** list will show the corresponding DRR in the **DRR** view and selecting a beam in the **Setup Beams** list will show the corresponding DRR in the **Setup DRR** view. The beams can also be selected via pie chart and mouse wheel. It is possible to change the selected beam in the BEV by clicking the beam name in the lower left corner of the view.

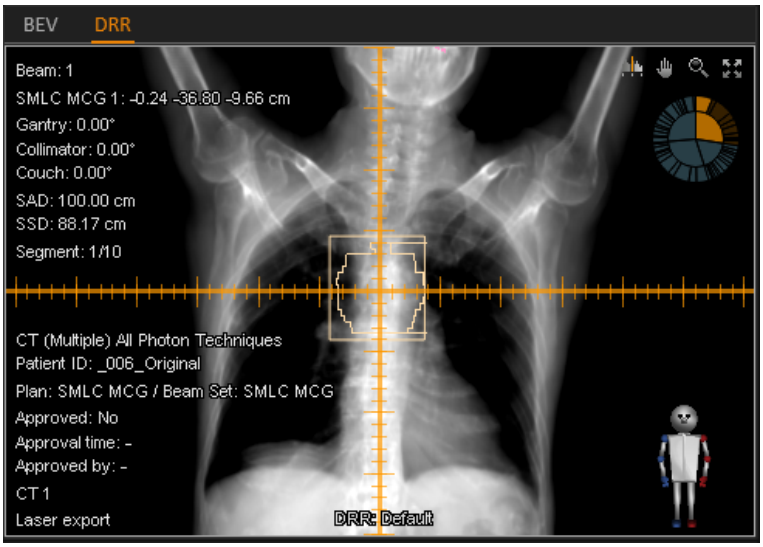


Figure 178. Example of the **DRR** view.

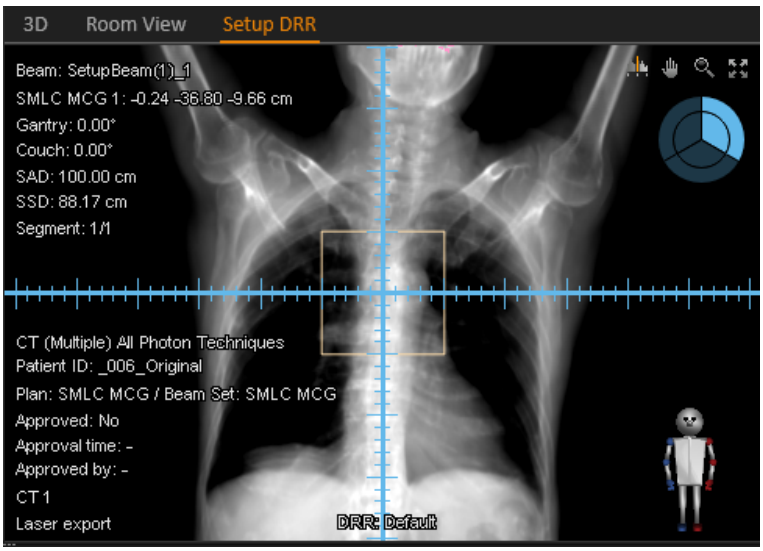
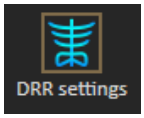


Figure 179. Example of the **Setup DRR** view.

Change DRR settings

To change DRR settings, click the **DRR settings** icon.



This opens the **Edit DRR Settings** dialog.

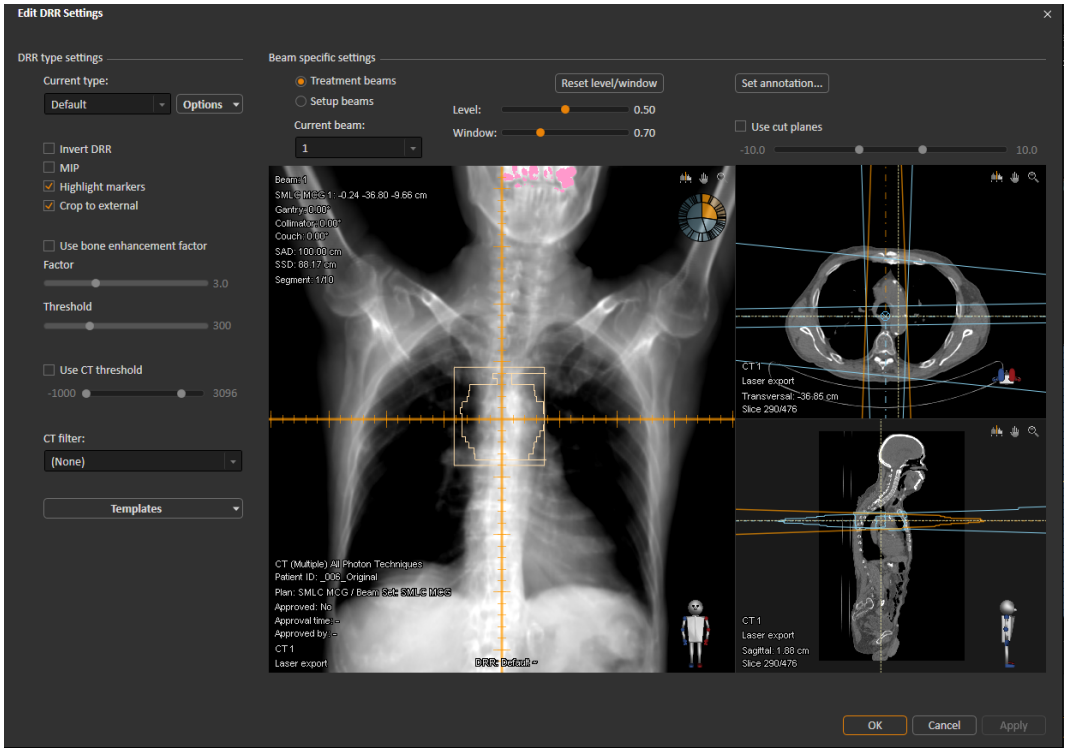


Figure 180. The **Edit DRR Settings** dialog.

The following DRR settings are available in the **Edit DRR Settings** dialog:

Parameter	Description
DRR type settings - common for all beams' DRRs of the selected type	
Current type drop-down list	For each beam set DRRs will be generated using the Default settings. To select another DRR type, click on the **Current type** drop-down list and select it from the list.

Parameter	Description
Options drop-down list	New DRRs can be created in two ways, either by copying the current DRR type or by creating one from a template. DRR templates are described in more detail below in DRR template settings. Before selecting another DRR type or creating a new DRR type, click the **Apply** button to confirm the current DRR settings. The following options are available from the **Options** drop-down list: • Select **Create new type from template** to create a new DRR type from a selected template. • Select **Copy current settings to new type** to copy the current settings to a new DRR type. • Select **Rename selected type** to rename the selected DRR type. • Select **Delete selected type** to delete the selected DRR type.
Invert DRR	Inverts the gray scale of the image, e.g., bones will be black on white background.
MIP	Maximum Intensity Projection (MIP) of patient data through the image.
Highlight markers	Enhances the contrast for existing markers, making them appear distinctively in the DRR. If the DRR generation algorithm finds a CT value higher than a threshold, that pixel is highlighted with a pink tint.
Crop to external	Excludes all CT data outside the External ROI when generating the image. This option is for example used to exclude the CT couch.
Use bone enhancement factor	This option is used to increase the contrast between bone and other tissue. **Threshold** - defines the lower CT limit on what is considered to be bone. **Factor** - defines how to scale the attenuation of the CT data above the selected threshold. Note that the factor can be set below 1 to suppress the bones (or values above the threshold).
Use CT threshold	This option is used to select which gray-value ranges of the CT data to include in DRR generation. Data below and above the sliders will be ignored in DRR calculation.

Parameter	Description
CT filter	The system provides pre-defined filters used to adjust how the CT data will be handled in the attenuation function. The filters modify how CT data are attenuated. To select a filter, click the **CT filter** drop-down list and select from the list. ***Note:*** *These filters are mainly kept for backwards compatibility. When creating DRRs on new plans, use bone enhancement factor and CT threshold instead.*
DRR template settings (available from the **Templates** drop-down list)	The DRR settings can be stored as a DRR template. The templates can simplify the planning process, as standard DRR types can be re-used when creating new plans. The default template is what is being applied to all new DRRs created in the plan. This template can be modified but it cannot be removed from the system. ***Note:*** *No beam specific settings are stored in the template.* The following actions can be performed from the **Templates** drop-down list: • Select **Load template** to load DRR settings from an existing DRR template. • Select **Create template** to create a DRR template based on the current settings. In the **Create Template** dialog, enter a **Name** for the new template and click **OK**. • Select **Update template from current settings** to update an existing DRR template based on the current settings. • Select **Delete template** to delete an existing DRR template.
Beam specific settings - specific for each beam's DRR image	
Treatment beams, **Setup beams**	Select to view DRRs for **Treatment beams** or for **Setup beams**.
Current beam drop-down list	Select the current beam from the **Current beam** drop-down list or in the pie chart in the **DRR** view. The selected beam is displayed in the **DRR** view.
Level, **Window** and **Reset level/window**	The DRR **Level** and **Window** sliders are used to change the contrast of the DRR image data. To reset the **Level** and **Window** sliders to default, click the **Reset level/window** button.

Parameter	Description
Set annotation...	Click the **Set annotation...** button to edit a text annotation for the **DRR** view.
Use cut planes	The **Use cut planes** option makes it possible to limit the CT data used for computing a DRR using two planes perpendicular to the beam angle. Only the CT data between the planes will be used. The cut planes are displayed in the 2D patient views and are moved using the sliders, or by using the **Move DRR cut planes** option in the **DRR** view, see *DRR options in BEV, DRR and Setup DRR views on page 335*.
DRRs created with RayStation versions earlier than 4.5	
Update to new DRR version button	When the **Edit DRR Settings** dialog is opened for a DRR type generated with RayStation versions earlier than 4.5, the **Update to new DRR version** button is displayed below the **DRR** view. Click this button to regenerate DRRs with the new algorithm. An old DRR will be regenerated with the new algorithm if changed in any way, whether the button is clicked or not.

DRR options in BEV, DRR and Setup DRR views

Views showing a DRR provide several options in the context menu:

Option	Description
Adjust DRR Level/Window	The DRR level window tool is activated for the current beam. Click the mouse button and move the mouse up and down to change level. Move the mouse left and right to change window.
Reset DRR Level/Window	Resets the current beam's DRR level and window to default.
DRR settings	Select which DRR type to show in a specific view. The options are: • **Off** - disables DRR visualization. • **Default** - creates a DRR type based on the default template. • **New setting from Template** - applies the settings from a saved template and creates a DRR type that is selectable within the current patient.

Option	Description
DRR Quality	Select rendering quality for the displayed DRRs. (Exported DRRs will always be of the same high resolution.) The selected DRR rendering quality might affect the performance of the system. The value defines a DRR sample rate and the effect is most obvious when using MIP. **Dynamic rendering threshold**: The system allows for dynamic on-screen quality degradation of DRRs to make the system more responsive during interaction. The value specifies how long time the DRR generation is allowed to run before the system automatically lowers the image quality. If the image quality is temporarily lowered, this is denoted with a "~" sign after the DRR type name in the view. As soon as the user interaction stops, the system renders an image with full quality (the selected **DRR Quality** value).
Use cut planes	The cut planes option makes it possible to limit the CT data used for computing the DRR using two planes perpendicular to the beam angle. Only the CT data between the planes will be used. The cut planes are displayed in the 2D patient views.
Move DRR cut planes	Selecting this option makes it possible to move the cut planes. To change position of the distal plane, press and hold down the mouse button while moving the mouse in the **BEV/DRR** view. To change position of the proximal plane, press and hold down the mouse button and the ALT key while moving the mouse in the **BEV/DRR** view.

6.1.9 Beam dose specification point

A beam dose specification point can be selected for each beam in the **Beam dose specification points** tab. This point and its values can be exported and used in external systems, for example RadCalc, to verify the dose calculation. The isocenter of each beam will, by default, be used as Beam dose specification point. Once clinical dose has been computed, different information is displayed for the Beam dose specification point depending on modality and treatment technique.

- For proton and carbon beams, **Dose per fraction** and **Physical depth** are displayed in the list.

  Physical depth is calculated as the distance between the skin surface intersection point and the beam dose specification point (BDSP) along a ray going from the beam source to the BDSP.

- For non-TomoHelical photon beams, values for **Dose per fraction**, **Physical depth** and **Water equivalent depth** are displayed. For VMAT, Conformal Arc and Static arc plans the **Physical depth** and the **Water equivalent depth** will be calculated as an unweighted mean over all control points. For Static arcs virtual control points are created maximum two degrees apart.

- For TomoHelical photon beams, only **Dose per fraction** is listed.

- For electron beams, **Electron density weighted depth**, which is the integrated depth from the surface weighted with the electron density relative to water, is given instead of **Water equivalent depth** in addition to **Dose per fraction** and **Physical depth**.

Note: *For carbon ions only: It is always the physical dose (not the RBE dose) that is displayed and exported for beam dose specification points.*

Note: *Ensure that the beam dose specification points are placed in a region where dose is not close to zero and where the dose gradient is low.*

Note: *For VMAT, Conformal Arc and Static arc plans, SSDs will be generated from the beam angle of the first segment of each beam.*

Select beam dose specification point

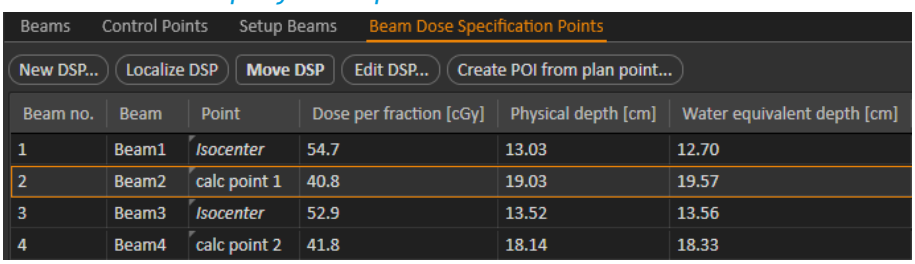


Figure 181. The **Beam dose specification points** tab.

Beams | Beam Dose Specification Points

Beam no.	Beam	Point	Dose per fraction (PHY) [cGy]	Physical depth [cm]
1	Left	*Isocenter*	30.4	7.66
2	Right	*Isocenter*	30.5	7.05

Figure 182. The **Beam dose specification points** tab for carbon ions.

Create a dose specification point

The beam dose specification point functionality is located in the **Beam Dose Specification Points** tab.

1. Click the **New DSP...** button or right-click in a patient view or select **Create dose specification point...** from the Context menu. Default point position is at the coordinates of the slice intersection.

Beams | Control Points | Setup Beams | Beam Dose Specification Points

New DSP... | Localize DSP | Move DSP | Edit DSP... | Create POI from plan point...

Beam no.	Beam	Point	Dose per fraction [cGy]	Physical depth [cm]	Water equivalent depth [cm]
1	Beam1	*Isocenter*	54.7	13.03	12.70
2	Beam2	calc point 1	40.8	19.03	19.57
3	Beam3	*Isocenter*	52.9	13.52	13.56
4	Beam4	calc point 2	41.8	18.14	18.33

Figure 183. The **Beam dose specification points** tab.

The **Create Dose Specification Point** dialog opens.

2. Select **Copy POI position** to create a dose specification point at the position of a POI.

Note: *The DSP will not move with the POI.*

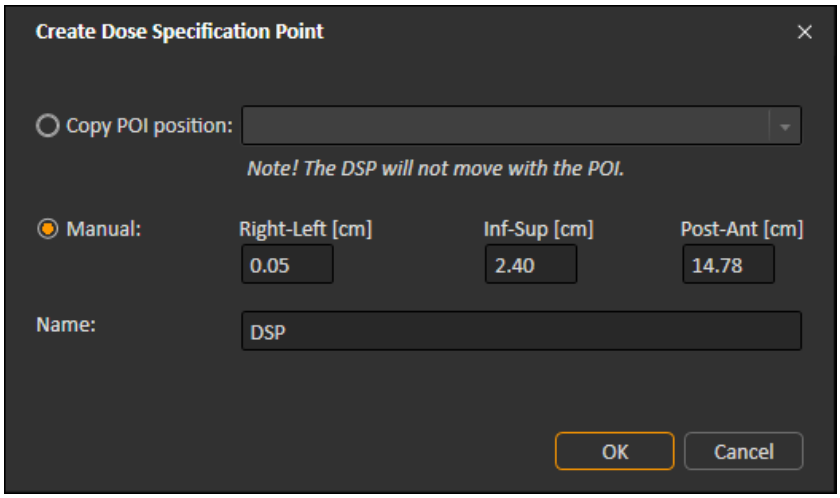


Figure 184. The Create Dose Specification Point dialog.

Localize dose specification point

Click the **Localize DSP** button to set the slice intersection to the position of the dose specification point of the currently selected beam.

Edit dose specification point

Click the **Edit DSP** button or right-click in a patient view to access the Context menu and select **Edit dose specification point...**. Select a point from the drop-down list and edit the positions as desired.

Move a dose specification point

Click the **Move DSP** button or right-click in a patient view to access the Context menu and select **Move dose specification point**. Drag and drop beam dose specification point(s) to desired positions. Click the **Move DSP** button again, or right-click the Context menu option, to exit edit mode.

Delete dose specification point

It is possible to delete a dose specification point from the Add/edit beam dialog.

6.1.10 Create POI from plan point

To create a POI from a plan point:

1. Click the **Create POI from plan point...** button or right-click in a patient view and select **Create POI from plan point...**. This opens the Create POI from Plan Point dialog.
2. Select to **Create POI from isocenter** or to **Create POI from dose specification point (DSP)**.
3. Specify POI properties such as **Name**, **Type** and **Color**.
4. Click **OK**.

6.1.11 Create bolus

Note: *Not applicable for carbon ions.*

To create a bolus:

1. Click the **Create bolus…** button in the **Beams** tab. This opens the Create bolus dialog.

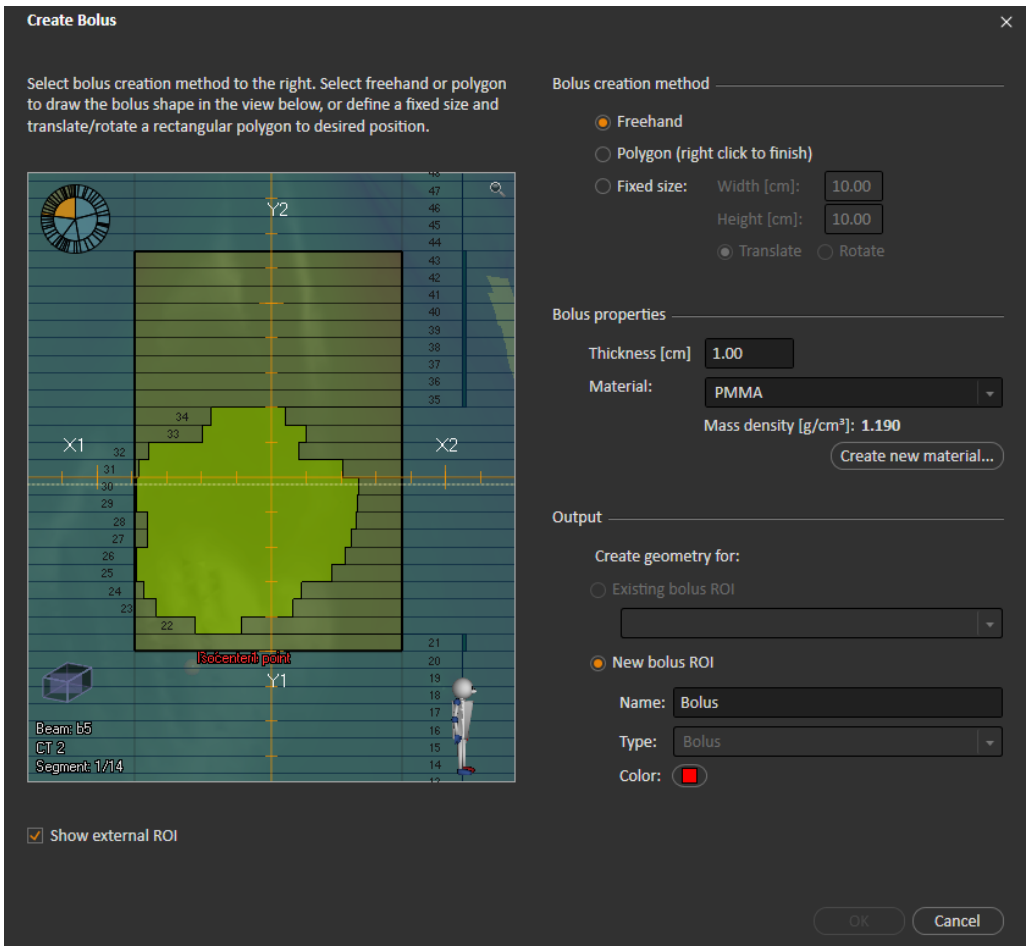


Figure 185. The Create bolus dialog.

2. Select to **Show the external ROI** by checking the corresponding checkbox.
3. Select **Bolus creation method**. The alternatives are; **Freehand**, **Polygon** and **Fixed size**. For a fixed size bolus, it is possible to **Translate** or **Rotate** the bolus in the BEV.

   Note: *When creating a bolus by drawing in the BEV, ensure that all surfaces on the bolus are visible in the BEV. Parts of the bolus that are hidden will not be included in the bolus.*

4. Enter a **Thickness** for the bolus.
5. Select a **Material** for the bolus.
6. Select to create geometry for an **Existing bolus ROI** or for a **New bolus ROI**.

   Note: *An existing bolus cannot be edited, but it is possible to create a new geometry for an existing bolus ROI.*

7. Click **OK**.

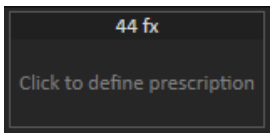
Note: *Dose will be calculated in boli ROIs also when the ROI is drawn outside of the CT images, as long as the ROI is inside the dose grid. Isodose lines and color wash will be visualized also outside of the CT images in the 2D views in RayStation.*

Note: *Dose computation with boli ROIs, as well as creation of boli ROIs from the Beams tab, is not supported for protons and carbon ions.*

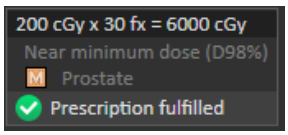
6.1.12 Define or modify prescription

To define or modify a dose prescription:

1. Click the **Define prescription** button to define a new prescription for the current plan,

   or click the **Prescription** button in the toolbar in order to modify an existing prescription.

   This opens the **Define Prescription** dialog.

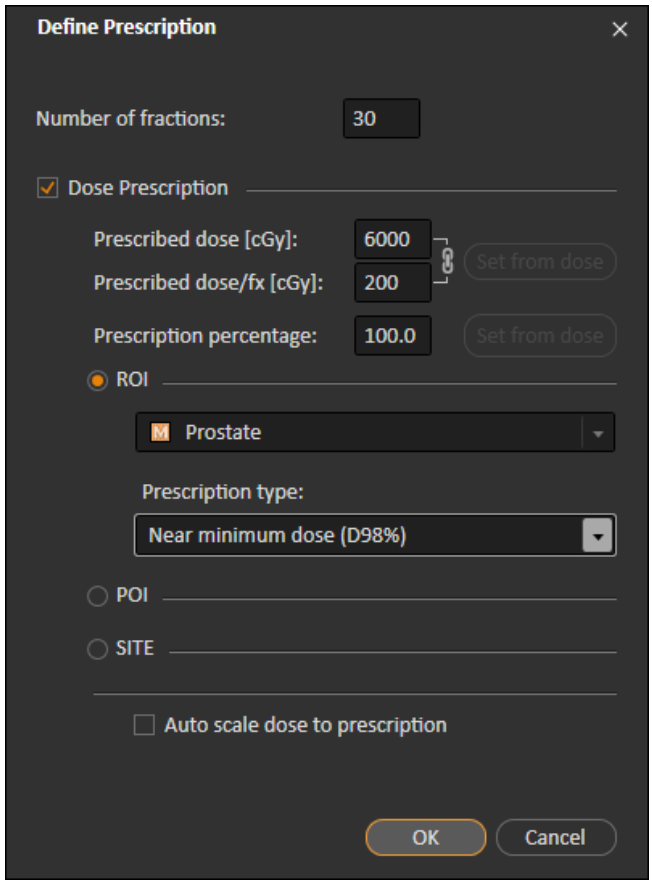


Figure 186. The **Define Prescription** dialog.

2. If desired, the **Number of fractions** can be changed.

   Note: *If an existing prescription is modified and the number of fractions is changed, only the prescribed dose will be updated based on the current prescribed dose per fraction.*

3. Check the **Dose Prescription** checkbox (if defining a new prescription).

   Note: *The dose color table by default uses the prescribed dose level as reference.*

   Note: *For carbon ions, prescription always relates to RBE dose.*

4. Enter either the **Prescribed dose** or the prescribed dose per fraction (**Prescribed dose/fx**).

   When changing the prescribed dose, the prescribed dose per fraction is updated based on the number of fractions. If instead the prescribed dose per fraction is changed, the prescribed dose will be updated based on the number of fractions.

   If the number of fractions is changed, only the prescribed dose will be updated based on the current prescribed dose per fraction.

   Note: *When having a background dose dependency, the prescribed dose per fraction is not defined. Therefore, when changing the number of fractions the prescribed dose will not change, so the underlying dose per fraction is scaled. The user is informed about this fact if changing the number of fractions.*

   If a dose exists, the **Set from dose** button can also be used to set the prescribed dose value from an existing dose in order to fulfill the prescription for the current dose distribution. The prescribed dose is then calculated in the following way:

   *Prescribed dose = Prescription percentage * Evaluated dose value*

   Example: Assume that the average dose in Prostate is 3332 cGy and the **Prescription percentage** is set to 100. The **Prescribed dose** value is then set to 3332 cGy when clicking the **Set from dose** button. The prescribed dose per fraction is updated according to the Prescribed dose value and the number of fractions.

5. Enter **Prescription percentage**.

   If a dose exists, the **Set from dose** button can also be used to set the prescription percentage value from an existing dose in order to fulfill the prescription for the current dose distribution. The prescription percentage is then calculated in the following way:

   Prescription percentage = Dose / Evaluated dose value

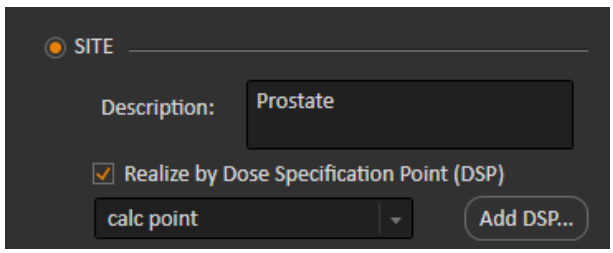
   Example: Assume that the **Dose** value is set to 3000 cGy and that the average dose in Prostate is 3332 cGy. The **Prescription percentage** is then set to 90% when clicking the **Set from dose** button.

6. Select to define a prescription for a selected **ROI**, **POI** or **SITE**.

   a. For a selected ROI there are several options in the **Prescription type** drop down list:

      - **Average dose** is defined as the average dose in the specified ROI.
      - **Near maximum dose (D2%)** is defined as the desired dose at 2% volume of the specified ROI.
      - **Median dose (D50%)** is defined as the desired dose at 50% volume of the specified ROI.
      - **Near minimum dose (D98%)** is defined as the desired dose at 98% volume of the specified ROI.
      - **Dose at volume** is defined as the desired dose at the entered volume [%] of the specified ROI.

   b. For a SITE prescription, a description of the prescribed site is required. A SITE prescription with only description will not be evaluated on if it is fulfilled or not.



      Optionally, the site prescription can be set to be realized by a selected dose specification point. The prescription will then be evaluated for the dose in the plan specific dose specification point.

      It is possible to click **Add DSP...** to add a dose specification point from the prescription dialogue. See *SITE prescription on page 347* for details.

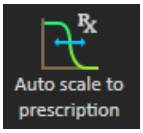
7. Click **OK**.

Remove prescription

To remove the prescription, uncheck the **Prescription** checkbox and click **OK**. The prescription button in the toolbar will be replaced with the **Define prescription** button.

Auto scale to prescription

If **Auto scale to prescription** is selected, the dose will always be scaled to fulfill the prescription, regardless of what change is done.

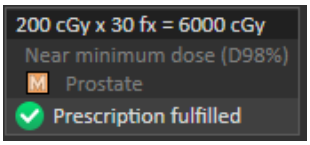


Note: *Auto scale to prescription is not available for carbon ions, nor for SITE prescriptions with a description only.*

For more information about auto scale to prescription, see *section 6.1.16 Auto scale to prescription on page 358*.

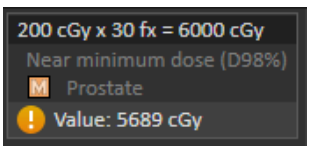
Fulfilled prescription

If the prescription is fulfilled, a green bullet and the text **Prescription fulfilled** will be displayed.



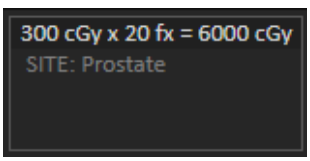
Note: *The prescription is evaluated with a one-sided relative tolerance of 0.5%. The prescription is considered to be fulfilled if the evaluated dose is equal to or larger than the prescription dose level and smaller than the prescription dose level times 1.005 (i.e., prescription dose level $\leq$ evaluated dose < prescription dose level · (1.005)).*

If the prescription is not fulfilled, a red bullet and the actual dose value will be displayed.

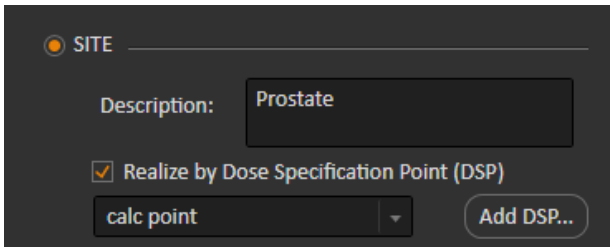


SITE prescription

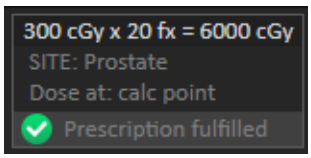
For a SITE prescription, a description of the prescribed site is required. A SITE prescription with only a description will not be evaluated regarding if it is fulfilled or not.



As an option, the site prescription can be set to be realized by a dose specification point. Check the corresponding checkbox and select the dose specification point to use. Click **Add DSP...** to add a dose specification point from the prescription dialog.



If a SITE prescription is realized by a dose specification point, the prescription will be evaluated for the dose in that dose specification point.



6.1.13 Beam entry validation

Beam entry validation is performed before optimization, before dose computation, at plan approval, and at DICOM export of unapproved plans. The purpose is to warn the user if the dose computation is likely to be wrong because of the way the dose grid is set up, or the way the External ROI and material override ROIs are defined.

Note: *Beam entry validation is a help for the user to detect setups that will cause an incorrect dose computation. For some cases there will be no warning, and the user is responsible to validate the proper beam and dose grid setup.*

Only material inside the dose grid is taken into account in the radiation transport steps in the dose computation. Not all material which is on the CT-scan is automatically included; the following materials are included:

- CT-values inside the External ROI
- Material overrides inside the External ROI
- Support and fixation ROIs both inside and outside the External ROI
- Bolus ROIs outside the External for the beams that the boli belong to

Make sure that the External ROI covers all parts of the CT images that are present at treatment and important for dose computation; the beam entry validation does not check the validity of the choice of External ROI but assumes that the External ROI is correct.

If the beam passes through parts of the External, support, bolus or fixation ROIs which are outside the dose grid, the dose computation will be wrong. Ensure that the dose grid always covers all parts of the External, support, bolus and fixation ROIs that are important for radiation transport. If there is doubt what should be considered as important include all density defining ROI regions.

Note: *No beam exit validation is performed. Missing density in the exit part may lead to an underestimation of the backscatter, the dose error due to missing backscatter is much smaller than the dose error due to missing attenuation.*

Note: *If the field borders are extended outside the radiation transport area (External ROI and material override ROIs inside the dose grid), there will be no dose computation in the outside parts and hence no dose contribution from the outside parts. If having this setup, an underestimation of the phantom scatter will occur, leading to dose errors.*

Note: *The beam entry validation assumes that the ROIs are correctly outlined.*

Note: *There is no beam entry validation performed on synthetic data.*

Beam entry validation before optimization and dose computation

Before optimization and dose computation it is checked if the centerline of the beam enters the External or any bolus, support or fixation ROIs outside the dose grid. In this case the optimization of dose computation is not allowed to proceed. For all these cases there is density outside the dose

grid and this is not taken into account in the dose computation; hence it is almost guaranteed that the dose computation is wrong.

Note: *For VMAT and Conformal Arc, all control points are tested. If no segments exist only the start angle is tested. This implies that before optimization the beam entry validation might pass, but before dose computation when there are segments, the beam entry validation might fail.*

Note: *For TomoHelical plans, no centerline check is performed. Instead dose grid entrance checks according to Dose grid entrance on page 352 will be performed at continued optimization and dose computation.*

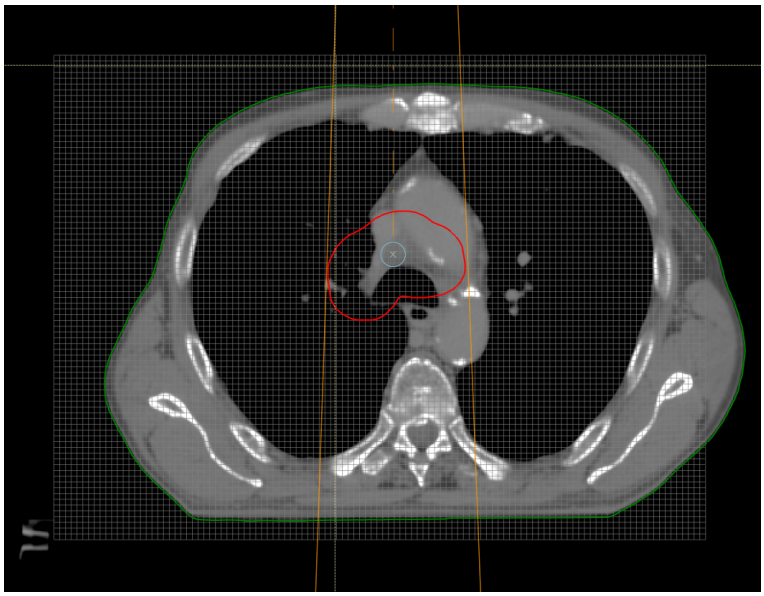


Figure 187. Example: Beam "b1" intersects the external ROI outside the dose grid.

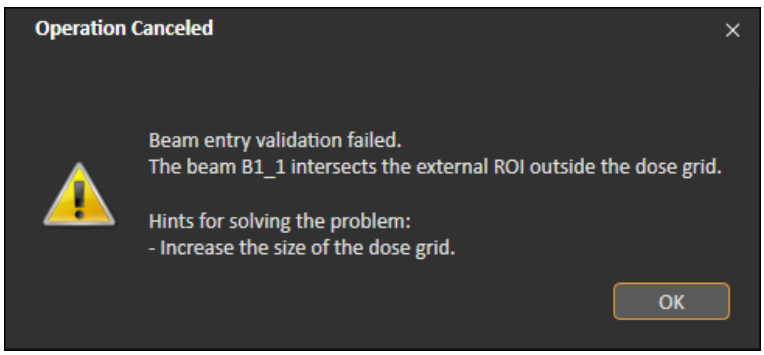

Operation Canceled
Beam entry validation failed.
The beam B1_1 intersects the external ROI outside the dose grid.
Hints for solving the problem:
- Increase the size of the dose grid.
OK

Figure 188. The warning dialog Operation canceled, beam entry validation failed. The beam "b1" intersects the external ROI outside the dose grid.

Beam entry validation before approval

Before approval, and DICOM export of unapproved plans, a more detailed beam entry validation is performed. This validation uses fluence levels across the beam.

Image stack entrance

It is not allowed for a beam to enter through an area where the image stack cuts the patient, unless remedied by material override ROIs outside of the image stack. An area less than 4 cm^2 indicates a proper endpoint of the ROI and is hence allowed.

If the projected beam area intersects an image border with more than 4cm^2 of the External, support or fixation ROIs the approval/export will be stopped.

Note that for photon beams, intersection with 10% to 50% of the max fluence will cause a warning only. This corresponds to the outer part of the fluence penumbra. It is then up to the user to estimate the importance of the missing attenuation and determine the proper measures.

Make sure to either:

- Modify the beam angles so that the beams do not intersect the ROI at the boundary of the image stack
- Remove the outermost contour of the ROI in the image stack
- Extend the ROI outside the image stack and ensure that the ROI is assigned a representative material

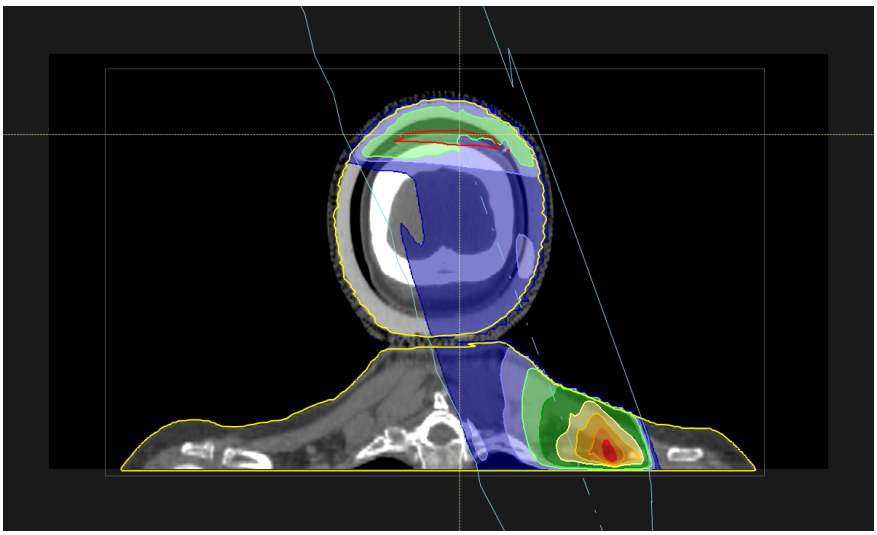


Figure 189. The beam is entering through an area where the External ROI has a non-negligible area.

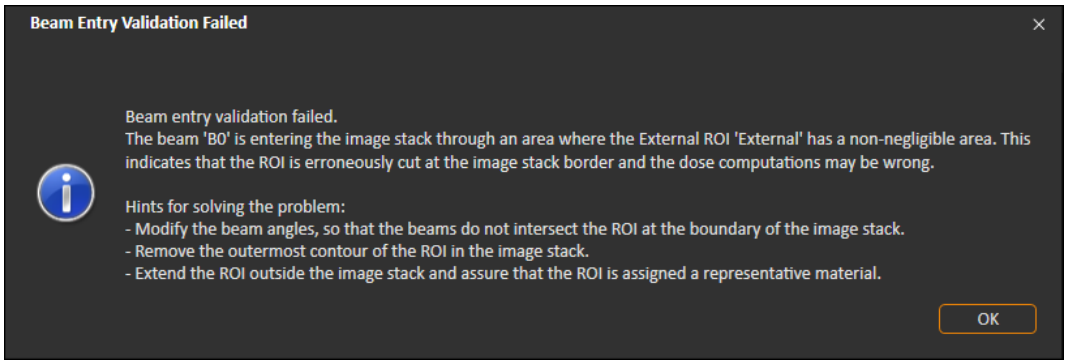

Beam Entry Validation Failed
Beam entry validation failed.
The beam 'B0' is entering the image stack through an area where the External ROI 'External' has a non-negligible area. This indicates that the ROI is erroneously cut at the image stack border and the dose computations may be wrong.
Hints for solving the problem:
- Modify the beam angles, so that the beams do not intersect the ROI at the boundary of the image stack.
- Remove the outermost contour of the ROI in the image stack.
- Extend the ROI outside the image stack and assure that the ROI is assigned a representative material.
OK

Figure 190. The warning dialog **Beam Entry Validation Failed**. The beam is entering through an area where the External ROI has a non-negligible area.

WARNING!

Beam Entry Validation for TomoHelical plans. Be aware that there is no image stack entrance control performed for TomoHelical plans. (254782)

Dose grid entrance

It is not allowed for a beam to enter through an area where the dose grid cuts away densities. If a projected beam area intersects the External, Support or Fixation ROIs outside of the dose grid, the approval/export will be stopped.

Note that for most photon beams, intersection with 10% to 50% of the max fluence will cause a warning only. This corresponds to the outer part of the fluence penumbra. It is then up to the user to estimate the importance of the missing attenuation and determine the proper measures.

Make sure to either:

- Modify the beam angles so that the beams do not intersect the ROI at the boundary of the dose grid
- Extend the dose grid

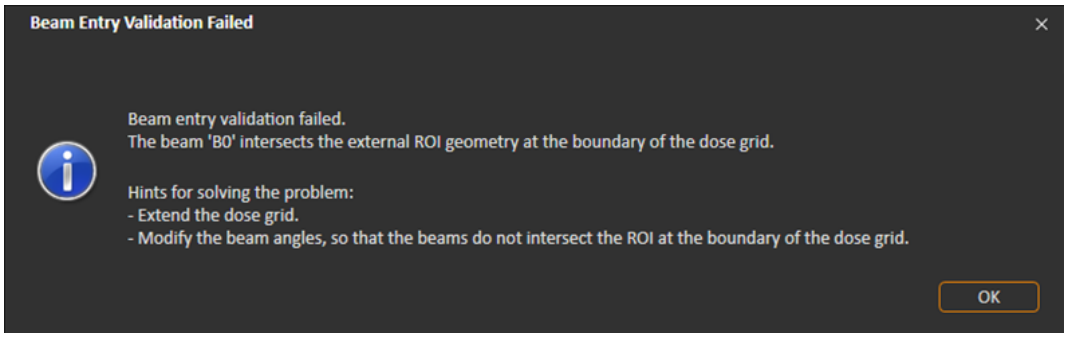
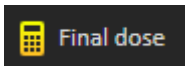

Beam Entry Validation Failed
Beam entry validation failed.
The beam 'B0' intersects the external ROI geometry at the boundary of the dose grid.
Hints for solving the problem:
- Extend the dose grid.
- Modify the beam angles, so that the beams do not intersect the ROI at the boundary of the dose grid.
OK

Figure 191. The warning dialog **Beam Entry Validation Failed**. The beam is entering through an area where the border of the dose grid cuts the External ROI.

6.1.14 Compute dose

Click the **Compute** button in the Final Dose section of the toolbar or type Ctrl + D to compute the dose for the current fluence.

For proton PBS/Line Scanning plans, the user can select several options for dose computation in a drop-down list.



Note: *If there already is a valid clinical dose computed with the same dose engine, it will not be recomputed.*

When the computation is completed, the dose will be displayed in the patient views. Click **Cancel** to abort a started dose computation.

The dose engines are described in the *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual*.

WARNING!

Dose computation region. Radiation transport and dose is computed only inside a region consisting of ROIs of type External, Bolus for beam, Support and Fixation. Image data not included in this region will be omitted from dose computation and is regarded as a vacuum (no interactions).

If the beam Field Of View covers part of the patient not inside the External ROI or any equipment not defined by Bolus, Support or Fixation ROIs, the dose computation will be incorrect.

Note also that the computation is limited to the dose grid. There is no warning if the dose grid does not cover the appropriate region. (7285)

WARNING!

Pixel padding. If pixel padding is present in the region used for dose computation, the calculated dose may be incorrect. Make sure that the pixel padded Hounsfield Units map to the desired density or make sure to add a material override to the pixel padded region.

If the CT-image has excluded material which will be present at treatment and which is inside the radiation scatter region, it is not recommended to use pixel padded values. Instead, add a material override to each material to include them in the dose computation. Failure to do so might lead to errors in the dose computation.

If everything that is important for radiation transport is inside the CT-image, but the External ROI covers image parts with pixel padding values that correspond to high density Hounsfield Units, this could also lead to errors in the dose computation. (56778)

WARNING!

Approximate dose is only intended for intermediate treatment planning steps. Approximate dose has lower accuracy compared to the dose displayed as "Clinical" and it must not be used for clinical decisions. A plan with approximate dose cannot be approved or exported. (126034)

WARNING!

MR planning: Bulk density assignment. RayStation planning based only on MR images relies on the user specified bulk-density assignment. Note that for certain configurations/regions, a bulk-density assignment using a homogeneous material will produce an unacceptable dosimetric error. (254454)

WARNING!

MR planning: Geometric distortion and field-of-view. MR images intended for planning must have negligible geometric distortion. RayStation does not include any algorithm for distortion correction. The MR image should cover the patient outline. (261538)

6.1.15 Scale dose

The dose can be scaled to fulfill the prescription or to fulfill an arbitrary dose-volume relation for a selected ROI or POI. To scale the dose:

1. Click the **Scale dose** button in the toolbar.

   This opens the **Scale Dose** dialog.

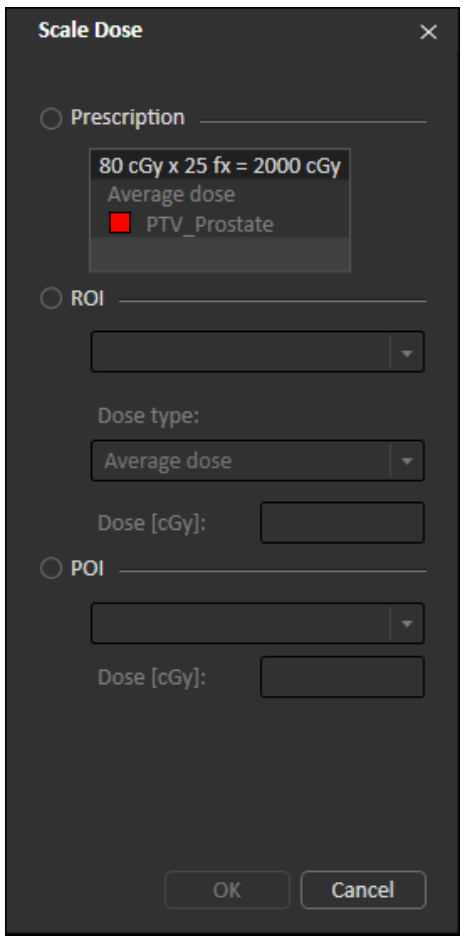
   

   Figure 192. The **Scale Dose** dialog.

2. Select to scale the dose to the current **Prescription**, or to a selected **ROI** or **POI**.

   For a selected ROI there are several options in the **Dose type** drop down list:

   - **Average dose** is defined as the average dose in the specified ROI.

- **Near maximum dose (D2%)** is defined as the desired minimum dose at 2% volume of the specified ROI.
- **Median dose (D50%)** is defined as the desired minimum dose at 50% volume of the specified ROI.
- **Near minimum dose (D98%)** is defined as the desired minimum dose at 98% volume of the specified ROI.
- **Dose at volume** is defined as the desired dose at the entered volume [%] of the specified ROI.

3. Click **OK**.

Note: *Due to machine constraints, scaling to an arbitrary dose level is not always possible. In case the scaling cannot be performed a warning dialog is displayed and the scaling operation is cancelled.*

Note: *If dose scaling is performed on a dose using a nonlinear RBE model, a dose computation will be automatically be triggered after clicking OK. This might be automatically iterated up to five times to achieve the desired dose level. Note that since the scaling factor is computed linearly, the resulting RBE dose will not, especially for large scaling factors, correspond with the desired value.*

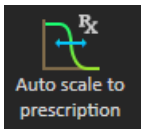
Note: *If dose scaling is performed on an imported RBE dose, only the physical dose will be scaled and the imported RBE dose will be invalidated, since there is no information about the linear nature of the underlying RBE model.*

Note: *For TomoHelical and Line Scanning beam sets the scaled dose will be approximate (non-clinical). Therefore, a clinical dose (final dose) needs to be computed after dose scaling. A Tomo Helical plan is scaled by changing the gantry speed. Since the machine supports a discrete number of gantry rotation periods, the scaling will generally result in a dose level that is slightly different than the specified value.*

Note: *For Mevion Hyperscan the scaled dose will be approximate (non-clinical). Therefore, a clinical dose needs to be computed after dose scaling.*

6.1.16 Auto scale to prescription

Click the **Auto scale to prescription** button in the toolbar to fulfil the prescription value regardless of any additional changes.



Note: *Auto scale dose to prescription can also be activated or deactivated from the New plan dialog, Edit plan dialog or from the Define prescription dialog.*

If auto scaling for any reason cannot be performed, the user will be informed about the reason, the function will be deactivated and the button will return to its non-pressed state.

Note: *To avoid dose being scaled in an inactive plan, the auto scale function will be deactivated if the prescription target ROI/POI's geometry is modified while the plan is inactive. The user will be asked to confirm this deactivation.*

Note: *Dose will only be rescaled if the prescription is not fulfilled. The prescription is considered to be fulfilled if the evaluated dose is equal to or larger than the prescription dose level and smaller than the prescription dose level times 1.005 (i.e., prescription dose level $\leq$ evaluated dose < prescription dose level $\cdot$ (1.005)). Small changes to the prescription dose level (within 0.5%) will therefore not lead to rescaling of dose.*

Note: *Auto scale to prescription is not available for carbon ions, nor for SITE prescriptions with a description only.*

6.1.17 Setup beams

Setup beams are created by checking the **Create setup beams** checkbox in the **New plan** dialog, see *section 6.1.3 Create a new plan on page 306*. Note that for ion treatment machines this is visible only if the machine has an imaging device. The setup beams isocenter positions and angles are displayed in the **Setup beams** tab in the beam list. Selecting a setup beam in the list will show the corresponding DRR in the **Setup DRR** view. The setup beams will be colored according to the selected isocenter.

The names, descriptions, gantry angles, couch angles and jaw positions can be edited directly in the **Setup beams** list.

Note: *Any changes to the setup beams are lost if the treatment machine for the Beam Set is changed.*

Setup beams for photon plans and electron plans

The setup beams shall be of energy 6 MV if possible. If the machine cannot deliver 6 MV, the lowest available energy is used.

Beams | Control Points | Setup Beams | Beam Dose Specification Points

Copy | Delete

No.	Name	Description	Isocenter [cm] Name	R-L	I-S	P-A	SSD [cm] To surface	To skin	Energy [MV]	Gantry angle [deg]	Couch [deg]	Jaw max aperture [cm] X1	X2	Y1	Y2
1	SB1_1	SetupBeam(1)_1	Iso 1	0.20	-4.75	-1.27	87.10	87.10	6	0.0	0.0	-5.00	5.00	-5.00	5.00
2	SB1_2	SetupBeam(1)_2	Iso 1	0.20	-4.75	-1.27	80.48	80.48	6	90.0	0.0	-5.00	5.00	-5.00	5.00
3	SB1_3	SetupBeam(1)_3	Iso 1	0.20	-4.75	-1.27	80.68	80.68	6	270.0	0.0	-5.00	5.00	-5.00	5.00
4	SB2_1	SetupBeam(2)_1	Iso 2	4.25	-4.75	-2.21	86.71	86.71	6	0.0	0.0	-5.00	5.00	-5.00	5.00
5	SB2_2	SetupBeam(2)_2	Iso 2	4.25	-4.75	-2.21	84.54	84.54	6	90.0	0.0	-5.00	5.00	-5.00	5.00
6	SB2_3	SetupBeam(2)_3	Iso 2	4.25	-4.75	-2.21	76.70	76.70	6	270.0	0.0	-5.00	5.00	-5.00	5.00

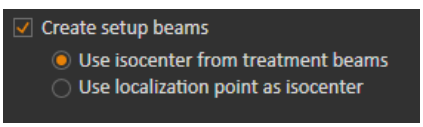
Figure 193. The **Setup Beams** tab for photon and electron plans.

Setup beams for proton plans and carbon plans

Setup beams can be created for proton and carbon plans only if the machine was commissioned with one or more setup imaging device(s). The setup imaging device can be selected in the setup beam list and specifies the virtual source-axis distance used for creating DRRs.

Localization point as isocenter

The localization point can be used as isocenter for the setup beams. This option is a clinic setting, see *section D.2 The Clinic Settings application on page 920*. This makes it possible to select between **Use isocenter from treatment beams** or **Use localization point as isocenter** in the **New plan** dialog:



If **Use localization point as isocenter** is selected, the generated setup beams and Setup DRRs will have the localization point as isocenter position.

6.1.18 Patient setup

If there is a localization point defined in the structure set, patient setup information is calculated for each isocenter in the plan.

As for all other POIs, the localization point can have different positions in different image sets, but only one localization point can be created in each image set. For instructions on how to create the localization point, see *Creating a POI on page 246*.

To review the patient setup information for the current beam set, click the **Patient setup** button in the beam list. This information is also printed in the plan report.

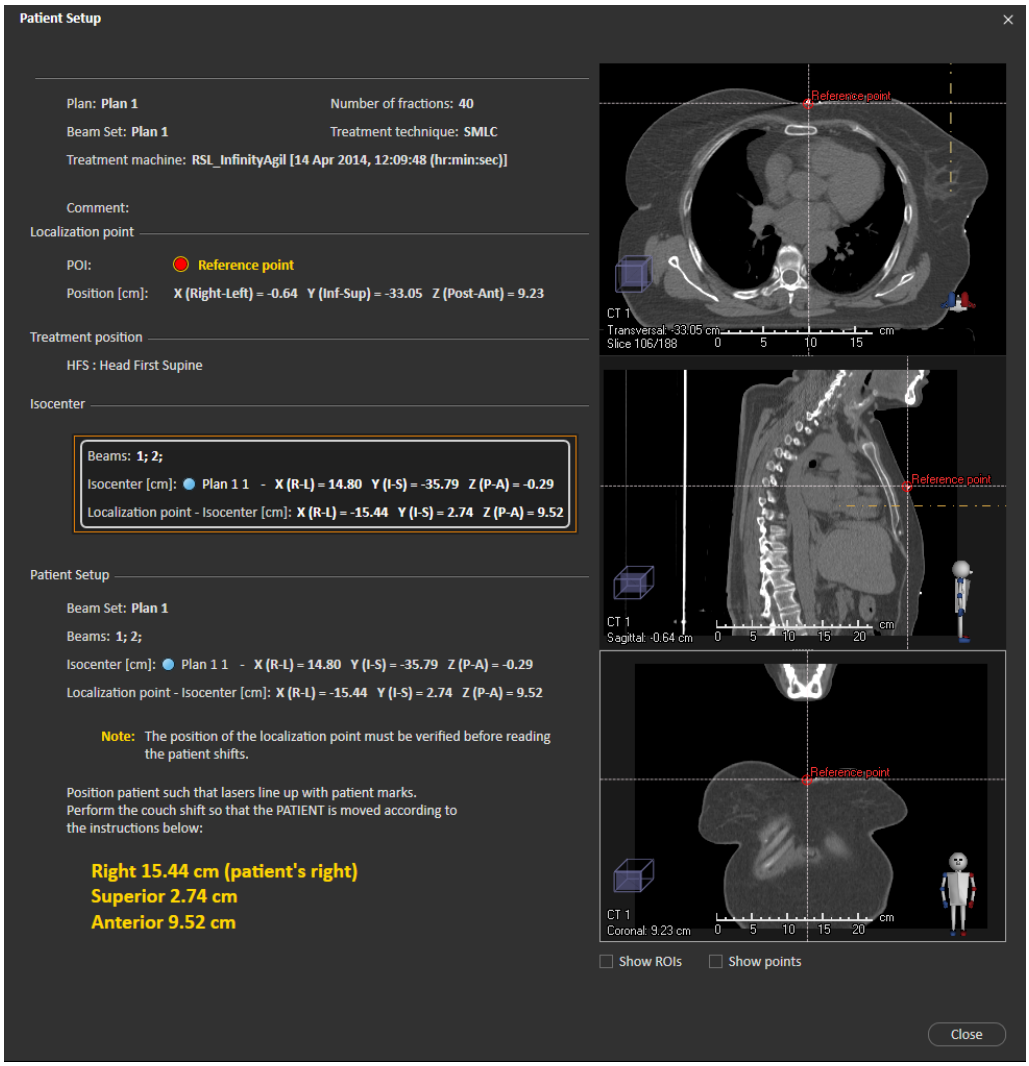

Patient Setup
Plan: Plan 1
Number of fractions: 40
Beam Set: Plan 1
Treatment technique: SMLC
Treatment machine: RSL_InfinityAgil [14 Apr 2014, 12:09:48 (hr:min:sec)]
Comment:
Localization point
POI: Reference point
Position [cm]: X (Right-Left) = -0.64 Y (Inf-Sup) = -33.05 Z (Post-Ant) = 9.23
Treatment position
HFS : Head First Supine
Isocenter
Beams: 1; 2;
Isocenter [cm]: Plan 1 1 - X (R-L) = 14.80 Y (I-S) = -35.79 Z (P-A) = -0.29
Localization point - Isocenter [cm]: X (R-L) = -15.44 Y (I-S) = 2.74 Z (P-A) = 9.52
Patient Setup
Beam Set: Plan 1
Beams: 1; 2;
Isocenter [cm]: Plan 1 1 - X (R-L) = 14.80 Y (I-S) = -35.79 Z (P-A) = -0.29
Localization point - Isocenter [cm]: X (R-L) = -15.44 Y (I-S) = 2.74 Z (P-A) = 9.52
Note: The position of the localization point must be verified before reading the patient shifts.
Position patient such that lasers line up with patient marks.
Perform the couch shift so that the PATIENT is moved according to the instructions below:
Right 15.44 cm (patient's right)
Superior 2.74 cm
Anterior 9.52 cm
Reference point
CT 1
Transversal: -33.05 cm
Slice 106/188
Reference point
CT 1
Sagittal: -0.64 cm
Reference point
CT 1
Coronal: 9.23 cm
Show ROIs
Show points
Close

Figure 194. The **Patient setup** dialog.

Couch shift

Couch shift (table top translation) instructions for positioning the patient are displayed in the **Patient Setup** part of the **Patient Setup** dialog and in the plan report.

The default couch shift presentation is **Patient**, i.e., the couch shift instructions in the **Patient setup** dialog are expressed in terms of patient anatomical directions.

If desired, the couch shift presentation can be changed to **Couch**, i.e., the couch shift instructions in the **Patient setup** dialog are expressed in couch directions. The couch shift presentation is changed in the Clinic Settings application (see *section D.2.2 The Preferences tab on page 922*).

Always verify that the couch shift displayed in RayStation and in the plan report are as intended and in accordance with clinical practice.

Another option for patient setup is to export the couch shift according to the DICOM standard. This option can be selected in RayPhysics. For more information, refer to the *RSL-D-RS-7.0-RPHY, RayStation 7 RayPhysics Manual* and the *RSL-D-RS-7.0-DCS, RayStation 7 DICOM Conformance Statement*.

WARNING!

Patient setup. Couch shift (table top translation) instructions for positioning the patient are displayed in the Patient setup dialog and in the plan report.

The default couch shift presentation is "Patient", i.e., the couch shift instructions in the Patient setup dialog are expressed in terms of patient anatomical directions.

If desired, the couch shift presentation can be changed to "Couch", i.e., the couch shift instructions in the Patient setup dialog are expressed in couch directions. The couch shift presentation is changed in the Clinic Settings application.

Before clinical use, always verify that the couch shift displayed in RayStation and in the plan report are as intended and in accordance with clinical practice.

Note that another option for patient setup is to export the couch shift according to the DICOM standard. This option can be selected in RayPhysics. (252059)

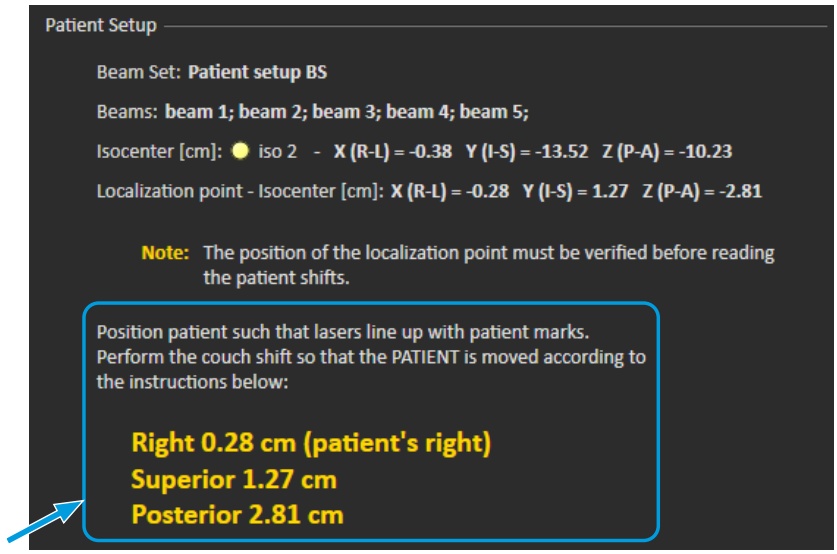

Patient Setup
Beam Set: Patient setup BS
Beams: beam 1; beam 2; beam 3; beam 4; beam 5;
Isocenter [cm]: iso 2 - X (R-L) = -0.38 Y (I-S) = -13.52 Z (P-A) = -10.23
Localization point - Isocenter [cm]: X (R-L) = -0.28 Y (I-S) = 1.27 Z (P-A) = -2.81
Note: The position of the localization point must be verified before reading the patient shifts.
Position patient such that lasers line up with patient marks.
Perform the couch shift so that the PATIENT is moved according to the instructions below:
Right 0.28 cm (patient's right)
Superior 1.27 cm
Posterior 2.81 cm

Figure 195. The couch shift instructions are displayed in the **Patient Setup** part of the **Patient Setup** dialog. This illustration shows an example of a couch shift expressed in terms of patient anatomical directions (couch shift presentation **Patient** in Clinic Settings).

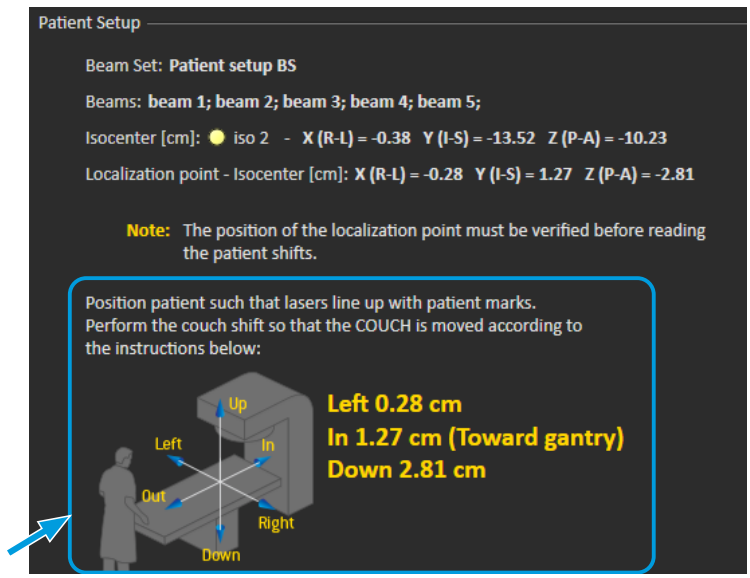

Patient Setup
Beam Set: Patient setup BS
Beams: beam 1; beam 2; beam 3; beam 4; beam 5;
Isocenter [cm]: iso 2 - X (R-L) = -0.38 Y (I-S) = -13.52 Z (P-A) = -10.23
Localization point - Isocenter [cm]: X (R-L) = -0.28 Y (I-S) = 1.27 Z (P-A) = -2.81
Note: The position of the localization point must be verified before reading the patient shifts.
Position patient such that lasers line up with patient marks.
Perform the couch shift so that the COUCH is moved according to the instructions below:
Up
Left
In
Out
Right
Down
Left 0.28 cm
In 1.27 cm (Toward gantry)
Down 2.81 cm

Figure 196. The couch shift instructions are displayed in the **Patient Setup** part of the **Patient Setup** dialog. This illustration shows an example of a couch shift expressed in couch directions (couch shift presentation **Couch** in Clinic Settings).

TomoTherapy red lasers' offset

For TomoHelical plans the red lasers' offset will be presented in the **Patient Setup** dialog and in the plan report. The localization point corresponds to the red lasers in the TomoTherapy system and the green lasers correspond to the isocenter.

The red lasers' offset is presented in the Tomo Fixed Coordinate System (IEC f). The coordinate system shows the current offset for the red lasers in the lateral (X), longitudinal (Y), and vertical (Z) directions relative to the virtual isocenter.

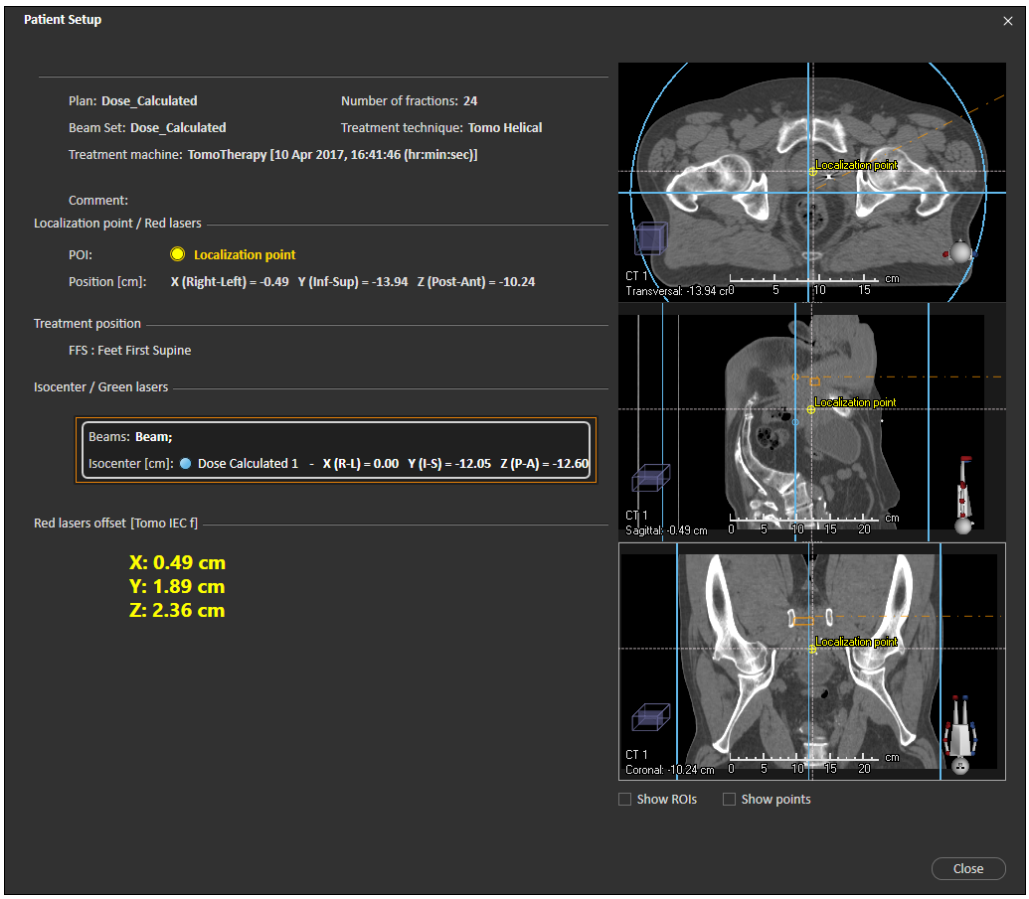

Patient Setup
Plan: Dose_Calculated
Number of fractions: 24
Beam Set: Dose_Calculated
Treatment technique: Tomo Helical
Treatment machine: TomoTherapy [10 Apr 2017, 16:41:46 (hr:min:sec)]
Comment:
Localization point / Red lasers
POI: Localization point
Position [cm]: X (Right-Left) = -0.49 Y (Inf-Sup) = -13.94 Z (Post-Ant) = -10.24
Treatment position
FFS : Feet First Supine
Isocenter / Green lasers
Beams: Beam;
Isocenter [cm]: Dose Calculated 1 - X (R-L) = 0.00 Y (I-S) = -12.05 Z (P-A) = -12.60
Red lasers offset [Tomo IEC f]
X: 0.49 cm
Y: 1.89 cm
Z: 2.36 cm
Localization point
CT 1
Transversal: -13.94 cm
Sagittal: -0.49 cm
Coronal: -10.24 cm
Show ROIs
Show points
Close

Figure 197. The **Patient setup** dialog for TomoTherapy machines.

Note: *For TomoHelical plans the localization point is compulsory, and its existence will be checked at export.*

Note: *If the red lasers' offset exceeds 20 cm in any direction, the red lasers will be out of range for patient setup. Such a plan will be stopped at dose computation (if the localization point it set) or at DICOM export.*

6.1.19 Volume Rendering settings

A Volume Rendering is a 3D image reconstructed from the CT data set slices. The surface rendering of the reconstructed 3D image is based on either 1D or 2D Modulation Transfer Functions (MTFs). The user can create a Volume Rendering filter and then add the desired number of MTFs in various colors to represent different densities in the reconstructed 3D image. 1D functions are usually good to cover big areas like bone and 2D functions are good to use to highlight certain materials (low gradients, and to show the edges of that material).

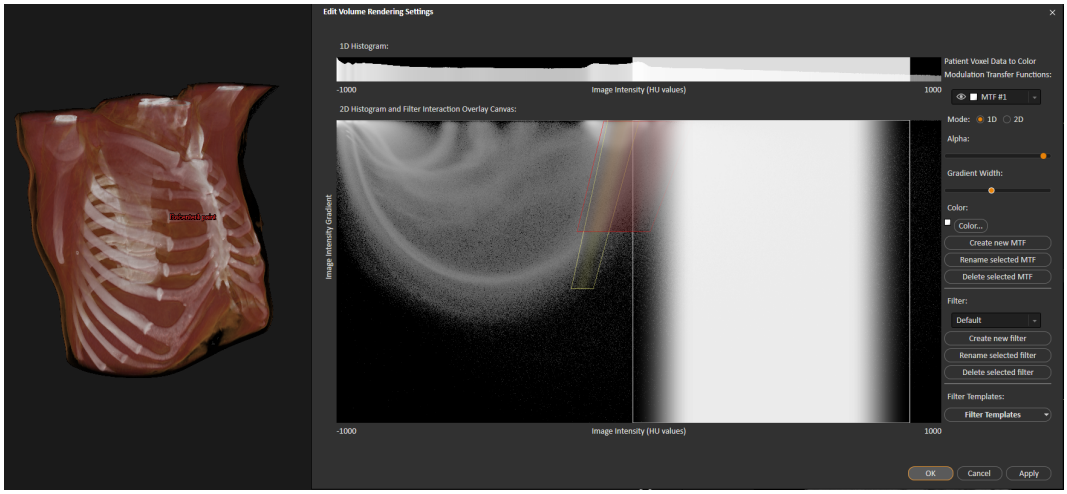


Figure 198. A Volume Rendering with a 1D MTF is coloring bone (white), a 2D MTF is coloring muscle (red) and another 2D MTF is used to highlight edge details of the muscle tissue (yellow).

A Volume Rendering filter can also be stored as a Volume Rendering template. Templates can simplify the planning process, as standard templates can be re-used when creating new plans. Two templates are included, one Default template and one Simple Bone template.

Note: *The Simple Bone template is only an example and might not be representative of all bone types.*

The Volume Rendering can be enabled in any 3D view and in the BEV. Right-click in a 3D view or in the BEV and select **Show Volume Rendering** to enable Volume Rendering in that view.

1D MTF functions

1D MTF functions will color a patient data range with a specific color without dealing with the gradient of the voxel (eg CT [-100,200] with red area). Note that the 1D histogram is covered with red color when using a 1D MTF.

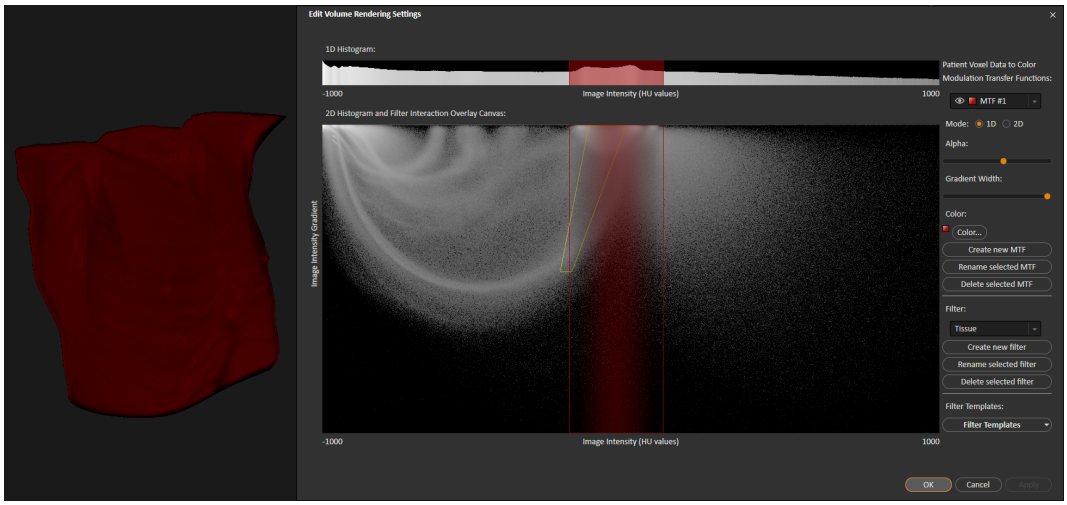


Figure 199. A Volume Rendering with a 1D MTF coloring the selected data range red.

2D MTF functions

2D MTF functions will color a patient data range with a specific color only if the gradient of the patient voxels are inside the area (eg CT[-100,200] and Grad[20,70] with a yellow area). Note that the volume rendered picture will emphasize edges, i.e., where gradients exist.

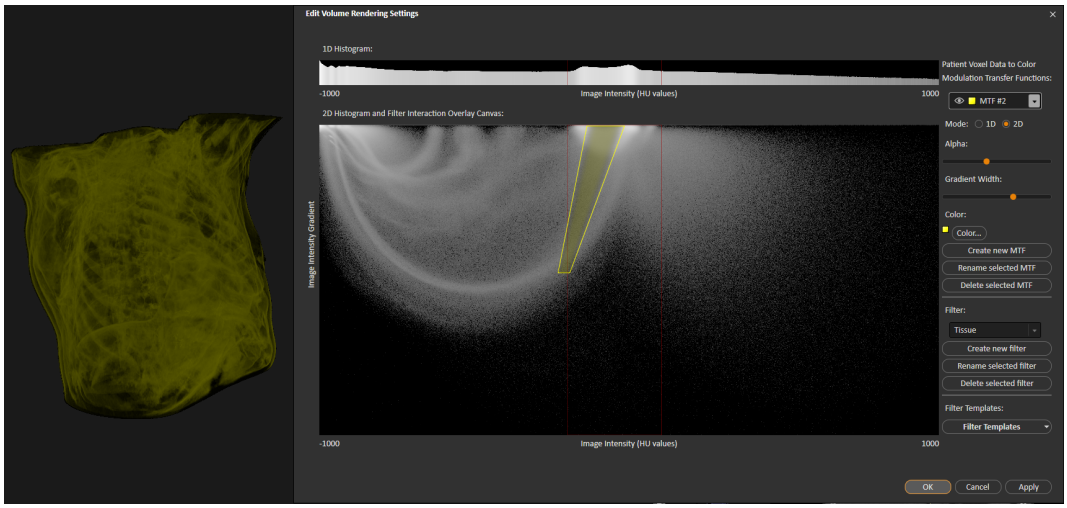


Figure 200. A Volume Rendering with a 2D MTF coloring the selected data range where there are gradients yellow.

2D functions can be used to emphasize differences of certain materials if there are gradients, i.e., edges of a certain level.

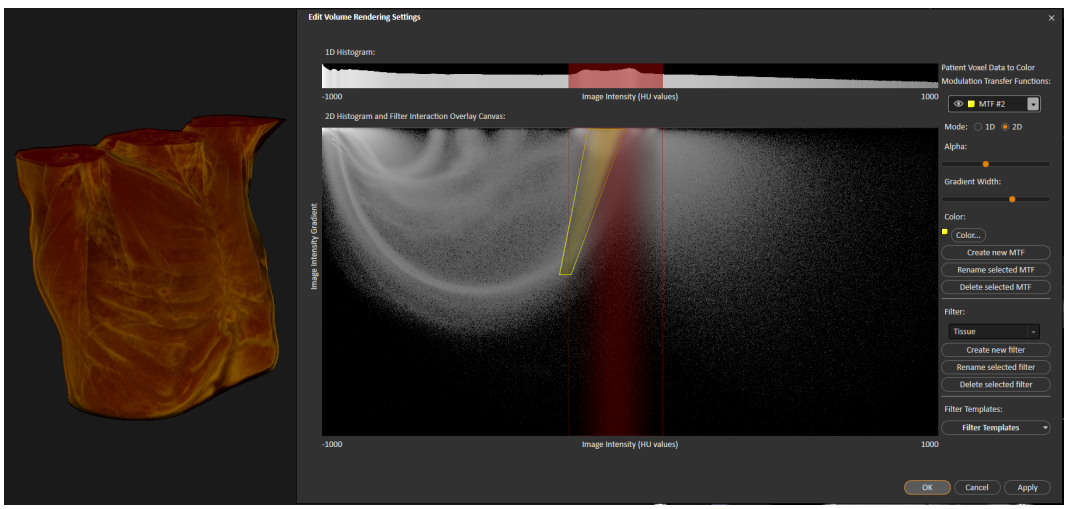


Figure 201. A Volume Rendering with a 1D MTF coloring the selected data range red and a 2D MTF coloring the selected data range where there are gradients yellow.

2D functions can also be used to emphasize areas with a continuous material with low gradients. See Figure 202 where the red region covers the 0 gradient level with some margin to emphasize minor fluctuations. The yellow 1D function is there to emphasize all gradient changes to the continuous material.

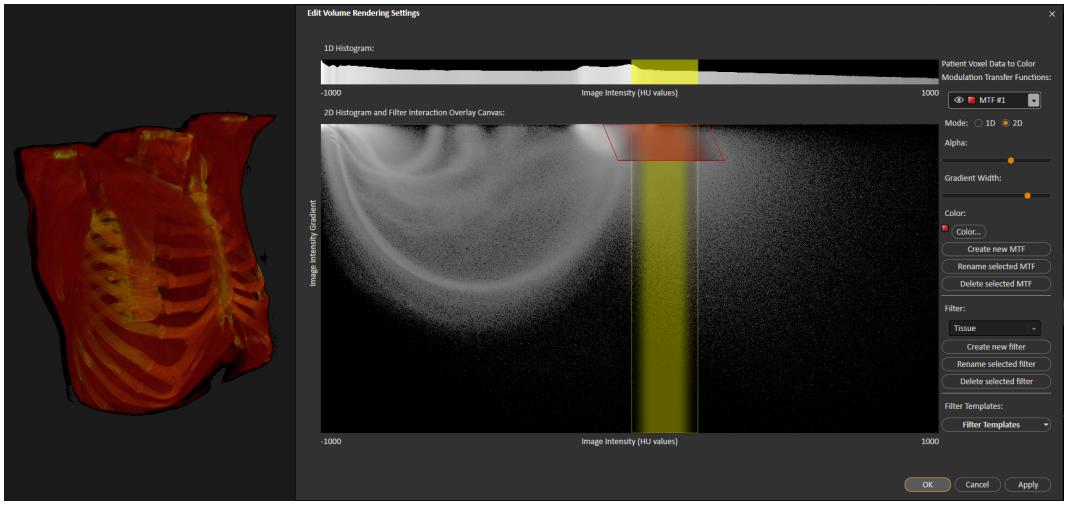


Figure 202. A Volume Rendering with a 1D MTF coloring the selected data range yellow and a 2D MTF coloring the selected data range where there are low gradients red.

Create a Volume Rendering filter

To create a Volume Rendering filter with one or more MTFs:

1. Right-click in a 3D view or in the BEV and select **Show Volume Rendering** to enable Volume Rendering in that view.
2. Right-click in a 3D view or in the BEV and select **Volume Rendering Settings...**. This opens the **Volume Rendering Settings** dialog.

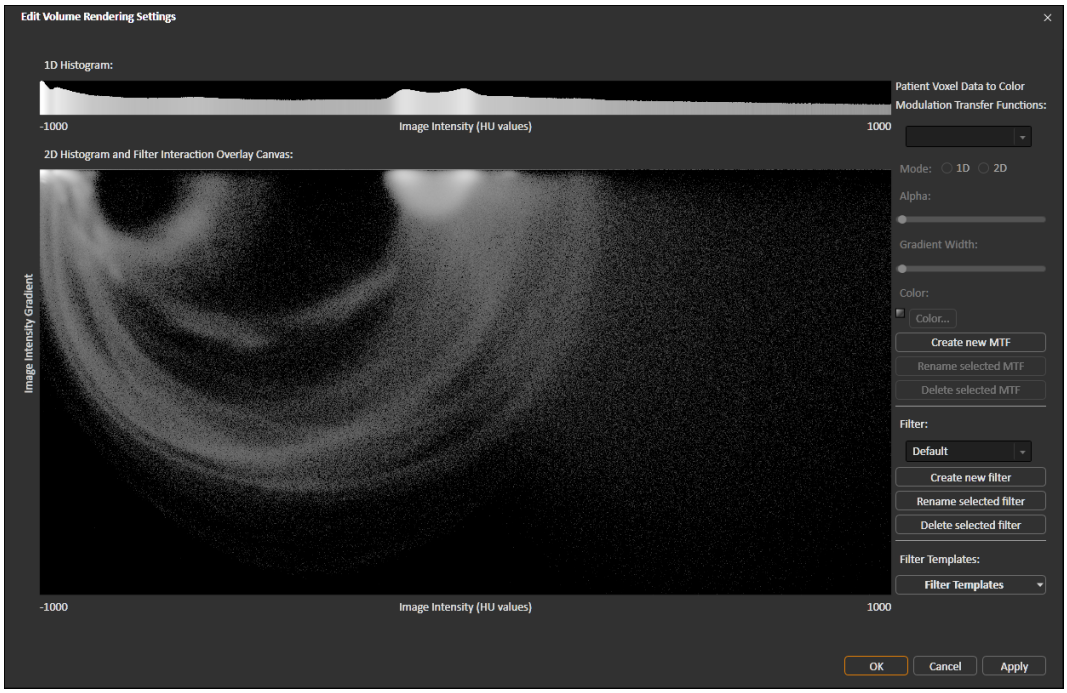
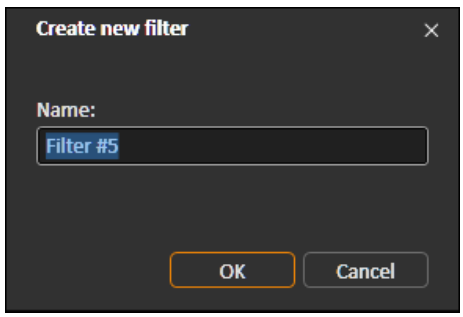


Figure 203. The **Volume Rendering Settings** dialog.

3. Click the **Create new filter** button. This opens the **Create new filter** dialog.



4. Enter the **Name** of the filter in the **Create new filter** dialog and click **OK**.

5. Click the **Create new MTF** button. A new MTF function will be created with a random size and color.
6. Modify the size and position of the MTF as desired. Left click and pan moves the MTF and the size of the MTF can be modified by clicking and moving the corners of the MTF. Any modifications can instantly be seen in the 3D view or in the BEV.
7. If desired, change the color of the MTF by clicking the **Color...** button. The fill type of the MTF can also be selected in the drop-down list next to the **Color...** button.
8. If desired, modify the transparency of the MTF by moving the **Alpha** slider.
9. If desired, modify the gradient width in the MTF by moving the **Gradient width** slider.
10. If desired, create another MTF by repeating the steps 5 to 9.
11. Click **OK**.

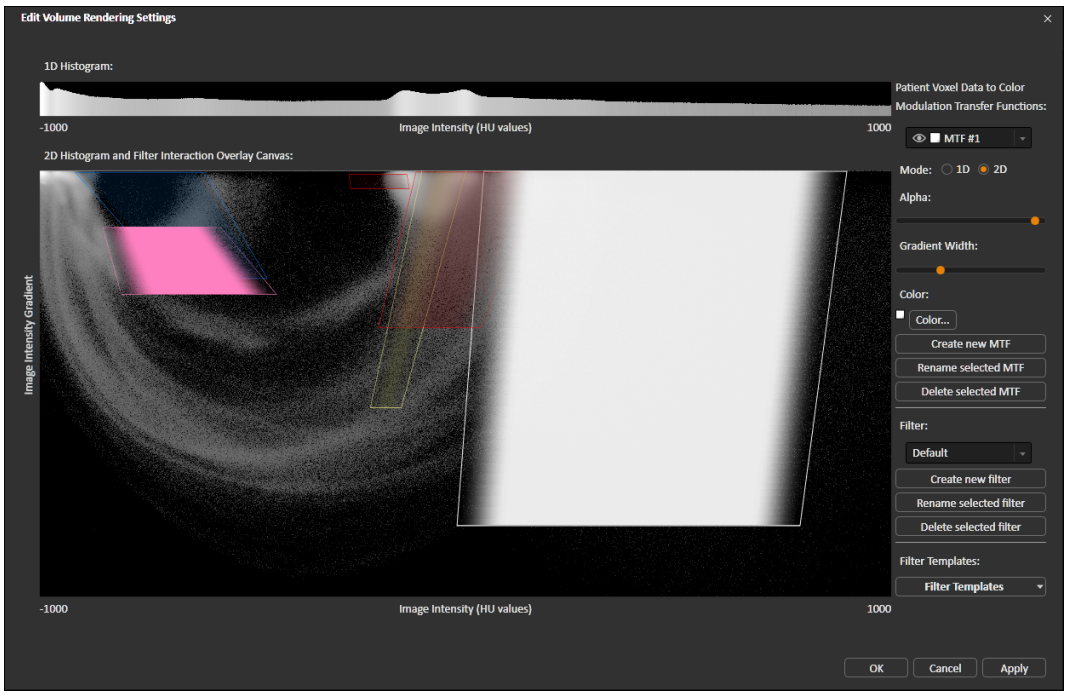
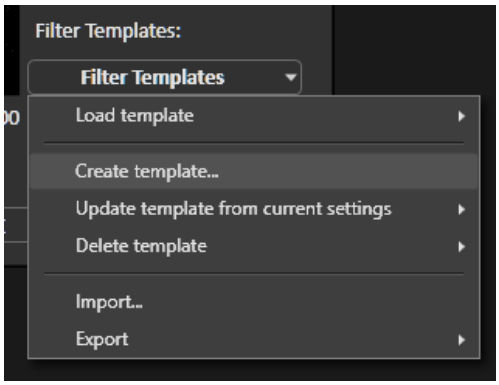


Figure 204. The **Volume Rendering Settings** dialog with MTFs in different colors.

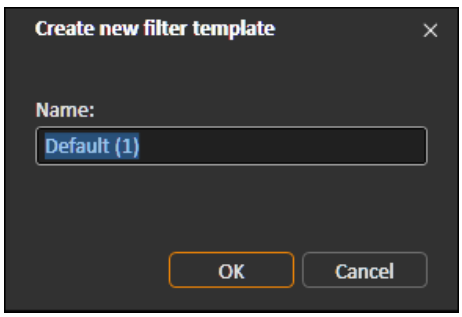
Create a Volume Rendering template

To create a Volume Rendering template:

1. Select **Volume Rendering Settings...** from the 3D view context menu or in the BEV context menu.
2. Click the **Filter Templates** drop-down list and select **Create template**.



This opens the **Create new filter template** dialog.



3. Enter the **Name** of the filter in the **Create new filter template** dialog and click **OK**.

Change Volume Rendering settings

Right-click in a 3D view or in the BEV and select **Volume Rendering Settings...** to open the **Volume Rendering Settings** dialog.

The following settings are available:

Settings	Description
MTF settings	• Modify the transparency of the MTF using the **Alpha** slider. • Modify the gradient width in the MTF using the **Gradient width** slider. • Change the color of the MTF by clicking the **Color...** button. The fill type of the MTF can also selected in the drop-down list next to the **Color...** button. • Modify the size and position of the MTF as desired. Left click and pan moves the MTF and the size of the MTF can be modified by clicking and moving the corners of the MTF. Any modifications can instantly be seen in the 3D view or in the BEV. • **Create new MTF**, **Rename selected MTF** or **Delete selected MTF** using the corresponding buttons.
Filter settings	• **Create new filter**, **Rename selected filter** or **Delete selected filter** using the corresponding buttons.
Filter template settings (available from the **Filter Templates** drop-down list)	• Select **Load template** to load an existing filter template. • Select **Create template** to create a filter template based on the current settings. • Select **Update template from current settings** to update an existing filter template based on the current settings. • Select **Delete template** to delete an existing filter template. • Select **Import template...** to import volume rendering filter templates. • Select **Export template...** to export volume rendering filter templates.

6.1.20 Multiple beam set planning

Multiple beam set planning is treatment planning using several beam sets with different beam configurations. When a plan is created, the first beam set is created automatically. This beam set and its corresponding dose distribution can either be created in RayStation 7 or imported via DICOM. The delivery order of multiple beam sets are set to the order in which they were created, dependency setup has no effect on the delivery order. The fractionation scheme can be edited in the fractionation schedule used in biological optimization and biological evaluation.

Add an additional beam set

To add an additional beam set:

1. Click the **Edit plan** button.

   This opens the Edit plan dialog.

2. Click the **Add beam set** button.

   This creates a new tab for the additional beam set in the plan.

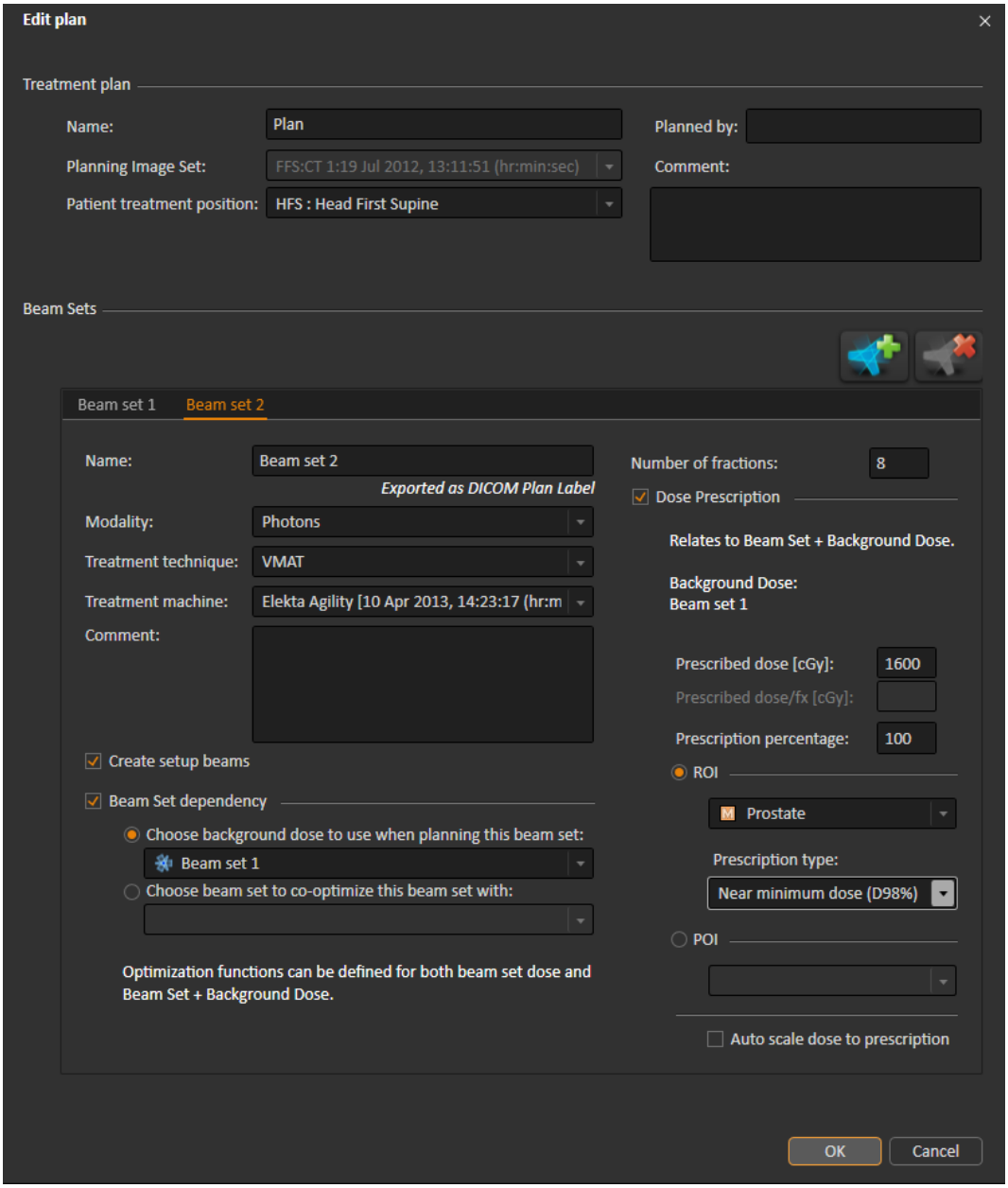


Figure 205. The Edit plan dialog.

3. Enter information for the new beam set in the same way as for the first beam set. For more information, see *Add beam set information on page 308*.

4. Optionally, check the **Beam Set dependency** checkbox to use dependent beam sets. One of the following two options can be selected:

   - To use another beam set as background dose, select **Choose background dose to use when planning this beam set** and select a beam set from the drop-down list. This will make the second beam set dependent of the dose from the selected beam set (and all its dependent doses). For more information, see *Create dose dependency on page 376*.
   - To co-optimize two beam sets, select **Choose beam set to co-optimize this beam set with** and select a beam set from the drop-down list. As a result, the two beam sets will be changed and optimized at the same time when performing plan optimization.

   Optimization of multiple beam sets is described in *section 7.1.19 Multiple beam set optimization on page 557*.

5. Click **OK**. The new beam set will be added to the beam set list.

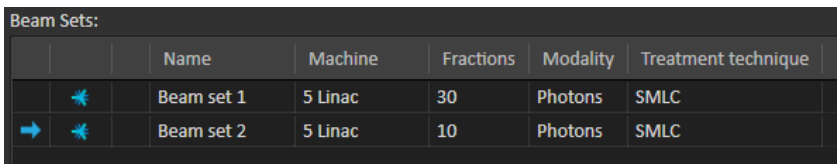


Figure 206. The beam set list for the current treatment plan. The blue arrow in the left column indicates which beam set that is currently active.

6. Repeat the steps above to add additional beam sets.

When an additional beam set is created it is possible to change the active beam set in the beam set drop-down list at the top right of the workspace or by right-clicking in the beam set list and selecting **Set as active**.

Delete a beam set

Delete an added beam set by clicking the **Delete beam set** button.

Dose presentation for multiple beam sets

When there are multiple beam sets in a plan, it is possible to display all the different planning doses by using the buttons in the toolbar. The selected dose presentation will influence all dose views, dose statistics, DVHs etc. in all modules presenting doses (except the Plan Evaluation module, the QA Preparation module and the Dose Tracking module).

The dose presentation buttons:

The **Plan dose** button displays the total dose, i.e. the dose from all the contributing beam sets in the plan.

The **Beam Set dose** button displays the total dose in the selected beam set.

The **Beam dose** button displays the dose for the selected beam.

The **Background dose** button displays the dose this beam set is dependent on during planning. This is the dose from all beam sets this beam set is set to be dependent on, and for adapted plans it is the dose from already delivered fractions.

The **Beam Set + Background dose** button displays the combined dose from this beam set and the background dose it is dependent on.

The **Combined dose** button displays the combined dose from the two beam sets that are to be co-optimized.

Note: *If two dose presentations are showing the same dose, only one of the dose presentation buttons will be displayed. For example, the Plan Dose and Beam Set + Background dose are the same if only two background dose dependent beam sets exist, then only the Plan Dose presentation button is visible.*

Use combined dose or separate beam set dose as objective/prescription for additional beam sets

The beam sets can be planned independently, with prescriptions and objective functions relating to only the separate beam set dose. It is also possible to create beam set dose dependencies, which is to set one beam set dependent of dose from one or more other beam sets (depending on the dependency type). Prescriptions and objective functions may then relate to the combined dose from the beam sets instead of the separate beam set dose.

Independent beam sets example:

If scaling to a prescription of Mean 60 Gy to the target, the beam set dose will be scaled to achieve a beam set dose of Mean 60 Gy to the target.

Dependent beam sets example when having background dose dependency:

If scaling the dependent beam set to a prescription of Mean 60 Gy to the target, the beam set dose will be scaled to achieve a combined beam set + background dose of Mean 60 Gy to the target.

Note: *The auto scale dose to prescription function will be deactivated if it is not possible to scale the beam set dose to achieve the desired beam set + background dose.*

Note: *For co-optimized beam sets dose prescription is always set for each individual beam set.*

For a dependent beam set, each objective function can be selected to relate to either the separate beam set dose or a combined dose. The combined dose is the sum of the background dose and the beam set dose for the case of background dose dependency, or the sum of the doses from the two co-optimized beam sets for the case of co-optimized beam sets.

Create dose dependency

A beam set can be set as dependent either on the background dose from one or more beam sets or on another collective/mutual beam set. When having background dose dependency the dose from the first beam set and its dependent doses will then serve as a pretreated dose when planning the current beam set. In the case of co-optimized dependency the two collective/mutual beam set doses will both be considered when planning any of the beam sets. In order to create background dose dependency it is possible to click on a beam set (i.e., on the beam set icon) in the list and drag and drop it onto another beam set in the list. This will make the first beam set dependent of the other.

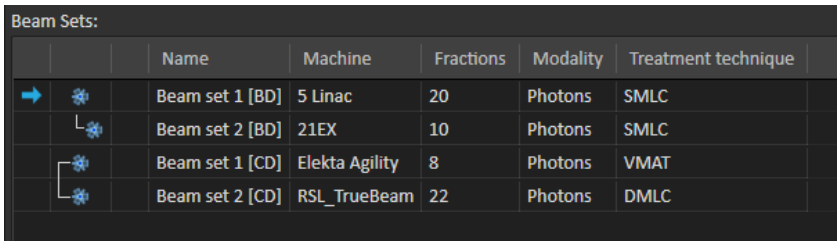
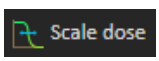


Figure 207. The beam set list, where the tree presentation shows the different dependencies. The connecting lines indicate the different dependencies here denoted by [BD] for background dose dependency and [CD] for co-optimized dose dependency. In the case of dependency [BD], the second beam set dose is dependent of the first beam set dose.

Another way of creating a dose dependency is to check the **Beam Set dependency** checkbox in the Edit plan dialog and selecting the desired option.

Scale dose for multiple beam sets

When having multiple beam sets, the endpoint of the scaling will be dependent on the dependency setup of the planned beam set. For independent beam sets and when having co-optimized dose dependency, the scaling will be performed to achieve a beam set dose that fulfills the level, for background dose dependent beam sets the beam set dose will be scaled to achieve a beam set + background dose of the desired dose level. The scale dose dialog will always display which type of scaling that will be performed. Click the **Scale dose** button.



This opens the **Scale Dose** dialog.

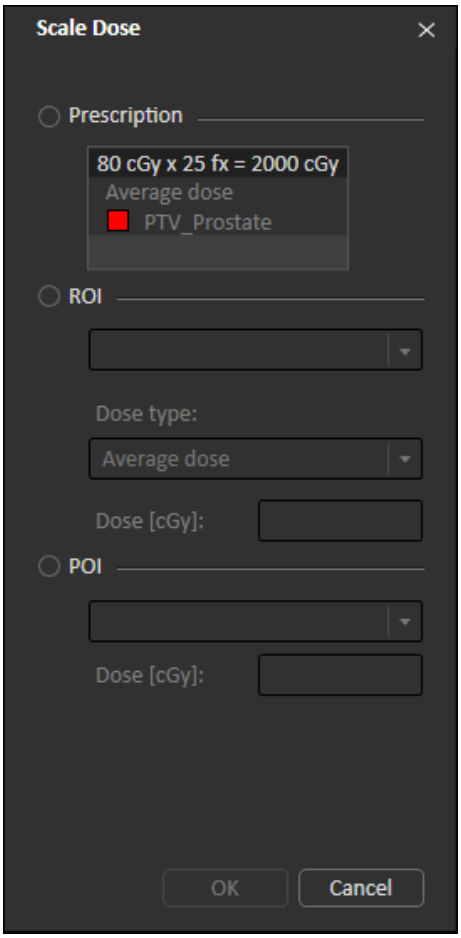


Figure 208. The **Scale Dose** dialog.

Use an imported dose as background dose

All imported doses are marked as approximate doses (non-clinical) in RayStation. To be able to approve a plan, the total dose needs to be clinical. When a plan includes an imported dose in one of the beam sets, the user has to approve that dose for background dose usage in a clinical plan. This is done by checking the **Consider imported dose clinical** checkbox in the Edit plan dialog. The imported dose will then be marked as clinical in the patient views and the beam set referring to that dose will be set as read-only. This is shown with a blue padlock next to the beam set in the beam set list.

WARNING!

Imported dose. An imported dose for an approved plan will automatically be considered clinical. (98967)

Note: *It is allowed to classify an imported dose as clinical even if the dose grid is coarser than 5 mm. If this dose is used as background dose, it will not be possible to continue with final dose computations due to the dose grid checks during the dose computation.*

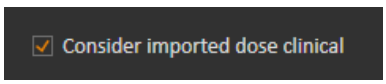


Figure 209. The Consider imported dose clinical checkbox in the Edit plan dialog.

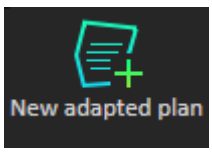
6.1.21 Create new adapted plan

In the Plan Setup module, the user can create an adapted treatment plan for a new planning image set, which is optimized using an imported dose as background dose.

Before an adapted treatment plan can be created, an approved deformable registration must exist between the original planning image set and the new planning image set, where the new planning image set is set as the reference image set and the original image set is set as the target image set.

To create a new adapted plan:

1. Click the **New adapted plan** button.



   This opens the New **Adapted Plan** dialog.

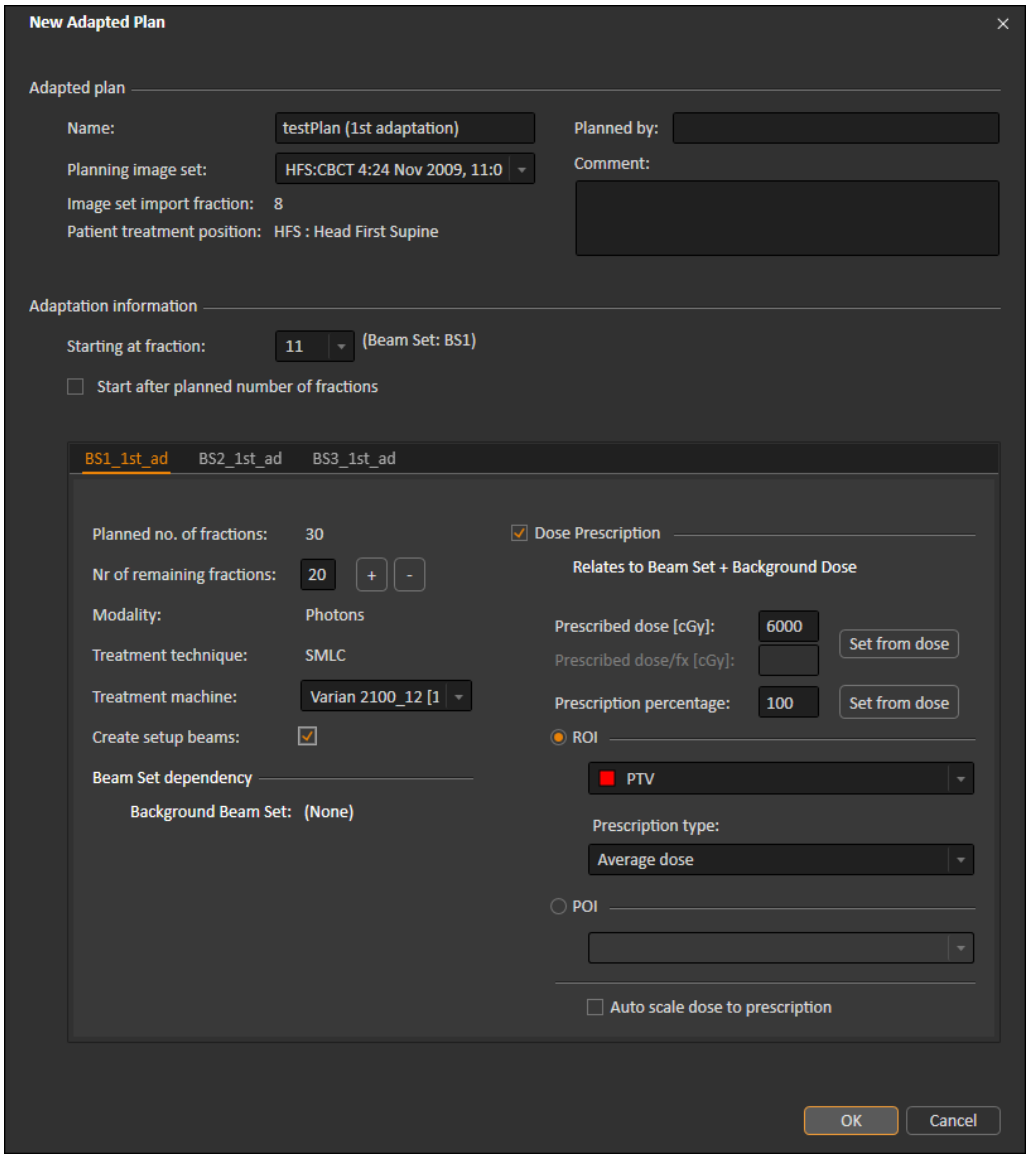


Figure 210. The New **Adapted Plan** dialog.

2. Enter a plan **Name**.
3. Select **Planning image set**.
4. Select starting fraction for the adaptation in the **Starting at fraction list** or check the **Start after planned number of fractions** checkbox.

   Note: *The planned fraction dose will be used as background dose during optimization.*

5. If desirable, the number of remaining fractions can be changed using the **+** and **-** buttons.
6. Select **Treatment machine**. The treatment machine selected for the original plan will be the default choice.
7. If desired, select to **Create setup beams**.

   Note: *Only possible for proton and carbon plans if the machine has an imaging device.*
8. Select to define a **Dose Prescription**. This is done in the same way as when creating a new plan, see *section 6.1.3 Create a new plan on page 306*.
9. Click **OK**.

A new plan will be created with the same number of beam sets as the original treatment plan.

The RayStation 7 system automatically:

- updates the beam list with beam geometry from the original plan moved to the new planning image set geometry. Isocenter for each beam is set to the isocenter for the original planning image set deformed to the new planning image set.
- updates the setup beams to the new beam geometry if the checkbox **Create setup beams** was checked in the New adapted plan dialog.
- sets a default dose grid which allows for dose computation on the new planning image set.
- sets the treatment machine for each beam set to the one selected in the New adapted plan dialog.
- sets the treatment delivery technique for each beam set to the same as for the respective beam set in the original plan.
- adds beam dose specification point (BDSP) corresponding to the BDSP for the original planning image set deformed to the new planning image set.
- sets the prescription for each beam set to the same as for the respective beam set in the original plan.

Note: *Always review the automatically generated adapted treatment plan data before proceeding with plan optimization and dose computation.*

6.1.22 Create template plans for fallback planning

In order to create fallback plans a number of fallback protocols needs to be available. A first step when creating these protocols is to create template plans that define how certain plan types should be handled on specific machines. The supported modality is photon and the supported treatment techniques are SMLC, 3DCRT, DMLC, VMAT and TomoHelical. The template plans are created in the Plan Setup module and shall solely be used for creating the protocols and shall not be used for treatment delivery.

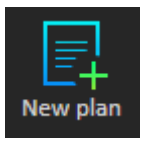
For more information about fallback planning and a suggested workflow, see *section 10.3 The Fallback Planning workflow on page 843*.

This section describes a suggested workflow for creating template plans for fallback planning. The workflow consists of three main parts and can be repeated as many times as needed:

1. Create a template plan without beams.
2. Add beams to the template plan.
3. Check settings for optimized techniques.

Part 1: Create a template plan without beams

1. Click the **New plan** button to open the **New plan** dialog.



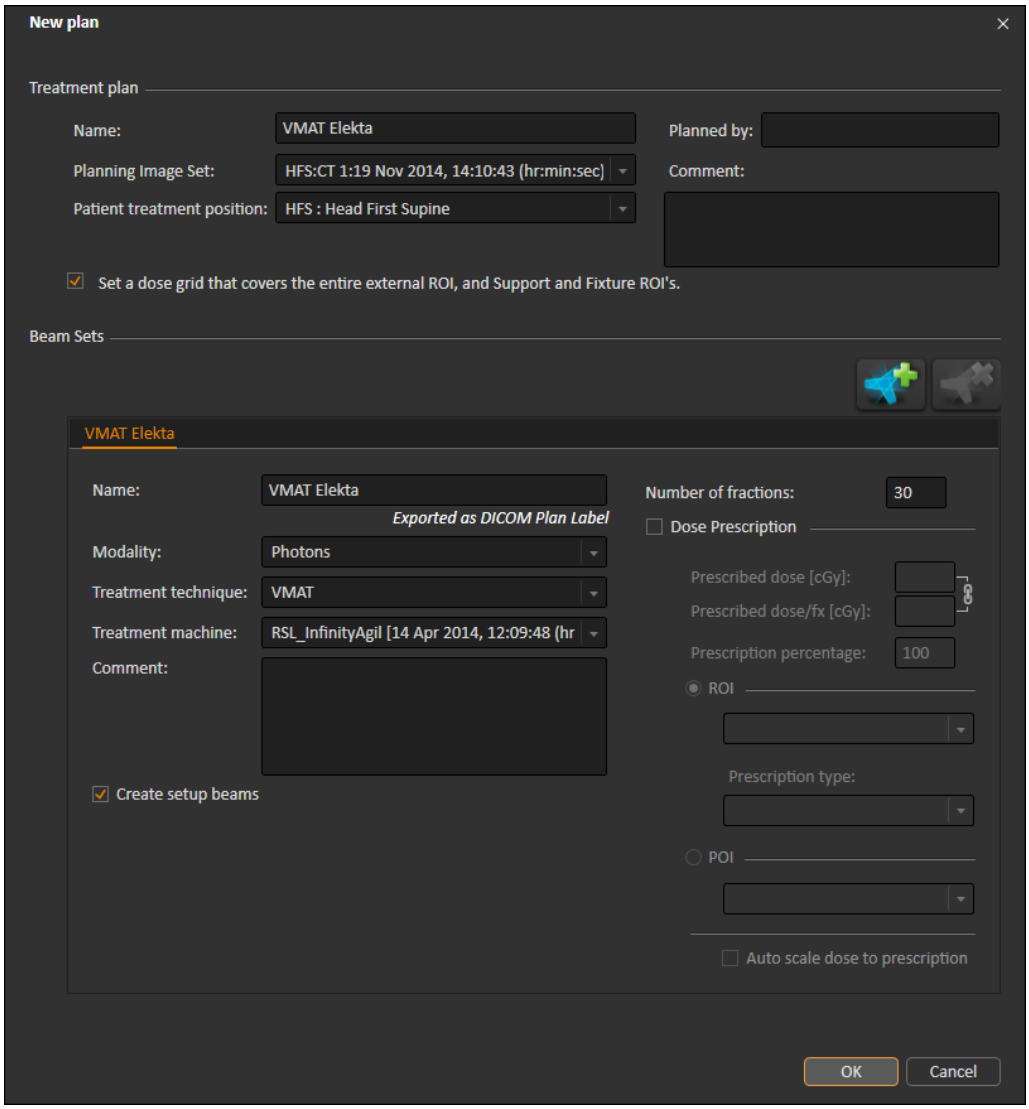


Figure 211. The **New plan** dialog for a fallback template plan. This example shows a photon VMAT plan.

2. Enter a plan **Name**.
3. Select **Planning image set** to base the protocol on.
4. Select **Patient treatment position**.
5. Select to **Set a dose grid that covers the entire external ROI and Support and Fixture ROIs** by checking the corresponding checkbox (this is checked by default if an External ROI has been assigned to the patient).

Note: *If a bolus will be added at a later stage, the dose grid has to be regenerated to cover it.*

6. Enter a beam set **Name**.
7. Select the relevant **Modality**, **Treatment technique** and **Treatment machine** for the protocol.
8. Select any **Number of fractions**. This does not impact the protocol.
9. Do not add a prescription as it will not be used.
10. Select to **Create Setup beams** by checking the corresponding checkbox.

For more information on how to create a new plan, see *section 6.1.3 Create a new plan on page 306*.

Part 2: Add beams to the template plan

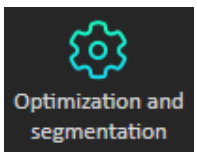
Add beams to the template plan and enter the gantry and collimator angles for the fallback plan. There is no need to create a beam opening. The field size and segments will be created during the protocol generation.

For more information on how to add beams, see *section 6.1.6 Add, edit, copy or delete beams on page 316*.

Part 3: Check settings for optimized techniques

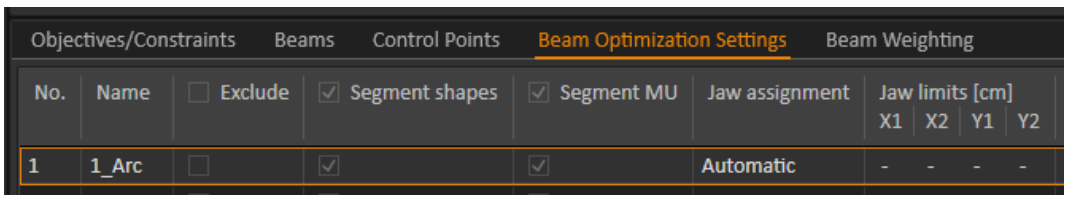
If an optimized technique (optimized 3D-CRT, DMLC, SMLC or VMAT) is selected:

- Make sure that the Optimization and segmentation settings in the Plan Optimization module correspond to what is required for the fallback protocol.



For more information about Optimization and segmentation settings, see *section 7.1.5 Specify optimization and segmentation settings on page 530*.

- Make sure that the Beam Optimization Settings in the Plan Optimization module correspond to what is required for the fallback protocol.



For more information about Beam Optimization Settings, see *section 7.1.9 Beam optimization settings on page 542*.

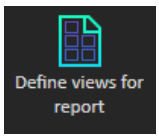
6.1.23 Define views for plan report

In the Plan Setup module, it is possible to define specific dose views that will be includes in the plan report. The views for the plan report are defined by report view definition points that are intended to be used in reports, if the report templates supports it. The report view definition points can be managed through the **Define views for report** dialog or by scripting (refer to the *RSL-D-RS-7.0-SG, RayStation 7 Scripting Guideline*).

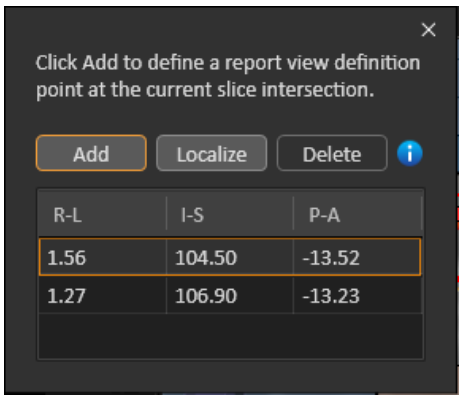
The report can be designed to include transversal, sagittal and/or coronal views through the report view definition points. Views related to these points are included in the report only when using a report template designed for dose view selection.

To add, localize or delete views for a plan report:

1. Click the **Define views for report** button. A dialog will open showing all currently specified points in a list.



2. A dialog will open showing all currently specified report view definition points in a list.



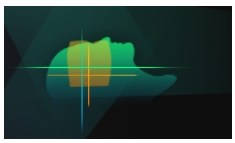
In the dialog it is possible to:

- Add view: Click **Add** to define a report view definition point at the current slice intersection of the views.
- Localize view: To navigate to a specific report view definition point in the list, click **Localize**.
- Delete view: Select a report view definition point in the list and click **Delete**.

6.2 THE VIRTUAL SIMULATION MODULE

The Virtual Simulation module is a workspace designed for fast and straightforward planning. The module supports image import and one click default plan creation with an orthogonal pair of beams. Multiple tools for easy isocenter adjustments is provided, including two DRR beam views. The module provides laser export ability for marking the patient on the planned isocenter position.

In the Virtual Simulation module a complete set of 3D-CRT planning features can be reached including editing of virtual jaws, center beam in field and functionality to set isocenter midplane patient. For field shaping manual tools to draw and conform to aperture field shapes in BEV are provided as well as the ability to conform the field to contoured ROIs. Plans are stored in the common RayStation patient database for continued planning in the full RayStation framework.



In this section

This section contains the following sub-sections:

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6.2.6	Edit beam properties	p. 402
6.2.7	Laser export	p. 408
6.2.8	Field shaping in BEV	p. 412
6.2.9	Specify settings in the Treat and Protect tab	p. 415
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6.2.12	Patient setup	p. 420

Precautions

WARNING!

Block/cutout verification. Always verify that the blocks and electron beam cutouts created in the Beam design modules are physically realizable. It is not possible to define any block manufacturing constraints in RayStation.

For proton blocks, the size of the block milling tool is taken into consideration in the automatic block generation tools. However, it is possible to obtain a block that cannot be manufactured using the manual block editing/creation tools. It is then possible to run the milling tool algorithm manually after the block editing. However, since it is not done automatically, the responsibility that the block is physically realizable still lies with the user.

Always check the created block against the block aperture printout. (27064)

6.2.1 The Virtual Simulation user interface

Workspace

There are two tool panels in the Virtual Simulation module; a **General** tab where all the common operations are performed and a **Laser** tab where a reference localization point can be exported to a laser system.

The Virtual Simulation workspace contains three sub-windows to the left showing **2D** image data in different patient planes, making it possible to simultaneously work in three dimensions. It is possible to change the patient direction using shortcuts. Click in a patient view and type T (Transversal), C (Coronal) or S (Sagittal). The sub-windows can also display image data in **Room View** and **3D** view.

The workspace also contains two sub-windows to the right that each show a Beam's Eye View (**BEV**) with **DRR visualization**. For more information about DRR settings, see *section 6.1.8 The DRR views and settings on page 330*.

The lower part of the workspace contains the beam list, which contains the tabs **Beams** and **Treat and Protect**.

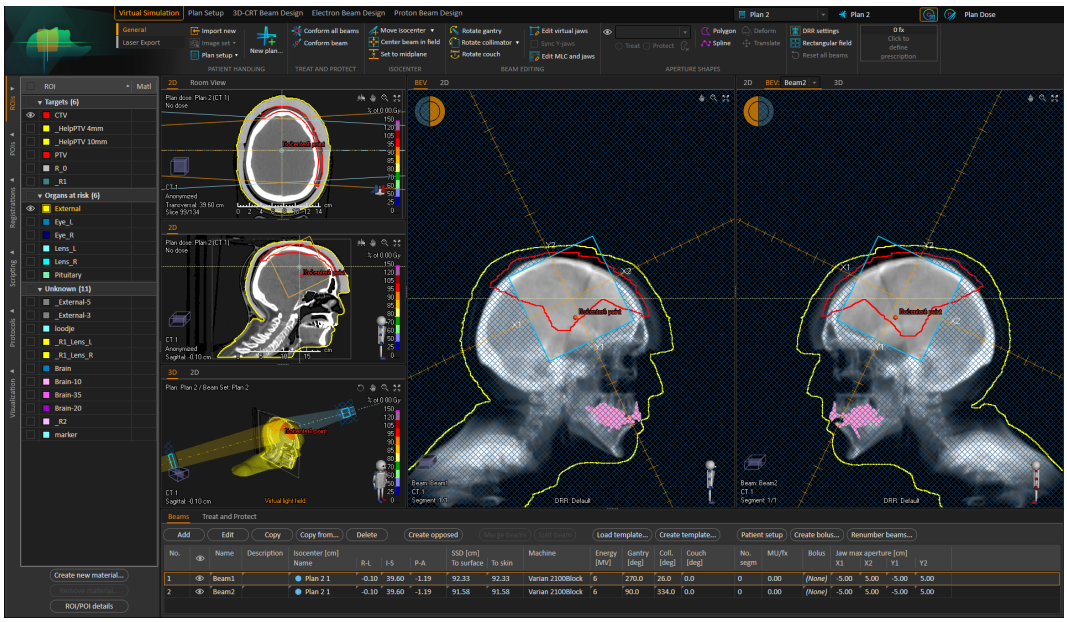


Figure 212. The Virtual Simulation workspace.

Graphical User Interface

For more information about the tools, operations and various view types in the Graphical User Interface, see *chapter 3 The Graphical User Interface*.

Context menus

Each view has a context menu which is opened by right-clicking in the view. For a description of the general context menu options, see *section 3.9 The context menu on page 102*.

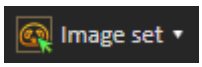
6.2.2 Virtual Simulation Workflow

This section describes a suggested workflow for the entire Virtual Simulation planning process. The suggested workflow for Virtual Simulation consists of the following stages:

1. **Preparations.** Define the default treatment machine and the default beam energy that will be used when creating a default plan. For more information, see *section D.2 The Clinic Settings application on page 920*. If laser export is going to be used this has to be enabled in RayPhysics. Refer to *RSL-D-RS-7.0-RPHY, RayStation 7 RayPhysics Manual* for more information.

2. **Import new patient data.** Import new patient data by clicking the **Import new** button. For more information, see *section 4.3.1 Import new patient data on page 112*. To import a new image to an existing case: Go to the **RayStation** menu and select **DICOM import: Import to current patient/case**.

3. **Select Image set.** Select the CT image set that will be used for treatment planning from the **Image set** drop-down list.

   For information on how to edit the image set properties for the CT image set, see *section 4.7.1 Setting image set properties for CT image sets on page 147*.

4. **Create default plan.** In this step a default plan with a set of predefined settings will created automatically, with only one click. For more information, see *section 6.2.3 Create default plan on page 391*. It is also possible to create a plan manually. See *section 6.2.4 Create a new plan manually on page 393* for more information.

   Note: *Creating a default plan will create a plan without a set number of fractions. When creating a plan manually, the number of fractions has to be set.*

5. **Edit the isocenter position.** It is possible to edit the isocenter position. For more information, see *Edit the isocenter position on page 402*.

6. Optional: **Laser export.** For more information, see *section 6.2.7 Laser export on page 408*.

7. Optional: **Manually draw aperture field shapes in BEV or select Treat and Protect ROIs to use for planning**. How to perform manual field shaping in BEV is described in *section 6.2.8 Field shaping in BEV on page 412*. How to specify Treat and Protect ROIs is described in *section 6.2.9 Specify settings in the Treat and Protect tab on page 415*.

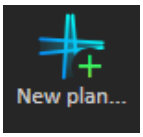
8. Optional: **3D-CRT-conform**.

9. **Save patient and plan to database**.

10. **Continued planning can be performed in the appropriate other planning modules in RayStation.** Here continued 3D-CRT planning can be performed, also with a different treatment machine selected, dose can be computed and plan can be exported. It is also possible to create new plans of all types using the marked isocenter position.

6.2.3 Create default plan

A default plan with a set of predefined settings can be created automatically, with only one click. To create a default plan, click the **New plan** button.



As a result, RayStation automatically creates a default plan with the following properties:

Property	Value
Treatment plan **Name**	Plan 1 (Plan 2, Plan 3, etc.)
Planning Image Set	The image set displayed in the Virtual Simulation workspace views, i.e., the selected primary image set.
Patient treatment position	The patient treatment position is set to be the same as the CT scanning position. For more information, see *section D.2 The Clinic Settings application on page 920*.
External ROI	An external ROI is created.
Dose grid	A default dose grid that covers the External ROI is created.
Treatment machine	The default treatment machine selected in Clinic Settings. The latest commissioned machine version with the matching name is selected. ***Note:*** *If the entered name does not exist or if no name is entered, the system will select the first available treatment machine in alphabetical order.*
Energy	The default energy selected in Clinic Settings. (If a default energy is not defined or not supported by the machine, the lowest energy of the machine is set as the default energy.) For more information, see *section D.2 The Clinic Settings application on page 920*.
Number of fractions	The number of fractions is left empty.
Modality	Photons
Treatment technique	3D-CRT
Beam Set **Name**	Beam Set 1 (Beam Set 2, Beam Set 3, etc.)
Beams	An orthogonal pair of beams are created, at 0 and 90 degree gantry angles. The beam names are set to Beam 1 and beam 2.

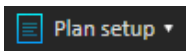
Property	Value
Isocenter	Isocenter is set to current slice intersection.
Angles	**Gantry**, **Couch** and **Collimator** angles are all set to 0 degrees.
Field size	10 x 10 virtual jaws independent of treatment machine.
Setup beams	Setup beams are created to the isocenter of the beams.

Note: *The default plan will not contain any fractions. These has to be added in the Edit plan dialog before dose computation.*

The result is visible in the Virtual Simulation workspace views.

6.2.4 Create a new plan manually

1. Select **Plan setup: New plan...**.



This opens the **New plan** dialog.

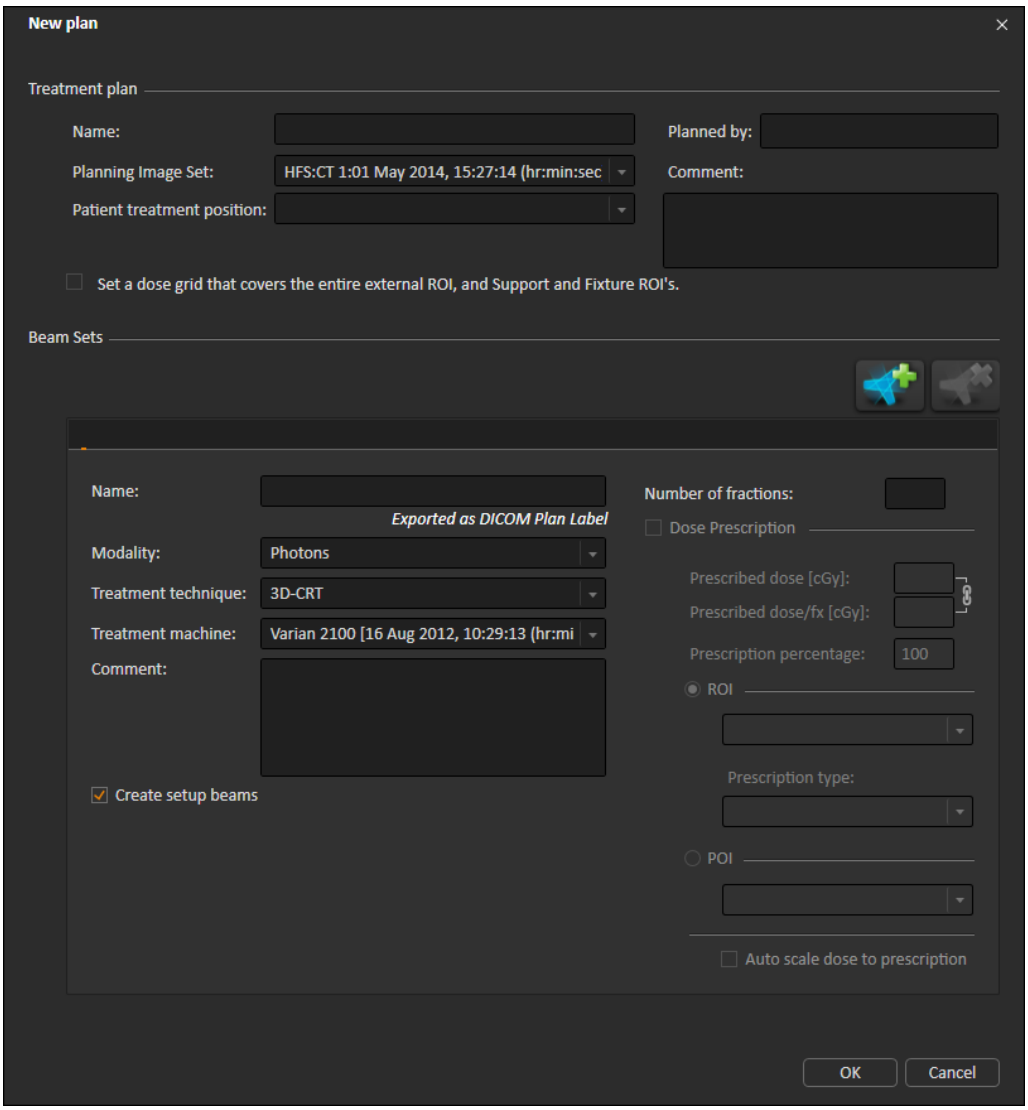


Figure 213. The **New plan** dialog.

Add treatment plan information

Enter information about the treatment plan:

1. Enter a plan **Name**.

   Note: *The plan name is exported as DICOM RT Plan Name [300A,0003].*

2. Select **Planning image set** from the drop-down list to use as a basis for the treatment plan. The image set selected for treatment planning in the toolpanel is preselected.
3. Select **Patient treatment position**.
4. Enter information in the **Planned by** field (optional).
5. Enter a **Comment** in free text (optional).
6. Select to **Set a dose grid that covers the entire external ROI and Support and Fixture ROIs** by checking the corresponding checkbox (this is checked by default if an External ROI has been assigned to the patient).

   Note: *If a bolus will be added at a later stage, the dose grid has to be regenerated to cover it.*

Add beam set information

Enter beam set information. This information is dependent on the treatment technique.

1. Enter a beam set **Name**.

   Note: *The radiation set name is exported as DICOM RT Plan Label [300A, 0002].*

2. Select **Modality**. The only available option is photons (preselected).
3. Select **Treatment technique**.
4. Select **Treatment machine**. The list contains treatment machines that are commissioned for the selected treatment technique. Beam Commissioning is described in *RSL-D-RS-7.0-RPHY, RayStation 7 RayPhysics Manual*. The treatment machine defined in Clinic Settings is preselected.
5. Enter a **Comment** in free text (optional).
6. Select to **Create Setup beams** by checking the corresponding checkbox. See *section 6.1.17 Setup beams on page 359* for more information about setup beams.
7. Enter **Number of fractions**.
8. Check the **Dose Prescription** checkbox to add a **Prescription** for an ROI, POI or SITE.

9. Enter either the **Prescribed dose** or the prescribed dose per fraction (**Prescribed dose/fx**).

   When changing the prescribed dose, the prescribed dose per fraction is updated based on the number of fractions. If instead the prescribed dose per fraction is changed, the prescribed dose will be updated based on the number of fractions.

   If the number of fractions is changed, only the prescribed dose will be updated based on the current prescribed dose per fraction.

10. Enter **Prescription percentage**.

11. For a selected ROI there are several options in the **Prescription type** drop down list:

    - **Average dose** is defined as the average dose in the specified ROI.
    - **Near maximum dose (D2%)** is defined as the desired dose at 2% volume of the specified ROI.
    - **Median dose (D50%)** is defined as the desired dose at 50% volume of the specified ROI.
    - **Near minimum dose (D98%)** is defined as the desired dose at 98% volume of the specified ROI.
    - **Dose at volume** is defined as the desired dose at the entered volume [%] of the specified ROI.

    Note: *The dose color table by default uses the prescribed dose level as reference.*

    Note: *SITE prescriptions that only contain a description are not evaluated. As an option, a dose specification point can be added to the SITE prescription which will then be evaluated on the dose to that dose specification point. For more information, see SITE prescription on page 347.*

12. If desired, select to **Auto scale dose to prescription** by checking the corresponding checkbox. For more information, see *section 6.1.16 Auto scale to prescription on page 358*.

13. If desired, add an additional beam set to the plan by clicking the **Add beam set** button.

    Repeat steps 1 to 7 for the new beam set. See *section 6.1.20 Multiple beam set planning on page 372* for more information.

14. Click **OK**. The plan (without beams) is opened. The image set selected for the plan is displayed in the patient views.

Edit plan settings

To edit plan settings, select **Plan setup: Edit plan...**. This opens the **Edit Plan** dialog.

Copy plan

To make a copy of the current plan, select **Plan setup: Copy plan...**. In the **Copy Plan** dialog, enter a **Name** for the new plan and click **OK**. The new plan will be opened as the selected current plan, i.e. the plan that is displayed in **Virtual Simulation** workspace.

Close plan

In order to change the selected image set and create a new plan on that other image set, the current plan has to be closed. To close the current plan, select **Plan setup: Close plan...**

Delete plan

Select **Plan setup: Delete plan...** This will delete the plan from the plan list.

Edit dose grid settings

The dose grid is the 3D grid in which the dose distribution is calculated. To edit the dose grid:

1. Select **Plan setup: Dose grid settings...** This opens the **Edit Dose Grid Settings** dialog.

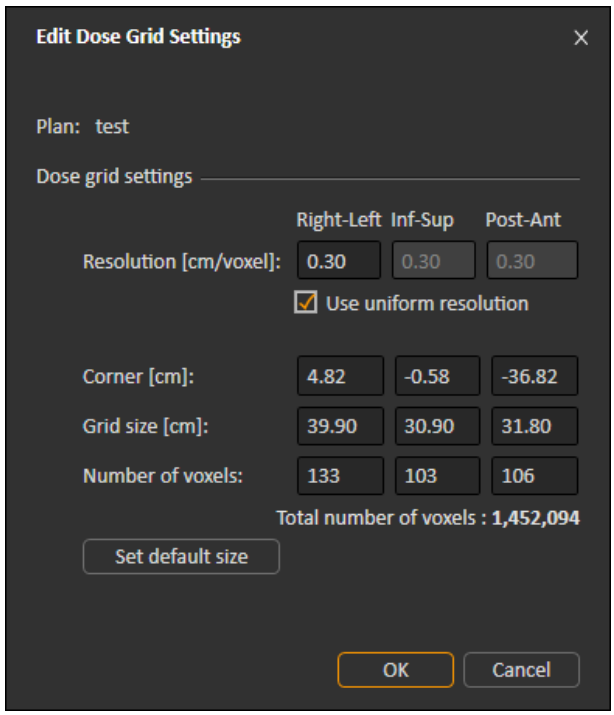


Figure 214. The Edit Dose Grid Settings dialog.

2. Enter **Resolution** values. This is the size of the voxels in the dose grid. Uncheck the **Use uniform resolution** checkbox to define individual values per direction. The default resolution is specified in the ClinicSettings application, see *Appendix D System administration* for more information.

3. Click the **Set default size** button to create a grid that covers the entire External geometry, support and fixture ROIs or select to enter **Corner** value, **Grid size** and/or **Number of voxels**.
4. Click **OK**.

6.2.5 Add, edit, copy or delete beams

Beams can be added to a plan in several ways;

- by specifying beam properties
- by copying an already existing beam, either from the current beam set or from another beam set
- by adding a set of pre-defined beams from a template. See *section 6.1.7 Beam list templates on page 328* for more information.
- by creating an opposed beam (only available for 3D-CRT planning)

The beam properties vary depending on the selected treatment modality, but the steps to create, copy, and delete beams are the same.

Note: *Adding a new beam after dose computation will invalidate the dose since the new beam will automatically get the MU value 1 when the first control point is added. In order to add a new beam and modify the shape without losing the dose, make a copy of an existing beam. The result is a beam with the MU value 0 and the beam can then be shaped on top of an existing dose distribution. The MU value must however be changed prior to dose computation to avoid a beam with the MU value 0.*

Add photon beams

1. Click the **Add** button in the beam list. This opens the **Add Beam** dialog.

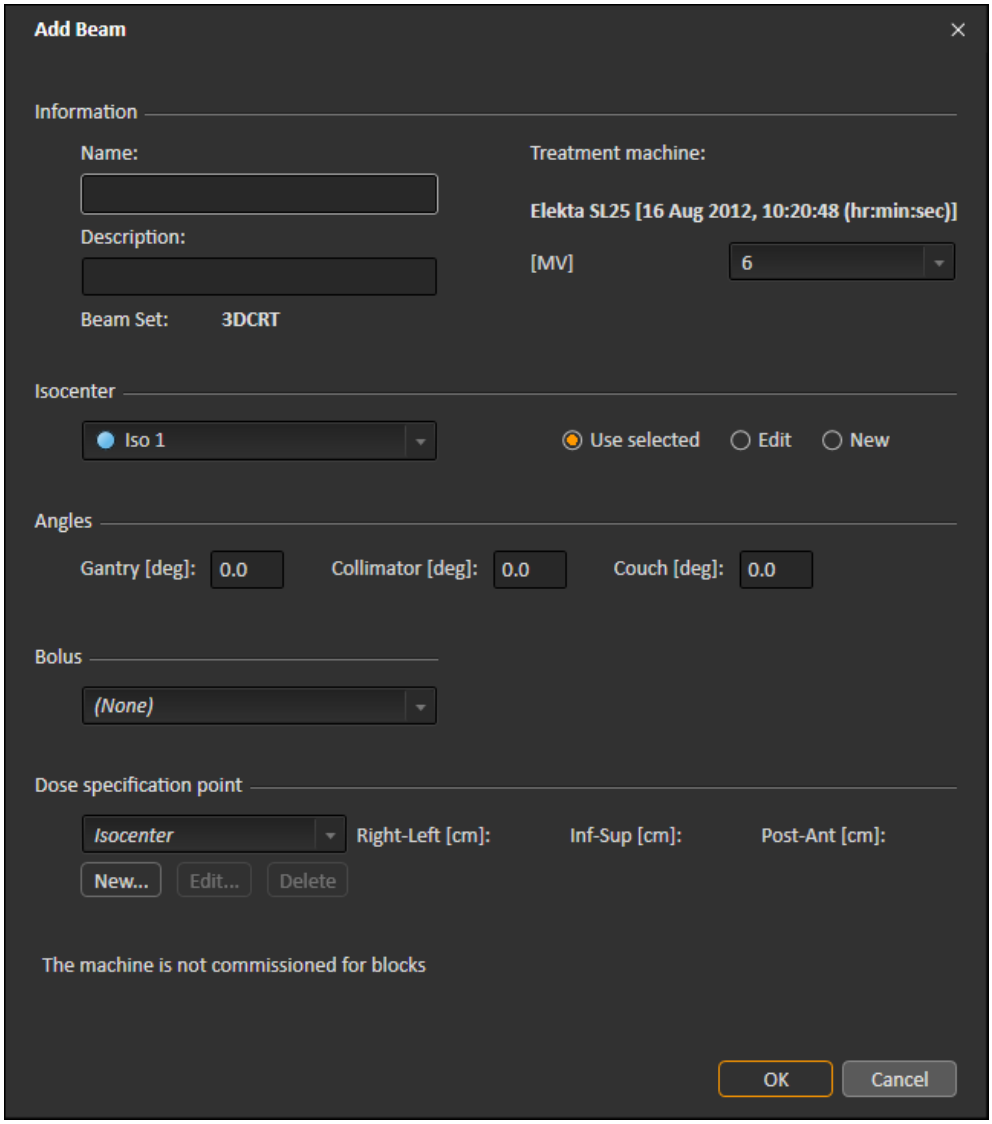


Figure 215. The **Add Beam** dialog.

2. Enter a beam **Name**.
3. Enter a beam **Description** (optional).
4. Select **Energy**.

5. Select **Isocenter**. Select to use an existing isocenter (**Use selected**), edit the existing isocenter (**Edit**) or define a new isocenter manually (**New**) or by copying the bounding box center positions of an ROI or a POI.

   - **Use selected**: If an isocenter already exists it will linked to this beam by default. The isocenter of the selected beam in the beam list will be the default selection. If there are no beams but an isocenter exists, this isocenter will be used by default when adding beams.
   - **Edit**: Edit the selected isocenter. Name and color is assigned by default but can be changed.
     - If the isocenter shall be in the center of an ROI, select an ROI from the **Center of ROI** drop-down list.
     - If the isocenter shall be in the same position as a POI position, select a POI from the **POI** drop-down list.
     - If the isocenter shall be in the center of the image set, select the **Center of image set** checkbox.
     - Multiple beam sets only: If the isocenter shall be in the same position as an isocenter in another beam set, select the isocenter from the drop-down list.

     Note: *Any edits will affect all beams sharing this isocenter.*
   - **New**: Create a new isocenter for this beam by defining it manually or by copying the bounding box center positions of an ROI or a POI. Name and color is assigned by default but can be changed. When creating a new isocenter it is possible to copy positions in the same way as when editing an isocenter (described in the previous bullet point). If the isocenter shall be in the center of the image set, click the **Center of image set** button.

   It is also possible to assign a separate isocenter to the beam by right-clicking the isocenter in the beam list and select "Duplicate isocenter".

   Note: *Isocenter names must be unique within the plan. If multiple plans uses the same isocenter names, but the isocenters have different coordinates at the time of approval, export or plan report printout, the isocenters need to be renamed to prevent misinterpretation.*

6. Enter **Gantry angle**, **Collimator angle** and **Couch angle**.
7. If desired, select a **Bolus** from the list. If there is no bolus in the list, it has to be created, see *section 6.1.11 Create bolus on page 341* for more information.
8. A **Beam Dose Specification Point** can be selected or created. (This point and its dose value are exported and may be used as reference for independent verification of the dose calculation. See *section 6.1.9 Beam dose specification point on page 337* for more information.)
9. Click **OK**. The created beam will be visible in the beam list.

To add additional beams, repeat steps 1-8 above, or copy the created beam by clicking the **Copy** button (see *Copy a beam in the current beam list on page 326*) or the **Copy from...** button (see *Copy beams from another plan or another beam set on page 326*).

Beams can also be added from a template by clicking the **Load template** button (see *Add beams from template on page 328*).

Copy beam

In the beam list, select the beam to copy and click the **Copy** button. The name of the new beam will be the name of the old beam with a 'n' at the end (where n is 1 for the first beam, 2 for the second one etc.).

Note: *The beam set dose is not invalidated when copying an existing beam. The copied beam will get the value MU=0.*

Note: *For VMAT, Conformal Arc and Static Arc plans the copied beam will get the same MU as the original beam and therefore the beam set dose is invalidated when a beam is copied. For other treatment techniques, the beam set dose is not invalidated when a beam is copied since the copied beam will get the value MU=0.*

Delete beam

In the beam list, select the beam to delete and click the **Delete** button.

Create opposed beam

For 3D-CRT plans, an opposed beam can be created. Select a beam in the list and click the **Create opposed** button. This creates a new beam with an opposed gantry angle and mirrored field shape.

Merge beams

The beams can be merged for a field-in-field approach. The beams to be merged must have the same isocenter position, energy, gantry angle, collimator angle and couch angle.

Select the desired beams to merge by Shift or Ctrl mouse-click. The beam that shall become the first segment of the merged beam shall be selected first (it will be highlighted with the orange selection color). Click the **Merge beams** button to merge the beams.

Split beam

A beam containing several segments can be split into separate beams. The new beams will have the same Treat and Protect ROIs, ensure that the field openings for these beams are ok. To split the current beam segments into individual beams, click the **Split beam** button.

Renumber beams

The beams will be delivered in ascending order. To renumber the beams, click the **Renumber beams** button.

6.2.6 Edit beam properties

The beams can be manually optimized by changing the isocenter positions, beam angles and segment shapes.

Edit the isocenter position

After plan generation two DRRs are displayed in the BEV. The isocenter that was set to slice intersection in the default plan is displayed and can be edited. As a help when editing the isocenter, the intersection point of the beam center with the patient is displayed as a cross on the External ROI surface.

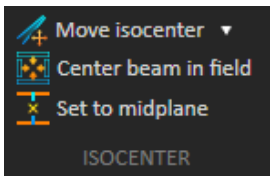
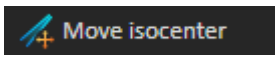


Figure 216. The Isocenter tools.

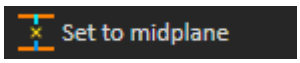
There are several options for editing the isocenter using the the **Isocenter** tools.



Move isocenter: Move the isocenter to the desired position by click and drag in the BEV.

Set to intersection: Move the isocenter to the slice intersection.

Center beam in field: Move the isocenter to the center of the field opening.



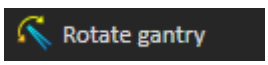
Set to midplane: Set isocenter at depth midplane patient based on the external ROI geometry.

Edit beam angles

The beam angles for gantry, collimator and couch can be edited manually directly from the BEV or a 2D patient view.

Rotate gantry

Click the **Rotate gantry** button in the toolbar. Click and drag to left/right in the lower part of the BEV or in a 2D patient view to adjust the gantry angle.



Rotate collimator

Click the **Rotate collimator** button in the toolbar. Click and drag up/down in the BEV to adjust the collimator angle. A block will always remain in its original position related to the patient. The MLC opening will rotate with the collimator.

There are also a set of predefined rotation states that can be used when setting a wedge, that will rotate the collimator and aim to reshape the leaves to preserve the old target coverage. They are reached by the drow-down menu on the **Rotate collimator** button.

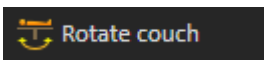
- +90 auto conform
- +180 auto conform
- +270 auto conform
- +90 keep edited opening
- +180 keep edited opening
- +270 keep edited opening

Auto conform is the preferred option if possible. The collimator will be rotated and MLC reconformed based on virtual jaws, drawn aperture shapes and treat and protect ROIs. **Keep edited opening** will do its best to imitate the shape of the current leaf positions, but target and protect areas are not guaranteed. See note below.

Note: *If "Keep edited opening" is selected in the Beam list, be aware of the following: The area that was exposed (i.e., the area not covered by the leaves) before the rotation, is guaranteed to also be exposed after the rotation. However, due to the finite width of the leaves, the exposed area may increase after rotating the collimator. Therefore it is important to always evaluate the aperture after rotating the collimator.*

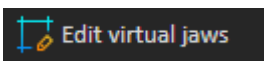
Rotate couch

Click the **Rotate couch** button in the toolbar. Click and drag up/down in the right part of the BEV to adjust the couch angle.



Edit virtual jaws

Use the **Edit virtual jaws** tool to manually pull the virtual jaws in the BEV to desired positions. Positions of the virtual jaws will be presented in the Jaw max aperture area of the beam if the beam have no real physical jaws, otherwise positions of the real jaws will be presented.



Click and drag on the active (blue) jaw to move it. Each jaw can be moved separately but it is also possible to move both x- and y-jaws at the same time. This is done by hovering and clicking in the corner area (the intersection between the x- and y-jaw) and dragging the jaws to a desired position. Clicking in the middle moves the complete field opening. Restrict movement of the complete field opening to the x- or y-direction by pressing Ctrl or Shift.

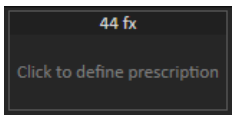
Select to synchronize the y-jaws, for example to set the upper and lower limits of the tumor, by checking the **Sync Y-jaws** checkbox. This will make the edited virtual jaw equally positioned in all beams in the beam set that share the same isocenter. Positions of the virtual jaws will be presented in the Jaw max aperture area of the beam if beam have no real physical jaws, otherwise positions of the real jaws will be presented.

Create rectangular field

Click the **Rectangular field** button to open the **Create Rectangular Fields** dialog (see section *section 6.3.18 Create rectangular fields on page 458*).

Define Prescription

Click the **Define prescription** button to open the **Define Prescription** dialog (see section *section 6.1.12 Define or modify prescription on page 343*.



Edit segment shapes

Click the **Edit MLC and jaws** button.

This opens the **Edit MLC and jaws** dialog which provides several tools to manually edit the segment shape.

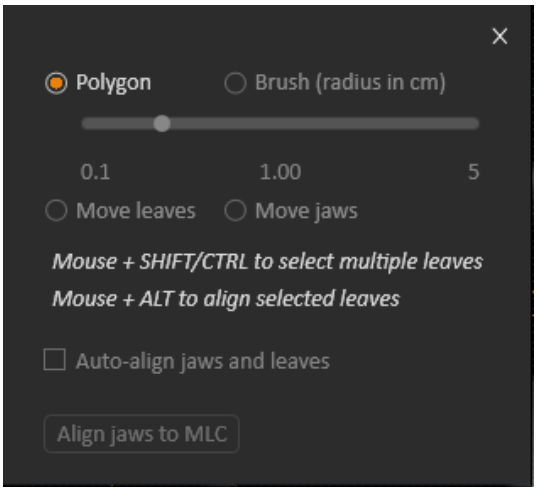


Figure 217. The **Edit MLC and jaws** dialog.

- Use the **Polygon** tool to manually draw a polygon shape in the BEV. Right-click in the view to close the polygon shape.

  Note: *To keep the polygon shape so that it can be edited after the leaves have been conformed, use the aperture shape polygon tool or the spline tool instead.*

- Use the **Brush** tool to push the leaves in the BEV to a desired position. The Brush tool can be adjusted using the slider in the Editing window, or by pressing the + and - keys on the numerical keyboard, or by using the mouse wheel while pressing the ALT key. (By using the smallest size of the Brush tool individual leaves can be moved.)
- Use the **Move leaves** tool to manually pull the leaves to a desired position. Left-click and press SHIFT/CTRL to select multiple leaves. Left-click and press ALT to align the selected leaves.
- Use the **Move jaws** tool to manually pull the jaws in the BEV to desired positions. Click with the mouse on the (blue) jaw to move it.
- Uncheck **Auto-align jaws and leaves** to move leaves without affecting jaws with the **Brush** tool, or jaws without affecting leaves with the **Move jaw** tool.
- Click the **Align jaws to MLC** button to align the jaws with the MLC opening.

Note: *Although it is possible to manually move a jaw and thereby collimate using the jaws also inside a field, this is not advisable. E.g., for an Elekta machine where the x-jaw is relatively thin compared with an MLC leaf, the jaw collimation will not be very effective.*

Retract MLC

Right-click in the BEV to open the context menu and select **Retract MLC**.

Edit beam properties directly in the beam list

In the beam list, select the beam to edit and click the **Edit** button, or double click on a non-editable area of the beam in the beam list. The **Edit Beam** dialog presents the same beam properties as the **Add Beam** dialog. Some beam properties can also be edited directly in the beam list, for example: name, description, isocenter position, gantry angle, couch angle, and MU/fx. For photon beams the following properties are also editable: Energy, Collimator angle, Bolus, and Max jaw aperture. Editable fields has a mark in the upper left corner. Click on the desired property field to set the list in edit mode.

Note: *When editing the gantry angle, the beam will be rotated around the current isocenter. If the isocenter has been manually changed, the new isocenter will be used as center of rotation.*

Beam visibility can be toggled on or off by checking/unchecking the visibility checkbox.

Note: *When visibility is unchecked for a beam, only the 2D beam graphics are hidden. The beam's dose contribution will still be displayed and taken into account in dose statistics.*

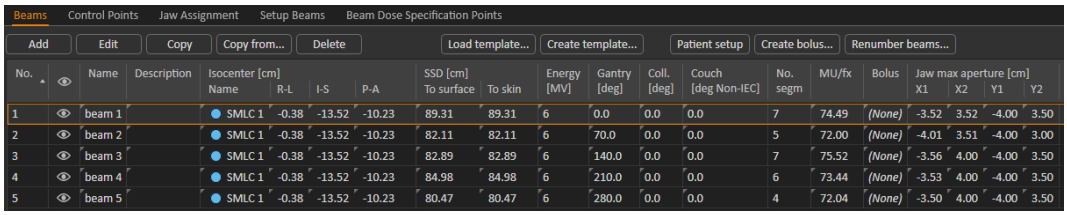
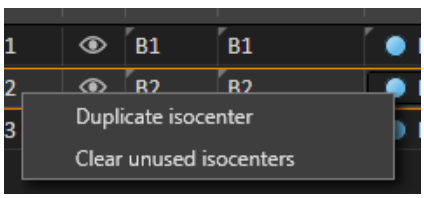


Figure 218. The **Beams** tab for a photon plan. To edit a beam, select it and click the **Edit** button, or edit the beam by clicking the desired property field.

Assign a separate isocenter to a beam

Define a new separate isocenter for the beam by right-clicking on an existing isocenter in the list and select **Duplicate isocenter**.



Select other isocenter

To select another existing isocenter for a beam, click on the isocenter in the beam list and select another isocenter from the drop-down list.

Clear unused isocenters

If undesired and unused isocenters exist in the beam sets, select **Clear unused isocenters**. All isocenters in the beam set that are not used by a beam will be deleted.

Jaw max aperture

The **Jaw max aperture** column in the beam list displays virtual jaws if no real physical jaws exist, otherwise values for the physical jaws will be presented. This is only applicable for 3D-CRT beams.

The Jaw max aperture can only be edited for a machine with the following jaw movement rules:

- **Per segment**: Editable if there only is one segment, except for Static Arc where editing is enabled regardless of segment count. Only applicable for physical jaws.
- **Per beam**: Editable if all segments have the same jaw position. Only applicable for physical jaws.

Wedges

If a treatment machine that supports wedges is selected, there is a multiple choice of wedge angles and orientations in the list.

6.2.7 Laser export

If an initial laser isocenter (reference point) is defined and a treatment beam isocenter exists, the distance between these two points, the laser shift, can be exported to the laser system. The lasers can then be positioned to the treatment machine isocenter and the patient can be marked directly on that position. During treatment, the treatment machine isocenter will be correct directly without having to shift the treatment couch.

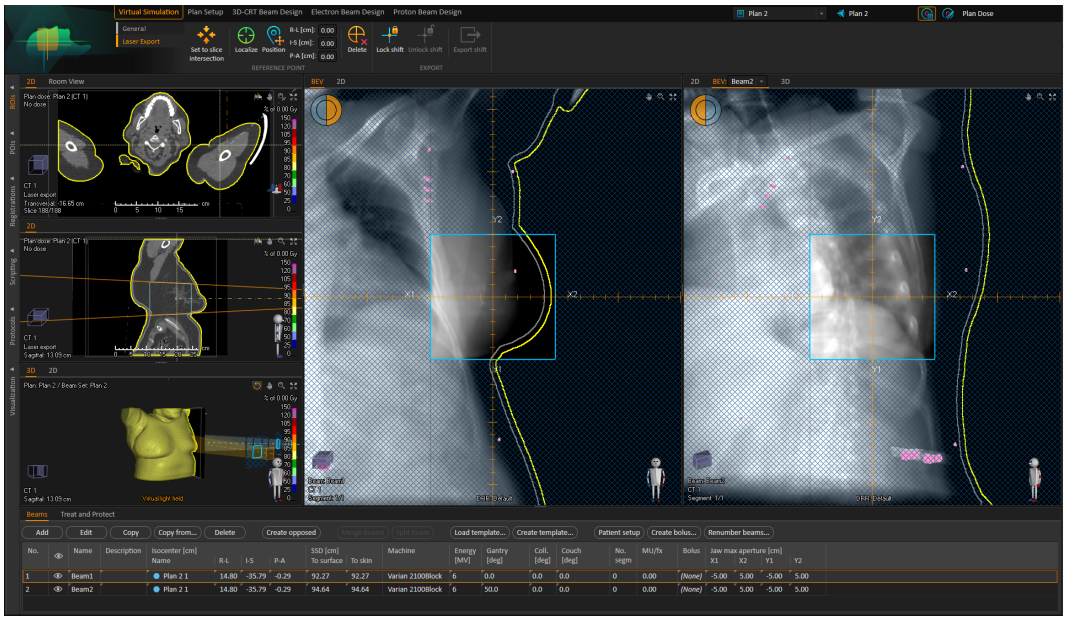


Figure 219. The **Laser** tab.

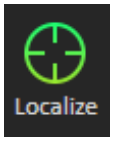
Prerequisites

- The CT machine must be commissioned with **Laser export enabled** in RayPhysics. See *RSL-D-RS-7.0-RPHY, RayStation 7 RayPhysics Manual* for more information.
- The plan must have an isocenter.

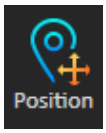
The Reference Point editing tools

The Reference Point editing tools can be used to set the reference point to a desired position.

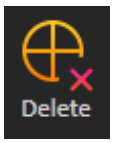
The **Set to slice intersection** button can be used to move the reference point to the intersection of the transversal, sagittal, and coronal views.



The **Localize** button repositions all patient views to the reference point position.



The **Position** button can be used to position the reference point by drag and drop. Click anywhere in the view and drag the reference point to the desired position.



Delete the current reference point by clicking the **Delete** button.

Set reference point and export to laser system

1. Scroll through the slices to identify the CT markers on the patient. The green cross corresponds to the position where the reference point will be set.

   Note: *If 'Set reference point to CT origin' is selected in RayPhysics, the reference point will always be set to (0,0,0) and cannot be modified.*

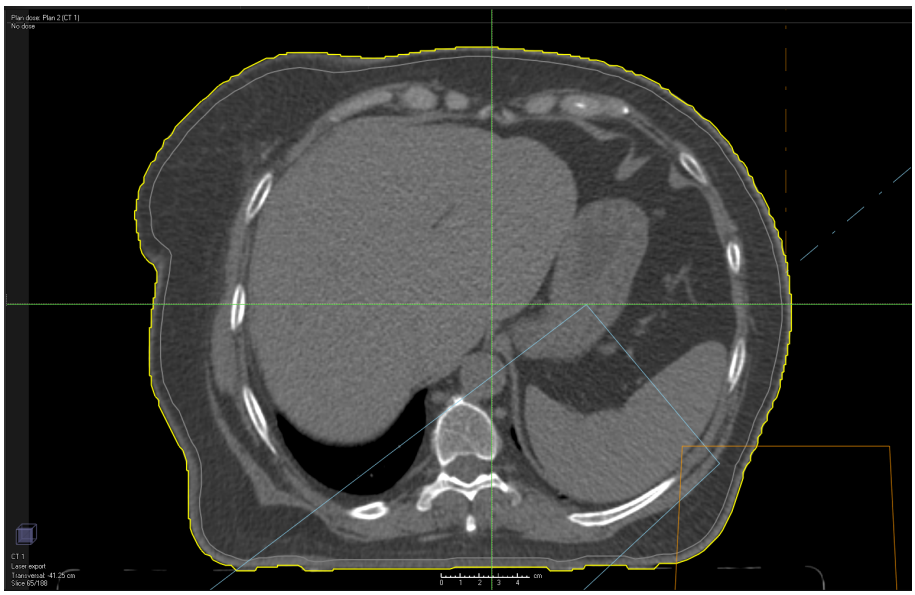
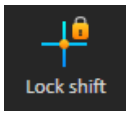


Figure 220. The green cross in the patient 2D views corresponds to the reference point.

2. Position the reference point marker using the **Reference Point** tools.

3. Lock the shift for editing by clicking the **Lock shift** button.



The reference point will be visible as an 'initial laser isocenter' in the **POI** list and in the patient views. A localization point corresponding to the treatment machine isocenter will also be created. The difference between the initial laser isocenter and the localization point is called the laser shift and can be exported to the laser system. When the laser shift has been locked, the initial laser isocenter and the localization point cannot be modified.

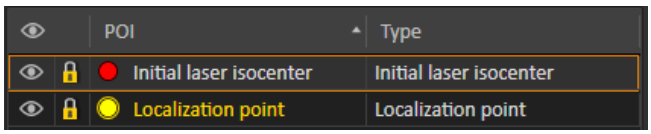


Figure 221. The initial laser isocenter and the localization point (treatment machine isocenter) visualized in the POIs list.

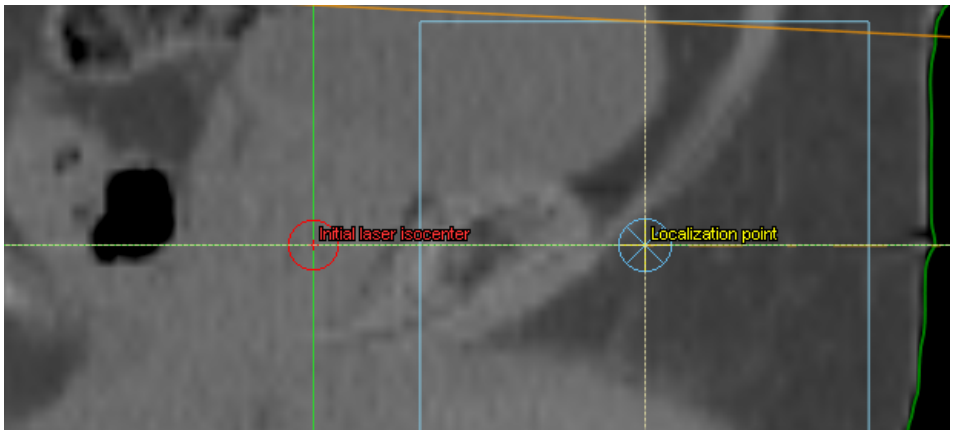
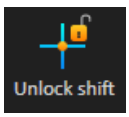
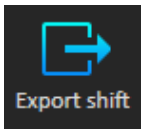


Figure 222. The initial laser isocenter and the localization point (treatment machine isocenter) visualized in a patient 2D view.

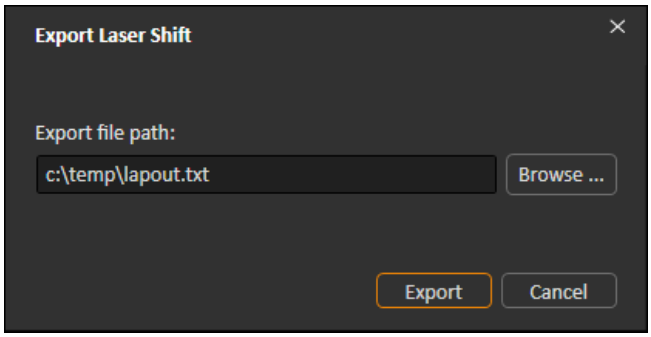
To unlock the reference point and make it editable, click the **Unlock shift** button. To enable laser export, the shift must be locked again.



4. Export the laser shift by clicking the **Export shift** button.



5. The **Export file path** is automatically assigned to the destination specified in the imaging system. This file path can however be modified if needed. Click **OK** to export the laser shift file.



Planning

The localization point represents the marked isocenter position. When creating plans for this setup, the localization point shall be used as isocenter position for the beams.

6.2.8 Field shaping in BEV

Machine independent field shaping can be performed in the BEV by using the **Aperture shaping** tools. Drawn shapes can define areas to treat or protect. Drawn areas to treat or protect can be combined with selected ROIs to treat or protect. If no other treat shapes are defined, or treat ROIs selected, the virtual jaws will be used as treat area. This is supported for 3D-CRT, but not for Conformal Arc or Static Arc.

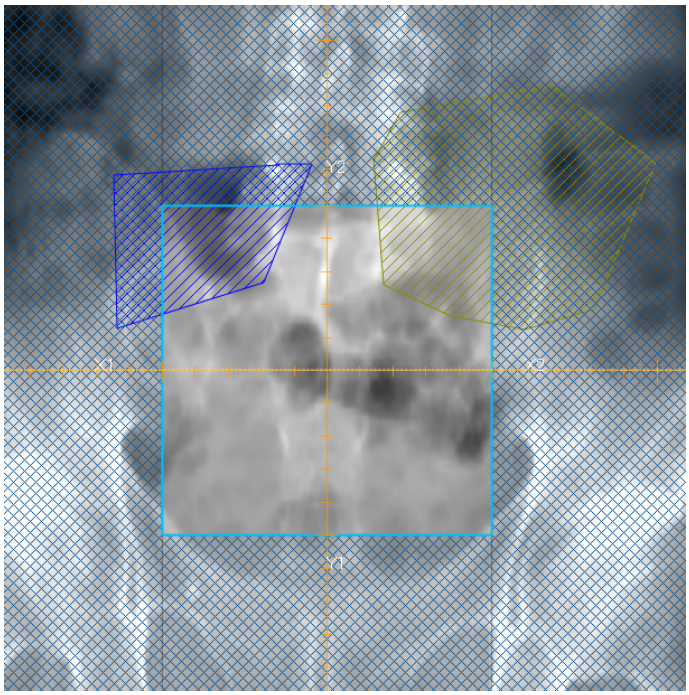


Figure 223. An example of drawn aperture shapes in the BEV.

The Aperture shaping tools

The aperture shaping tools are located in the Aperture shaping toolbar.

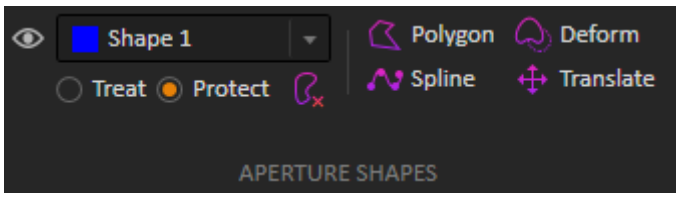
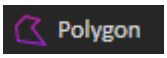


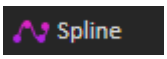
Figure 224. The **Aperture shaping** tools.

Draw an aperture shape

If the starting point is outside all aperture shape edges and 'Polygon' or 'Spline' is selected, a new aperture shape can be defined.



Add a **Polygon** shape: Click to add a contour line. Right-click to exit drawing mode, the first and the last points in the slice will be connected.



Add a **Spline** shape. The **Spline** tool adds smoothly curved lines between the points marked by a click. Click to add a curved contour line. Right-click to exit drawing mode, the first and the last points in the slice will be connected.

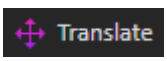
Editing aperture shapes

If hovering over a drawn aperture shape in the BEV views, name and type (treat/protect) will be displayed, independently of the aperture shaping tool enable status, when inside a margin of 0.75 cm on each side. If hovering over multiple drawn aperture shape edges, the nearest will be chosen. The aperture shape will get a brighter color and will be selected if left-clicked when the aperture shape editing tool is active.

If the starting point (first left-click) is near an existing aperture shape edge, the aperture shape will be enabled for editing.

- **Extend** – A drawn area is added to the original shape if the starting point is inside the original shape (close enough to an edge to have the shape selected).
- **Subtract** - A drawn area is subtracted from the original shape if the starting point is outside the original shape (close enough to an edge to have the shape selected).
- **Cut** – A part of the aperture shape is cut if a polygon or spline editing divides the shape in parts. The cutting can be done by a shape area, or by a two click line – left click to start and right click to close. The smaller part will be cut off.

The **Deform** tool deforms the drawn shape. The size of the cursor ring is proportional to the extent of the deformation. Move the cursor to the contour, click the mouse button and move the mouse to deform the shape. To change the size of the deformation tool, use the slider in the **Deformation range** dialog, type the + and - keys on the keyboard, or by using the mouse wheel while pressing the CTRL key.



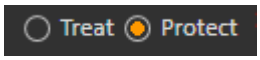
The **Translate** tool allows translation of a contour by clicking its border and moving the mouse.

Cancel editing

Pressing 'Esc' interrupts current editing of polygons and splines.

Define a Treat or Protect property for the drawn aperture shape

Select if the drawn shape is going to be used as an area to **Treat** or **Protect** by clicking the corresponding radio button.



The drawn shapes and the treat and protect settings will be used as input to the conform calculation, together with virtual jaws and selected treat and protect ROIs, to conform the aperture that is realized with MLC or an aperture block. Note that the protect areas will be used as areas to protect when creating an aperture block in the same manner as when using protect ROIs. Protect shapes cannot be used to create a shielding block.

Toggle visibility on or off

Visibility of the drawn shapes can be toggled on or off by checking/unchecking the visibility checkbox.

DRR Settings

There are several settings in the DRR view that can be used to facilitate drawing of aperture shapes and editing physical block contours.

It is also possible to **Use cut planes** in the DRR view. This is described in detail in *section 6.1.8 The DRR views and settings on page 330*.

Skin view

In order to use skin information when shaping the field, it is possible to visualize the **External as a mesh** in BEV. Toggle the **Transparent external ROI** in the Context menu off in order to see the skin better.

When contouring around beam overlap it is possible to turn on **Light field** in BEV.

Note: *Light field in BEV and overlapping beams. The External ROI is often based on a rather low resolution CT image and may therefore be imprecise. This should be taken into account when using Light field to position the patient or when viewing overlapping beams.*

These settings are described in detail in *section 3.4.5 The Visualization tab on page 62*.

6.2.9 Specify settings in the Treat and Protect tab

To specify the treat and protect settings, use the **Treat and Protect** tab at the bottom of the workspace.

Note: *Adding treat and protect aperture shapes are done from the tool panel.*

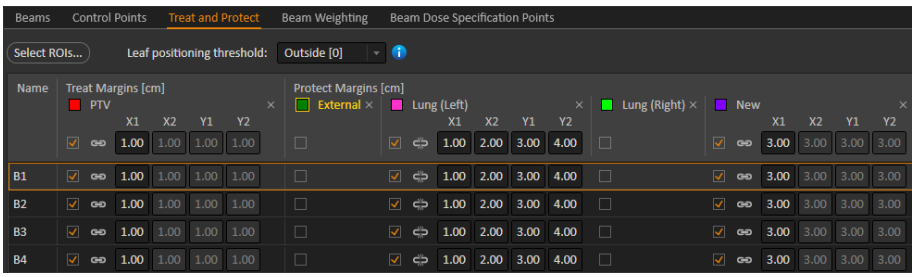


Figure 225. The **Treat and Protect** tab.

ROI usage

The header list in the **Treat and Protect** tab contains all the ROIs that are selected to use for planning. For conformal treatments, the list is default populated by all ROIs classified as Target or OAR. For primarily optimized treatment techniques, the list is empty per default.

To add or remove ROIs from the presented list in the **Treat and Protect** tab, click the **Select ROIs...** button. This opens the **Select ROIs** dialog. It is also possible to click the "x" next to the ROI's name in the column head to remove that ROI from the list.

Select ROIs to treat or protect

The outlines of ROIs selected as treat or protect will be input to the automatic aperture generation. An ROI will be classified as being treated or protected based on its type. All ROIs classified as Unknown/Other will be classified as ROIs to protect.

To select to treat or protect an ROI for a beam, check the checkbox for that ROI in the row for that beam.

To simultaneously select to treat or protect an ROI for all current beams in the beam set, click the checkbox in the header section for the ROI.

Leaf positioning threshold

The leaf positioning threshold represents the amount of relative area of the target that a leaf shall overlap at the target boundary.

To add leaf positioning threshold, click the drop-down list and select:

- Outside: If the threshold is set to 0, leaves are positioned to barely touch the target boundary.
- Inside: If the threshold is set to 1, the leaves are moved inwards such that there is no non-target area exposed between the leaf and the target.

- Mid: Set the threshold value to 0.5. An intermediate threshold value implies that a leaf is positioned such that the ratio of the covered target area, and the covered target area had the threshold been set to 1, equals the threshold value.
- Custom: For old plans or plans edited from scripting a custom leaf positioning threshold can be set.

Note: *Leaf positioning threshold is applied to polygon drawn MLC openings, Treat ROIs and aperture shapes of treat type. Protect shapes and protect ROIs are always fully protected.*

Note: *For Conformal Arc, Treat ROIs are supported but not Protect ROIs.*

Margins used when conforming to Treat and Protect ROIs

A margin to use around a treat or protect ROI can be set. The margin recipe can be set as either a uniform margin or individual margins in all beam directions. The selection can be done per each beam by clicking the icon for that beam, or for all current beams simultaneously by clicking the link icon in the header.

Uniform margins: the margins are all set to the first/X1 margin value.

Non uniform margins: the margins can be edited separately.

Margin values can be entered per ROI for each individual beam, or edited in the header to apply the margin values for the ROI for all current beams in the beam set.

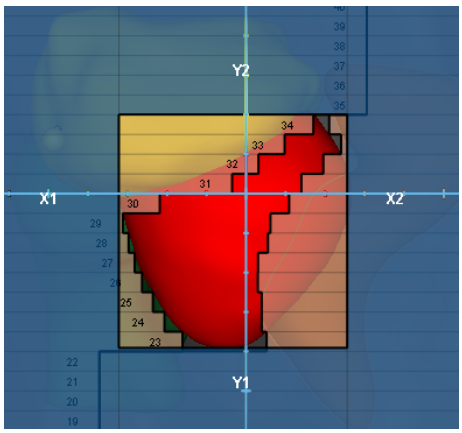


Figure 226. Apertures generated without margins. Rectum and bladder (blue and yellow) are protected. PTV (red) is treated.

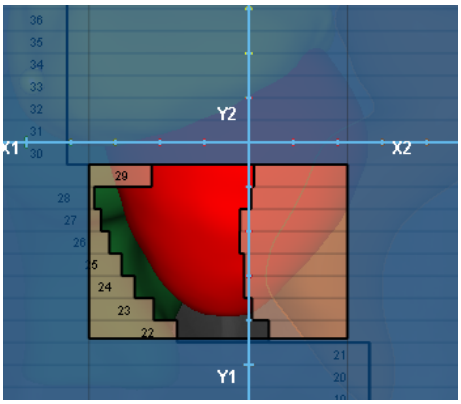


Figure 227. Apertures generated with a 0.5 cm margin. The field is broadened where this does not harm the protected ROIs.

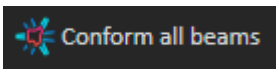
6.2.10 Conform field openings

The conform field openings tool is used to shape the field openings based on drawn aperture shapes and ROIs selected for Treat and Protect, and using the defined margins for the ROIs. For each beam the generated opening will conform to the drawn shape(s) and ROI(s) selected for treatment while shielding the shape(s) or ROI(s) selected for protection.

Note: *The virtual jaws, the drawn aperture shapes and the selected treat and protect ROIs are preserved when changing treatment machine. This to allow the user to change treatment machine and reconform the beam aperture.*

Conform field openings for all beams

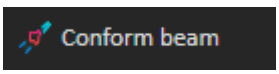
To conform field openings for all beams in the current beam set according to the treat and protect settings, drawn shapes and virtual jaws, click the **Conform all beams** button.



As a result, all aperture blocks in the beam will be conformed, otherwise the MLC field opening will be conformed.

Conform field openings for a selected beam

To conform a field opening for the current beam according to the treat and protect settings, drawn shapes and virtual jaws, click the **Conform beam** button.



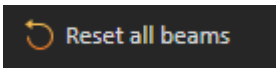
If there is an aperture block in the beam this will be conformed, otherwise the MLC field opening will be conformed.

Conform field openings - rules and exceptions

- The area to be treated is the union of treat ROI outlines and treat aperture shape. If no treat ROI or aperture shape is selected, the Virtual jaws will define the area to treat
- The area to shield is the union of protect aperture shapes and protect ROI outlines.
- In conflict situations, the action will always strive to shield the full area to be protected, which can have impact on target coverage.

6.2.11 Reset all beams

The **Reset all beams** button resets all the beams in the beam set, i.e. removes all control points, blocks, cones and wedges and sets all beam MUs to zero.



Drawn aperture shapes, virtual jaw positions ant treat and protect ROI selections will be preserved.

6.2.12 Patient setup

For information on Patient Setup, refer to *section 6.1.18 Patient setup on page 360*.

6.3 THE 3D-CRT BEAM DESIGN MODULE

The 3D-CRT Beam Design module can be used to create plans using 3D-CRT, Conformal Arc or Static Arc treatment techniques. Beam orientations, apertures and various beam modifiers are designed by the user in order to manually optimize the plan. Tools are provided that make it possible to, with just a few clicks, compute:

- MLC shapes or aperture block openings based on the projection of the target ROIs that are to be treated and the OAR ROIs that are to be protected. Manually drawn areas to treat or protect can also be taken into account.
- MU as to fulfill the prescription.

In addition to this the user can also:

- define a prescription.
- edit isocenter position, gantry angle, couch angle, collimator angle, leaf and jaw positions.
- add wedges, aperture blocks, shielding blocks, circular cones and bolus.
- perform manual beam weighting.

In this section

This section contains the following sub-sections:

6.3.1	The 3D-CRT Beam Design user interface	p. 424
6.3.2	Setup plan	p. 426
6.3.3	Define or modify prescription	p. 427
6.3.4	Edit beam properties	p. 428
6.3.5	Field shaping in BEV	p. 434
6.3.6	Specify settings in the Treat and Protect tab	p. 437
6.3.7	Conform field openings	p. 440
6.3.8	Reset all beams	p. 441
6.3.9	Control points and MLC positions	p. 442
6.3.10	Calculate dose	p. 443
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6.3.12	Beam weighting	p. 445
6.3.13	Beam dose specification points	p. 447
6.3.14	Circular cones	p. 448
6.3.15	Aperture blocks	p. 450
6.3.16	Shielding blocks	p. 454
6.3.17	Static Arc	p. 457
6.3.18	Create rectangular fields	p. 458

Precautions

WARNING!

Block/cutout verification. Always verify that the blocks and electron beam cutouts created in the Beam design modules are physically realizable. It is not possible to define any block manufacturing constraints in RayStation.

For proton blocks, the size of the block milling tool is taken into consideration in the automatic block generation tools. However, it is possible to obtain a block that cannot be manufactured using the manual block editing/creation tools. It is then possible to run the milling tool algorithm manually after the block editing. However, since it is not done automatically, the responsibility that the block is physically realizable still lies with the user.

Always check the created block against the block aperture printout. (27064)

6.3.1 The 3D-CRT Beam Design user interface

Workspace

The 3D-CRT Beam Design workspace contains several views showing the Beam's Eye View (**BEV**), **2D** and **3D** views and **DVH**s.

The workspace also contains three sub-windows showing 2D image data in a specific patient plane, making it possible to simultaneously work in three dimensions. One of the two subwindows to the right shows **Dose Statistics** and **Clinical Goals**.

The lower part of the workspace displays the beam list, which contains the tabs **Beams**, **Control points**, **Treat and protect**, **Beam weighting** and **Beam dose specification points**. At the borders between the different views are handles which can be dragged to adjust the workspace as desired.

The 3D-CRT Beam Design workspace has three tabs: **General**, **Aperture block** and **Shielding block**.

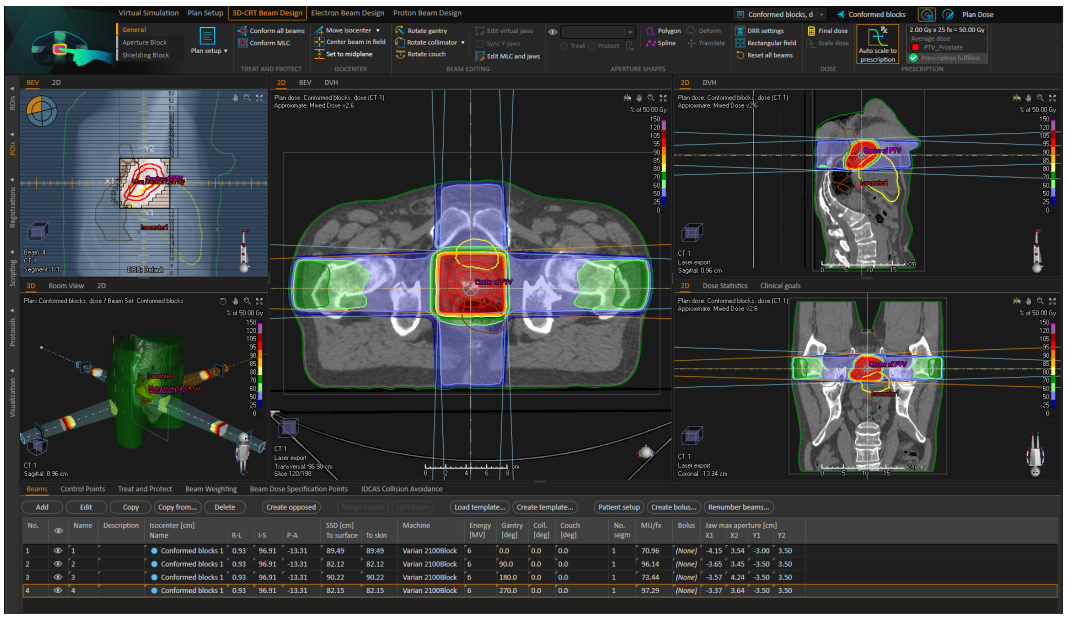


Figure 228. The 3D-CRT Beam Design workspace.

Graphical User Interface

For more information about the tools, operations and various view types in the Graphical User Interface, see *chapter 3 The Graphical User Interface*.

Context menus

Each view has a context menu which is opened by right-clicking in the view. For a description of the general context menu options, see *section 3.9 The context menu on page 102*.

DVHs, dose statistics and clinical goals

For detailed information on DVHs, dose statistics and clinical goals, see *section 3.7 Common graphs, tables and tools on page 77*.

6.3.2 Setup plan

The **Plan setup** button contains options for basic treatment setup:

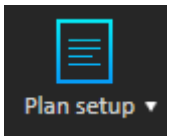


Figure 229. The **Plan setup** button.

Option	Description
Create new plan	To create a new plan, select **Plan setup: New plan...**. For more information on how to create a new plan, see *section 6.1.3 Create a new plan on page 306*.
Edit plan	To edit plan settings, **Plan setup: Edit plan...**. For more information, see *Edit plan settings on page 311*.
Copy plan	To copy the current plan, select **Plan setup: Copy plan...**. For more information, see *Copy plan on page 311*.
Close plan	To close the current plan, select **Plan setup: Close plan...**.
Delete plan	To delete a plan, select **Plan setup: Delete plan...**. This will delete the plan from the plan list.
Edit dose grid settings	To edit the dose grid settings, select **Plan setup: Dose grid settings...**. For more information, see *section 6.1.4 Define and edit the dose grid on page 312*.

6.3.3 Define or modify prescription

For instructions on how to to define or modify a dose prescription, see *section 6.1.12 Define or modify prescription on page 343*.

6.3.4 Edit beam properties

The beams can be manually optimized by changing the isocenter positions, beam angles and segment shapes.

Edit the isocenter position

After plan generation two DRRs are displayed in the BEV. The isocenter that was set to slice intersection in the default plan is displayed and can be edited. As a help when editing the isocenter, the intersection point of the beam center with the patient is displayed as a cross on the External ROI surface.

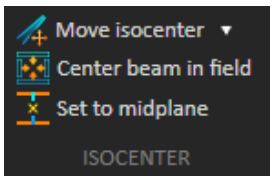
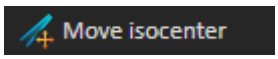


Figure 230. The Isocenter tools.

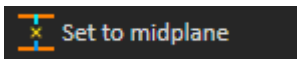
There are several options for editing the isocenter using the the **Isocenter** tools.



Move isocenter: Move the isocenter to the desired position by click and drag in the BEV.

Set to intersection: Move the isocenter to the slice intersection.

Center beam in field: Move the isocenter to the center of the field opening.



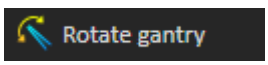
Set to midplane: Set isocenter at depth midplane patient based on the external ROI geometry.

Edit beam angles

The beam angles for gantry, collimator and couch can be edited manually directly from the BEV or a 2D patient view.

Rotate gantry

Click the **Rotate gantry** button in the toolbar. Click and drag to left/right in the lower part of the BEV or in a 2D patient view to adjust the gantry angle.



Rotate collimator

Click the **Rotate collimator** button in the toolbar. Click and drag up/down in the BEV to adjust the collimator angle. A block will always remain in its original position related to the patient. The MLC opening will rotate with the collimator.

There are also a set of predefined rotation states that can be used when setting a wedge, that will rotate the collimator and aim to reshape the leaves to preserve the old target coverage. They are reached by the drow-down menu on the **Rotate collimator** button.

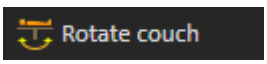
- +90 auto conform
- +180 auto conform
- +270 auto conform
- +90 keep edited opening
- +180 keep edited opening
- +270 keep edited opening

Auto conform is the preferred option if possible. The collimator will be rotated and MLC reconformed based on virtual jaws, drawn aperture shapes and treat and protect ROIs. **Keep edited opening** will do its best to imitate the shape of the current leaf positions, but target and protect areas are not guaranteed. See note below.

Note: *If "Keep edited opening" is selected in the Beam list, be aware of the following: The area that was exposed (i.e., the area not covered by the leaves) before the rotation, is guaranteed to also be exposed after the rotation. However, due to the finite width of the leaves, the exposed area may increase after rotating the collimator. Therefore it is important to always evaluate the aperture after rotating the collimator.*

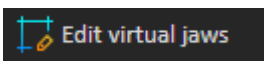
Rotate couch

Click the **Rotate couch** button in the toolbar. Click and drag up/down in the right part of the BEV to adjust the couch angle.



Edit virtual jaws

Use the **Edit virtual jaws** tool to manually pull the virtual jaws in the BEV to desired positions. Positions of the virtual jaws will be presented in the Jaw max aperture area of the beam if the beam have no real physical jaws, otherwise positions of the real jaws will be presented.



Click and drag on the active (blue) jaw to move it. Each jaw can be moved separately but it is also possible to move both x- and y-jaws at the same time. This is done by hovering and clicking in the corner area (the intersection between the x- and y-jaw) and dragging the jaws to a desired position. Clicking in the middle moves the complete field opening. Restrict movement of the complete field opening to the x- or y-direction by pressing Ctrl or Shift.

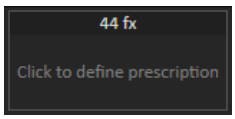
Select to synchronize the y-jaws, for example to set the upper and lower limits of the tumor, by checking the **Sync Y-jaws** checkbox. This will make the edited virtual jaw equally positioned in all beams in the beam set that share the same isocenter. Positions of the virtual jaws will be presented in the Jaw max aperture area of the beam if beam have no real physical jaws, otherwise positions of the real jaws will be presented.

Create rectangular field

Click the **Rectangular field** button to open the **Create Rectangular Fields** dialog (see section *section 6.3.18 Create rectangular fields on page 458*).

Define Prescription

Click the **Define prescription** button to open the **Define Prescription** dialog (see section *section 6.1.12 Define or modify prescription on page 343*.



Edit segment shapes

Click the **Edit MLC and jaws** button.

This opens the **Edit MLC and jaws** dialog which provides several tools to manually edit the segment shape.

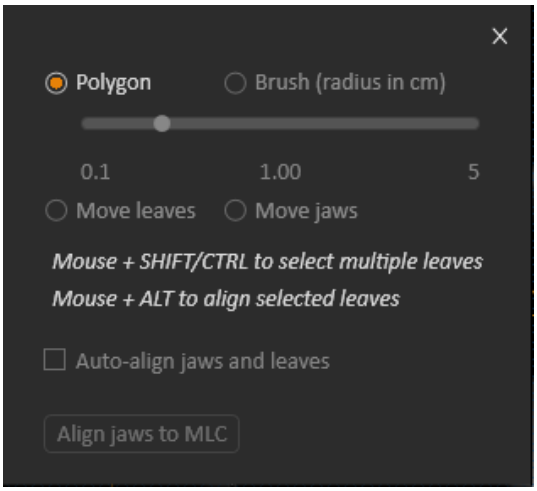


Figure 231. The **Edit MLC and jaws** dialog.

- Use the **Polygon** tool to manually draw a polygon shape in the BEV. Right-click in the view to close the polygon shape.

  Note: *To keep the polygon shape so that it can be edited after the leaves have been conformed, use the aperture shape polygon tool or the spline tool instead.*

- Use the **Brush** tool to push the leaves in the BEV to a desired position. The Brush tool can be adjusted using the slider in the Editing window, or by pressing the + and - keys on the numerical keyboard, or by using the mouse wheel while pressing the ALT key. (By using the smallest size of the Brush tool individual leaves can be moved.)
- Use the **Move leaves** tool to manually pull the leaves to a desired position. Left-click and press SHIFT/CTRL to select multiple leaves. Left-click and press ALT to align the selected leaves.
- Use the **Move jaws** tool to manually pull the jaws in the BEV to desired positions. Click with the mouse on the (blue) jaw to move it.
- Uncheck **Auto-align jaws and leaves** to move leaves without affecting jaws with the **Brush** tool, or jaws without affecting leaves with the **Move jaw** tool.
- Click the **Align jaws to MLC** button to align the jaws with the MLC opening.

Note: *Although it is possible to manually move a jaw and thereby collimate using the jaws also inside a field, this is not advisable. E.g., for an Elekta machine where the x-jaw is relatively thin compared with an MLC leaf, the jaw collimation will not be very effective.*

Retract MLC

Right-click in the BEV to open the context menu and select **Retract MLC**.

Edit beam properties directly in the beam list

In the beam list, select the beam to edit and click the **Edit** button, or double click on a non-editable area of the beam in the beam list. The **Edit Beam** dialog presents the same beam properties as the **Add Beam** dialog. Some beam properties can also be edited directly in the beam list, for example: name, description, isocenter position, gantry angle, couch angle, and MU/fx. For photon beams the following properties are also editable: Energy, Collimator angle, Bolus, and Max jaw aperture. Editable fields has a mark in the upper left corner. Click on the desired property field to set the list in edit mode.

Note: *When editing the gantry angle, the beam will be rotated around the current isocenter. If the isocenter has been manually changed, the new isocenter will be used as center of rotation.*

Beam visibility can be toggled on or off by checking/unchecking the visibility checkbox.

Note: *When visibility is unchecked for a beam, only the 2D beam graphics are hidden. The beam's dose contribution will still be displayed and taken into account in dose statistics.*

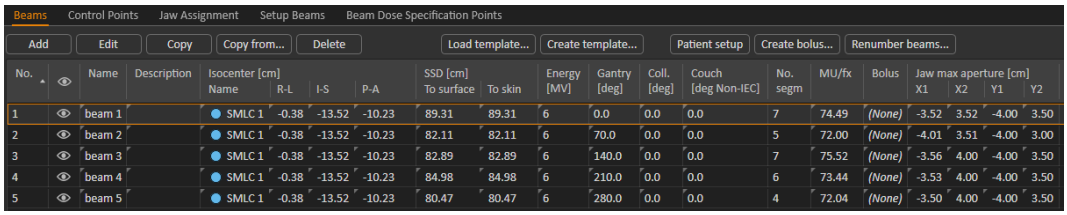
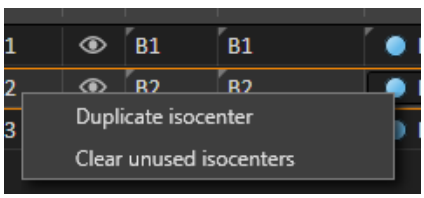


Figure 232. The **Beams** tab for a photon plan. To edit a beam, select it and click the **Edit** button, or edit the beam by clicking the desired property field.

Assign a separate isocenter to a beam

Define a new separate isocenter for the beam by right-clicking on an existing isocenter in the list and select **Duplicate isocenter**.



Select other isocenter

To select another existing isocenter for a beam, click on the isocenter in the beam list and select another isocenter from the drop-down list.

Clear unused isocenters

If undesired and unused isocenters exist in the beam sets, select **Clear unused isocenters**. All isocenters in the beam set that are not used by a beam will be deleted.

Jaw max aperture

The **Jaw max aperture** column in the beam list displays virtual jaws if no real physical jaws exist, otherwise values for the physical jaws will be presented. This is only applicable for 3D-CRT beams.

The Jaw max aperture can only be edited for a machine with the following jaw movement rules:

- **Per segment**: Editable if there only is one segment, except for Static Arc where editing is enabled regardless of segment count. Only applicable for physical jaws.
- **Per beam**: Editable if all segments have the same jaw position. Only applicable for physical jaws.

Wedges

If a treatment machine that supports wedges is selected, there is a multiple choice of wedge angles and orientations in the list.

6.3.5 Field shaping in BEV

Machine independent field shaping can be performed in the BEV by using the **Aperture shaping** tools. Drawn shapes can define areas to treat or protect. Drawn areas to treat or protect can be combined with selected ROIs to treat or protect. If no other treat shapes are defined, or treat ROIs selected, the virtual jaws will be used as treat area. This is supported for 3D-CRT, but not for Conformal Arc or Static Arc.

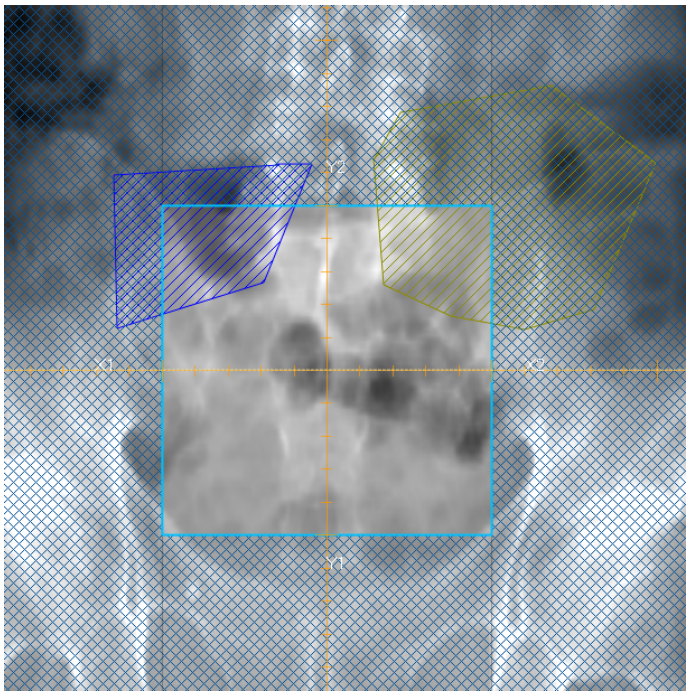


Figure 233. An example of drawn aperture shapes in the BEV.

The Aperture shaping tools

The aperture shaping tools are located in the Aperture shaping toolbar.

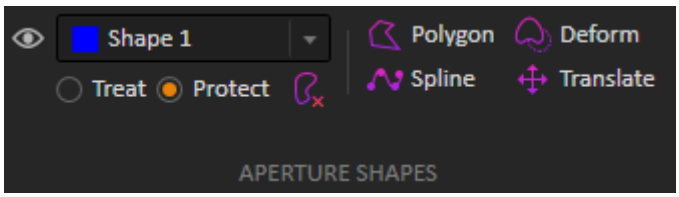
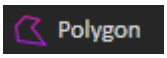


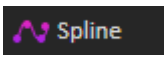
Figure 234. The **Aperture shaping** tools.

Draw an aperture shape

If the starting point is outside all aperture shape edges and 'Polygon' or 'Spline' is selected, a new aperture shape can be defined.



Add a **Polygon** shape: Click to add a contour line. Right-click to exit drawing mode, the first and the last points in the slice will be connected.



Add a **Spline** shape. The **Spline** tool adds smoothly curved lines between the points marked by a click. Click to add a curved contour line. Right-click to exit drawing mode, the first and the last points in the slice will be connected.

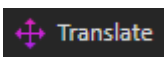
Editing aperture shapes

If hovering over a drawn aperture shape in the BEV views, name and type (treat/protect) will be displayed, independently of the aperture shaping tool enable status, when inside a margin of 0.75 cm on each side. If hovering over multiple drawn aperture shape edges, the nearest will be chosen. The aperture shape will get a brighter color and will be selected if left-clicked when the aperture shape editing tool is active.

If the starting point (first left-click) is near an existing aperture shape edge, the aperture shape will be enabled for editing.

- **Extend** – A drawn area is added to the original shape if the starting point is inside the original shape (close enough to an edge to have the shape selected).
- **Subtract** - A drawn area is subtracted from the original shape if the starting point is outside the original shape (close enough to an edge to have the shape selected).
- **Cut** – A part of the aperture shape is cut if a polygon or spline editing divides the shape in parts. The cutting can be done by a shape area, or by a two click line – left click to start and right click to close. The smaller part will be cut off.

The **Deform** tool deforms the drawn shape. The size of the cursor ring is proportional to the extent of the deformation. Move the cursor to the contour, click the mouse button and move the mouse to deform the shape. To change the size of the deformation tool, use the slider in the **Deformation range** dialog, type the + and - keys on the keyboard, or by using the mouse wheel while pressing the CTRL key.



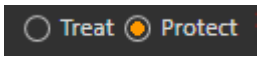
The **Translate** tool allows translation of a contour by clicking its border and moving the mouse.

Cancel editing

Pressing 'Esc' interrupts current editing of polygons and splines.

Define a Treat or Protect property for the drawn aperture shape

Select if the drawn shape is going to be used as an area to **Treat** or **Protect** by clicking the corresponding radio button.



The drawn shapes and the treat and protect settings will be used as input to the conform calculation, together with virtual jaws and selected treat and protect ROIs, to conform the aperture that is realized with MLC or an aperture block. Note that the protect areas will be used as areas to protect when creating an aperture block in the same manner as when using protect ROIs. Protect shapes cannot be used to create a shielding block.

Toggle visibility on or off

Visibility of the drawn shapes can be toggled on or off by checking/unchecking the visibility checkbox.

DRR Settings

There are several settings in the DRR view that can be used to facilitate drawing of aperture shapes and editing physical block contours.

It is also possible to **Use cut planes** in the DRR view. This is described in detail in *section 6.1.8 The DRR views and settings on page 330*.

Skin view

In order to use skin information when shaping the field, it is possible to visualize the **External as a mesh** in BEV. Toggle the **Transparent external ROI** in the Context menu off in order to see the skin better.

When contouring around beam overlap it is possible to turn on **Light field** in BEV.

Note: *Light field in BEV and overlapping beams. The External ROI is often based on a rather low resolution CT image and may therefore be imprecise. This should be taken into account when using Light field to position the patient or when viewing overlapping beams.*

These settings are described in detail in *section 3.4.5 The Visualization tab on page 62*.

6.3.6 Specify settings in the Treat and Protect tab

To specify the treat and protect settings, use the **Treat and Protect** tab at the bottom of the workspace.

Note: *Adding treat and protect aperture shapes are done from the tool panel.*

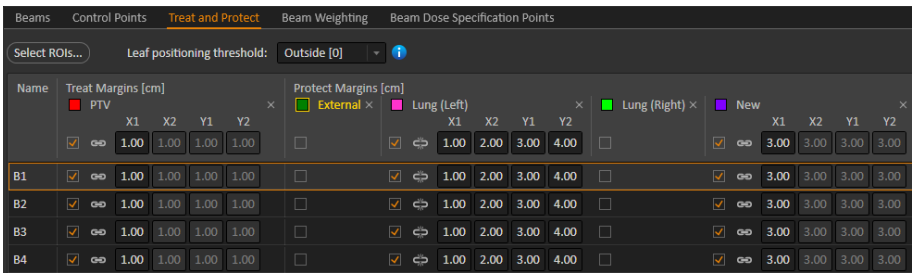


Figure 235. The **Treat and Protect** tab.

ROI usage

The header list in the **Treat and Protect** tab contains all the ROIs that are selected to use for planning. For conformal treatments, the list is default populated by all ROIs classified as Target or OAR. For primarily optimized treatment techniques, the list is empty per default.

To add or remove ROIs from the presented list in the **Treat and Protect** tab, click the **Select ROIs...** button. This opens the **Select ROIs** dialog. It is also possible to click the "x" next to the ROI's name in the column head to remove that ROI from the list.

Select ROIs to treat or protect

The outlines of ROIs selected as treat or protect will be input to the automatic aperture generation. An ROI will be classified as being treated or protected based on its type. All ROIs classified as Unknown/Other will be classified as ROIs to protect.

To select to treat or protect an ROI for a beam, check the checkbox for that ROI in the row for that beam.

To simultaneously select to treat or protect an ROI for all current beams in the beam set, click the checkbox in the header section for the ROI.

Leaf positioning threshold

The leaf positioning threshold represents the amount of relative area of the target that a leaf shall overlap at the target boundary.

To add leaf positioning threshold, click the drop-down list and select:

- Outside: If the threshold is set to 0, leaves are positioned to barely touch the target boundary.
- Inside: If the threshold is set to 1, the leaves are moved inwards such that there is no non-target area exposed between the leaf and the target.

- Mid: Set the threshold value to 0.5. An intermediate threshold value implies that a leaf is positioned such that the ratio of the covered target area, and the covered target area had the threshold been set to 1, equals the threshold value.
- Custom: For old plans or plans edited from scripting a custom leaf positioning threshold can be set.

Note: *Leaf positioning threshold is applied to polygon drawn MLC openings, Treat ROIs and aperture shapes of treat type. Protect shapes and protect ROIs are always fully protected.*

Note: *For Conformal Arc, Treat ROIs are supported but not Protect ROIs.*

Margins used when conforming to Treat and Protect ROIs

A margin to use around a treat or protect ROI can be set. The margin recipe can be set as either a uniform margin or individual margins in all beam directions. The selection can be done per each beam by clicking the icon for that beam, or for all beams simultaneously by clicking the link icon in the header.

Uniform margins: the margins are all set to the first/X1 margin value.

Non uniform margins: the margins can be edited separately.

Margin values can be entered per ROI for each individual beam, or edited in the header to apply the margin values for the ROI for all beams in the beam set.

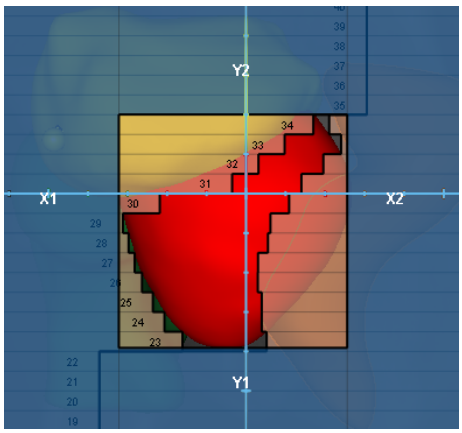


Figure 236. Apertures generated without margins. Rectum and bladder (blue and yellow) are protected. PTV (red) is treated.

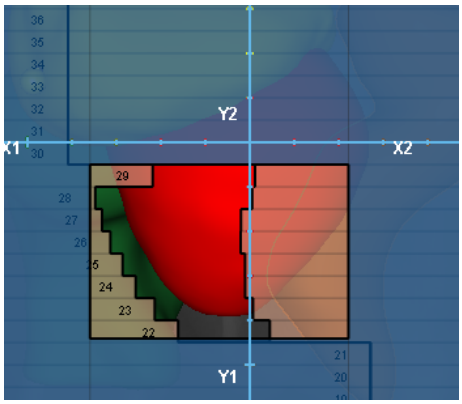


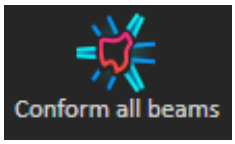
Figure 237. Apertures generated with a 0.5 cm margin. The field is broadened where this does not harm the protected ROIs.

6.3.7 Conform field openings

The conform field openings tool is used to shape the field openings based on the ROIs selected for treat and protect, and using the defined margins. For each beam the generated opening will conform to the ROI(s) selected for treatment while shielding the ROI(s) selected for protection. It is also possible to create a rectangular field and draw aperture shape of protect type to shield areas inside the opening.

Conform field openings for all beams

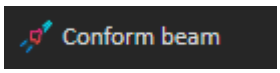
To conform field openings for all beams according to the treat and protect settings, click the **Conform all beams** button.



Note: *If a beam has both MLC and an aperture block defined, the Conform all function will conform the beam's aperture block opening.*

Conform field openings for a selected beam after modifying the treatment plan

To conform MLC settings for the current beam according to the treat and protect settings, click the **Conform beam MLC** button.



This generates MLC leaf and jaw positions.

Conform blocks

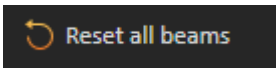
Aperture blocks can be shaped using the conform block tool, see *section 6.3.15 Aperture blocks on page 450* for more information.

Conform field openings - rules and exceptions

- The area to be treated is the union of treat ROI outlines and treat aperture shape. If no treat ROI or aperture shape is selected, the Virtual jaws will define the area to treat
- The area to shield is the union of protect aperture shapes and protect ROI outlines.
- In conflict situations, the action will always strive to shield the full area to be protected, which can have impact on target coverage.

6.3.8 Reset all beams

The **Reset all beams** button resets all the beams in the beam set, i.e. removes all control points, blocks, cones and wedges and sets all beam MUs to zero.



Drawn aperture shapes, virtual jaw positions ant treat and protect ROI selections will be preserved.

6.3.9 Control points and MLC positions

The **Control points** tab lists all segments and corresponding MLC positions for a selected beam. The **Delete segment** button will delete the current segment for a selected beam.

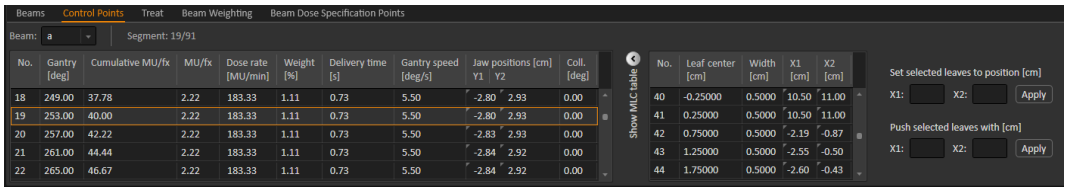


Figure 238. The Control points tab.

Edit jaw positions in the Control points tab

The Jaw positions for the selected segment are listed in the **Control points** tab and can be set to a desired position.

Note: *If there are several segments present and the machine demands the same jaw positions for all segments, all segments will be updated when one of the rows are edited.*

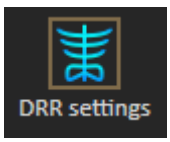
Edit the segment shapes in the control points tab

Click the control points tab at the bottom of the workspace. The leaves for the selected segment are listed in the MLC table, and can be set to a desired position or pushed a certain distance.

1. Select the leaf pairs to modify. Multiple rows are selected by Shift or Ctrl mouse click.
2. Add either new positions for **X1** and/or **X2**, or the distances (positive or negative) to push **X1** and/or **X2**. (Naming of positions is for an MLCX machine according to the Jaw labeling standard IEC 61217.)
3. Click **Apply**.

Edit DRR settings

To edit DRR settings, click the **DRR settings** icon. For more information, see section *section 6.1.8 The DRR views and settings on page 330*.



6.3.10 Calculate dose

Dose computation can be performed using the buttons in the **Dose** toolbar.

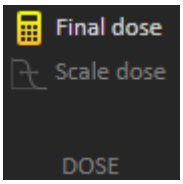
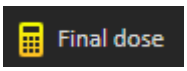


Figure 239. The Dose computation toolbar.

Calculate final dose

A final dose can be calculated using the Collapsed Cone dose engine. Click the **Final dose** button or type Ctrl + D to calculate the clinical dose.



The Collapsed Cone dose engine is described in detail in the *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual*.

6.3.11 Scale dose

The dose can be scaled to fulfill the prescription or to fulfill an arbitrary dose-volume relation for a selected ROI or POI. For instructions on how to scale dose, see *section 6.1.15 Scale dose on page 356*.

Note: *Conformal Arc plans cannot be scaled to an arbitrary dose level due to machine constraints.*

6.3.12 Beam weighting

The plan's dose distribution can be scaled and shaped, and individual beam doses can be scaled, in the **Beam weighting** tab at the bottom of the workspace. Absolute MU and dose values can be specified per beam, and relative beam weights can be defined. The beam weights can be either relative the MU value or, if point prescription is defined, relative the beam's dose contribution to the prescription point. For each beam the dose contribution to all POIs are displayed.

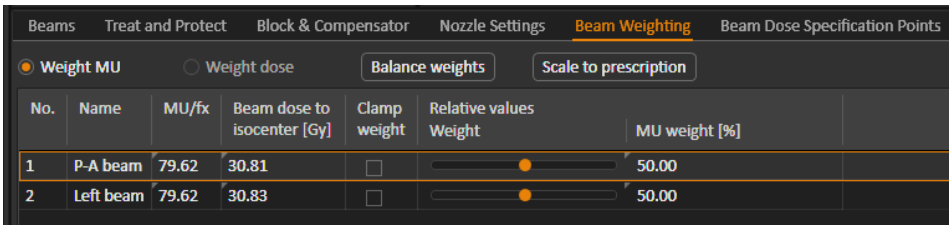
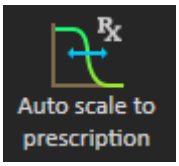


Figure 240. The **Beam weighting** tab.

Auto scale dose to prescription

Click the **Auto scale to prescription** button in the toolbar to fulfil the prescription value regardless of any additional changes. Note that the auto scale to prescription will scale for all beams. To scale only unclamped beams, use the **Scale to prescription** button in the **Beam weighting** tab.



If **Auto scale to prescription** is not selected, changes in the MU value or dose for a beam will not affect the other beams except for the relative weights that will be updated.

Note: *It is not possible to edit MU for a beam when Auto scale to prescription is selected.*

Note: *If dose is prescribed to a point, the values in the Beam dose column are the dose contributions to the prescription point. If dose is prescribed to an ROI, or no prescription is defined, the beam dose values are the dose contributions to each beam's isocenter point.*

Note: *For Line scanning and Mevion Hyperscan, an automatic scaling of the dose will lead to approximate dose values. A final dose computation will be necessary to get a clinical dose.*

Weight MU

If the option **Weight MU** is selected, the beam weights and sliders are relative to the beams' MU values. A change of the weight for one beam changes the weights of the rest of the beams to ensure that the sum of the weights remain 100%, while at the same time keeping the MUs proportional to the weights.

If **Auto scale to prescription** is selected, the MU values of all beams are scaled in order to retain the prescription value. If **Auto scale to prescription** is not selected, the MU values are scaled in order to retain the total MU of the plan.

Note: *It is not possible to edit point doses in Weight MU mode when Auto scale to prescription is selected.*

Weight dose

If the option **Weight dose** is selected, the beam weights and sliders are relative to the beams' dose contributions to the prescription point. A change of the weight for one beam changes the weights of the rest of the beams to ensure that the sum of the weights remain 100%, while at the same time keeping the point dose contributions proportional to the weights.

If **Auto scale to prescription** is selected, the MU values of the beams are scaled in order to retain the prescription value. If **Auto scale to prescription** is not selected, the MU values are scaled in order to retain the current dose to the prescription point. To scale dose of unclamped beams only, use the **Scale to prescription** button in the **Beam weighting** tab and deselect **Auto scale to prescription** in the toolbar.

Clamp the beam weight of a beam

It is possible to clamp (lock) the beam weight for one or several beams. This is done by checking the **Clamp** checkbox. If **Weight MU** is selected, clamping means that the relative beam weight for the beam will remain when MU, dose or weight for another beam is changed. If **Weight dose** is selected, clamping means that the MU for the beam will remain when MU, dose or weight for another beam is changed. Note that **Auto scale to prescription** will not take clamping into account. To scale unclamped beams only, use the **Scale to prescription** button in the **Beam weighting** tab.

Balance weights

The weights can be balanced, i.e. set to equal values, by clicking the **Balance weights** button.

Scale to prescription

If the dose is not scaled to fulfill the prescription, the dose (of unclamped beams) can be scaled to fulfill the prescription by clicking the **Scale to prescription** button.

6.3.13 Beam dose specification points

A beam dose specification point can be selected for each beam in the **Beam dose specification points** tab. When a clinical dose has been computed, values for Dose per fraction, Physical depth and Water equivalent depth are displayed in the list. This point and its values can be exported and used in external systems, for example RadCalc, to verify the dose calculation. Beam dose specification points can be created and edited graphically, see *section 6.1.9 Beam dose specification point on page 337* for more information.

6.3.14 Circular cones

Note: *The cones must be defined for each treatment machine in RayPhysics.*

Note: *When a cone is selected for a beam, the jaws and mlc leaves will be locked at the positions defined for the cone in RayPhysics.*

Add cone

Cones have to be defined for each beam when creating or editing a beam. To add a cone:

1. Select a beam in the beam list.
2. Double-click in a non-editable field or click the **Edit** button. This opens the Edit Beam dialog.

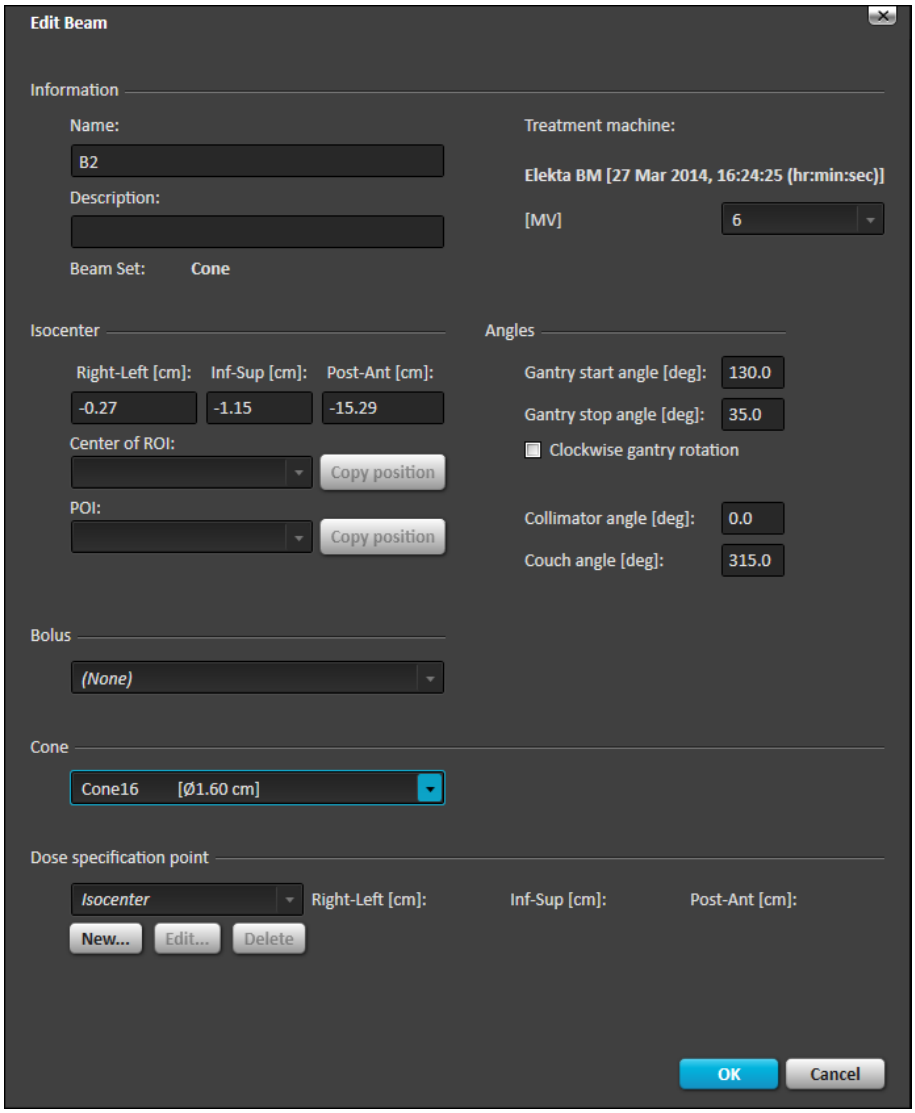


Figure 241. The Edit Beam dialog.

3. Select **Cone**. The Cone name and diameter is presented in the list.
4. Click **OK**.

When a cone is selected for a beam, there is a choice of all available cones in the beam list.

6.3.15 Aperture blocks

Note: *The block tray and the tray transmission must be defined for each treatment machine in RayPhysics.*

Enable aperture blocks

Aperture blocks have to be defined for each beam when creating or editing a beam.

To enable aperture blocks:

1. Select a beam in the beam list.
2. Double-click in a non-editable field or click the **Edit** button. This opens the **Edit Beam** dialog.

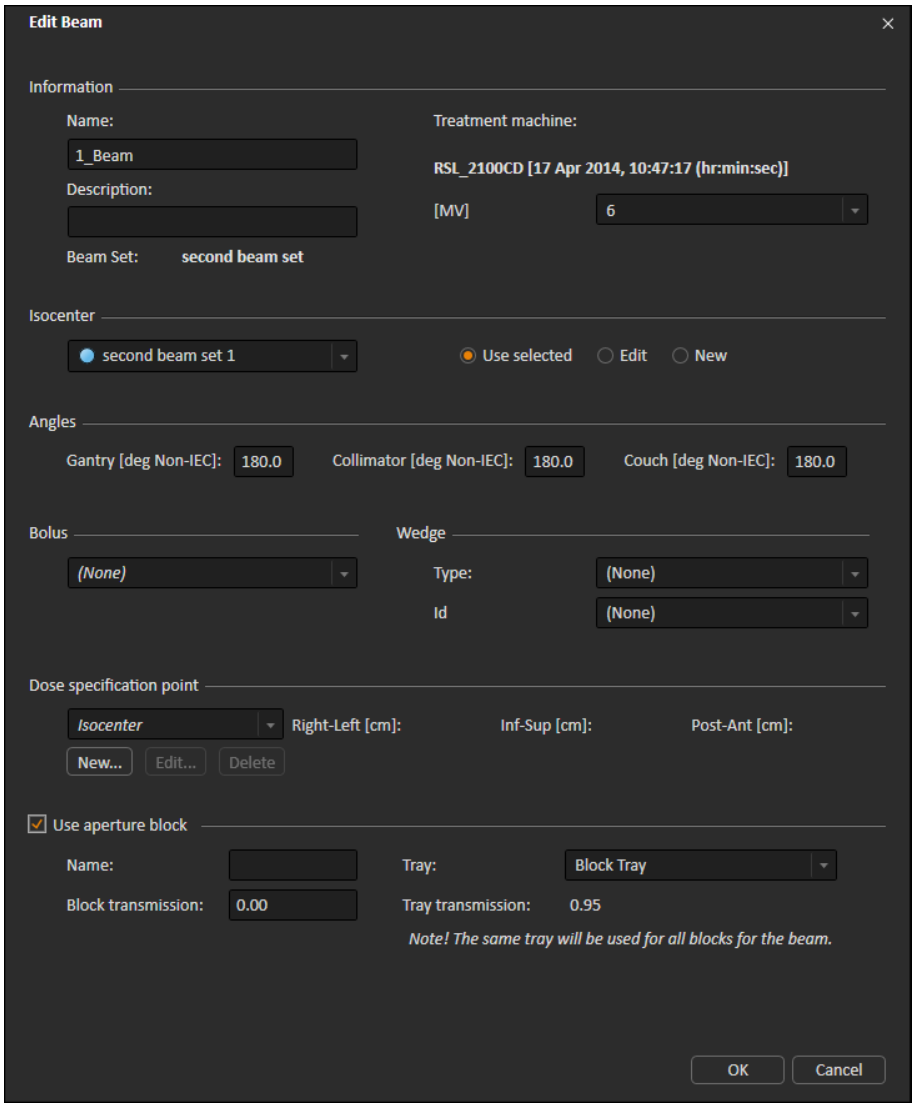
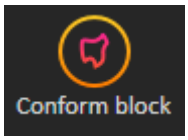


Figure 242. The **Edit Beam** dialog.

3. Check the **Use aperture block** checkbox.
4. Enter a block **Name**.
5. Select **Tray**.
6. Enter **Block transmission**.
7. Click **OK**.

Conform block parameters for a single beam

The block parameters for a selected beam can be computed according to the specified treat and protect settings and margins by clicking the **Conform block** button.



Note: *The dose will be invalidated after a new block has been calculated.*

Edit the block shape

The block shape can be edited in the BEV using the **Polygon** or **Brush** tool.

- **Brush**: The size of the ball can be adjusted using the slider in the **Block editing** toolbar, by pressing the + and - keys on the numerical keyboard, or by using the mouse wheel while pressing the ALT key. The smallest diameter of the brush is set to the milling tool diameter for the block.
- **Polygon**: A new contour is added to the original contour if the starting point is inside a contour on its edge, and finish point is inside the same contour. A new contour is subtracted from the original contour if the starting point is outside a contour on its edge, and the finish point is outside the same contour. If defining a two point polygon with both points outside the current aperture shape, and the line intersecting it twice, the smaller half will be cut off. If a polygon is drawn entirely outside an original block, fully inside or is fully containing the old block shape, the old block shape will be replaced by the new contour. Crossing contours are not allowed.

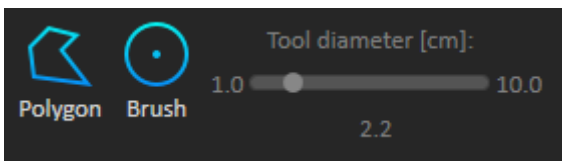
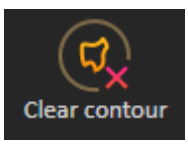


Figure 243. The block editing tools

Clear block contour

To clear the block contour, click the **Clear contour** button.



Remove aperture block contour

Remove the aperture block from the beam by unchecking the **Use aperture block** checkbox in the Edit beam dialog.

Print block contour

A block contour can be printed in its actual size on an office printer. This is done by first creating a block report in PDF format and then printing the PDF file using an office printer.

WARNING!

Verify the scale of the block/cutout printout. The printer settings will affect the actual size of the block/cutout in the printout. Before using the block/cutout printout for block/cutout manufacturing or verification, always check that the scale of the x- and y-axes are equal and that 1 cm on the verification scale corresponds to 1 cm using a ruler. (54970)

To print a block contour:

1. Click the **Print block contour** button.

2. Select a **Scale factor** in the Print Block Contour dialog. Default scale factor value is 1.
3. Click **OK**. A block report will be created in pdf format.

6.3.16 Shielding blocks

Block shapes can be generated based on ROI projections and can be manually edited in the BEV. The Shielding block tools are located under the **Shielding blocks** tab in the 3D-CRT Beam Design module.

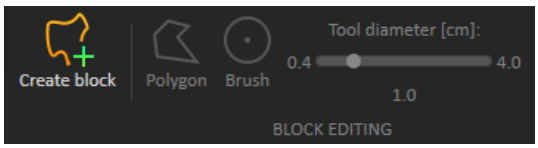


Figure 244. The Block editing tools.

Create blocks

To create a block:

1. Click the **Create block** button.

This opens the **Create Block** dialog.

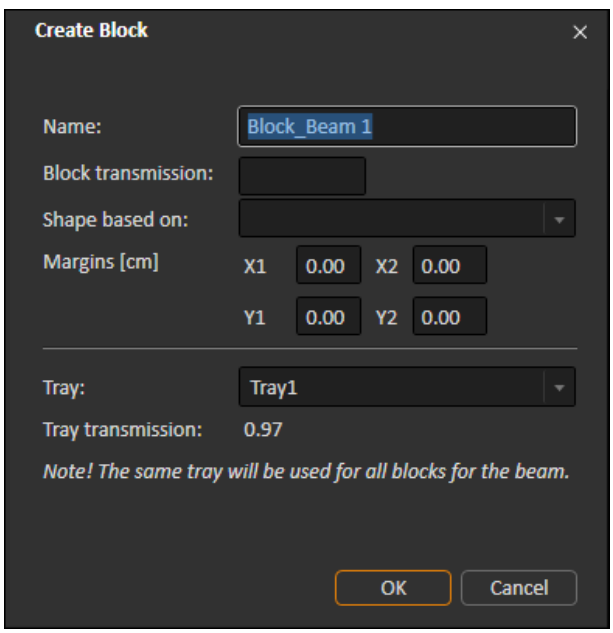


Figure 245. The **Create Block** dialog.

2. Enter a **Name for the block**.
3. Enter **Block transmission**.
4. Select an **ROI** from the drop-down list that the block shape will be based on.
5. Set block **Margins**.
6. Select **Tray**.
7. Click **OK**. The block is created and the block properties (Name, Block transmission and tray) are displayed in the **Beams** list.

Edit the block shape

The block shape can be edited in the BEV using the **Polygon** or **Brush** tool.

- **Brush**: The size of the ball can be adjusted using the slider in the **Block editing** toolbar, by pressing the + and - keys on the numerical keyboard, or by using the mouse wheel while pressing the ALT key. The smallest diameter of the brush is set to the milling tool diameter for the block.
- **Polygon**: A new contour is added to the original contour if the starting point is inside a contour on its edge, and finish point is inside the same contour. A new contour is subtracted from the original contour if the starting point is outside a contour on its edge, and the finish point is outside the same contour. If defining a two point polygon with both points outside the current aperture shape, and the line intersecting it twice, the smaller half will be cut off. If a polygon is drawn entirely outside an original block, fully inside or is fully containing the old block shape, the old block shape will be replaced by the new contour. Crossing contours are not allowed.

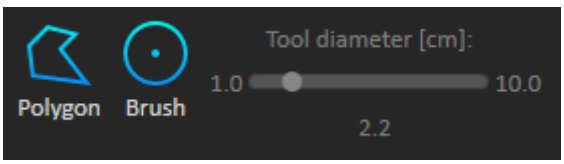
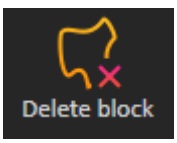


Figure 246. The block editing tools

Delete blocks

To delete a block, click the **Delete block** button.



Print block contour

A block contour can be printed in its actual size on an office printer. This is done by first creating a block report in PDF format and then printing the PDF file using an office printer.

WARNING!

Verify the scale of the block/cutout printout. The printer settings will affect the actual size of the block/cutout in the printout. Before using the block/cutout printout for block/cutout manufacturing or verification, always check that the scale of the x- and y-axes are equal and that 1 cm on the verification scale corresponds to 1 cm using a ruler. (54970)

To print a block contour:

1. Click the **Print block contour** button.

2. Select a **Scale factor** in the Print Block Contour dialog. Default scale factor value is 1.
3. Click **OK**. A block report will be created in pdf format.

6.3.17 Static Arc

A static arc plan consists of one or many static arc beams. The aperture of a static arc beam can be constructed in two ways, either by

- using the polygon tool in the Edit MLC and jaws dialog, see *section 6.2.6 Edit beam properties on page 402*, or by
- creating a rectangular field, see *section 6.3.18 Create rectangular fields on page 458*

The aperture of a Static Arc beam can be edited in the same way as the aperture of a 3D-CRT beam.

In the Control points list two control points are listed for a static arc beam. The first control point is located at the start gantry angle of the beam and the second at the stop gantry angle.

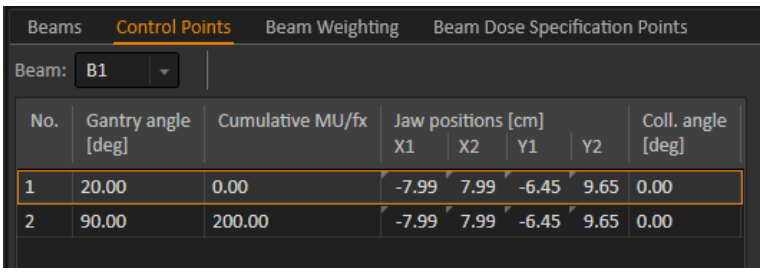


Figure 247. Static Arc beam starting with gantry start angle 20 and gantry stop angle 90.

Note: *The treat and protect feature is not supported for Static Arcs.*

Note: *Wedges and blocks are not supported for Static Arcs.*

6.3.18 Create rectangular fields

To create a rectangular field:

1. Click the **Create rectangular field** button.

This opens the Create rectangular field dialog.

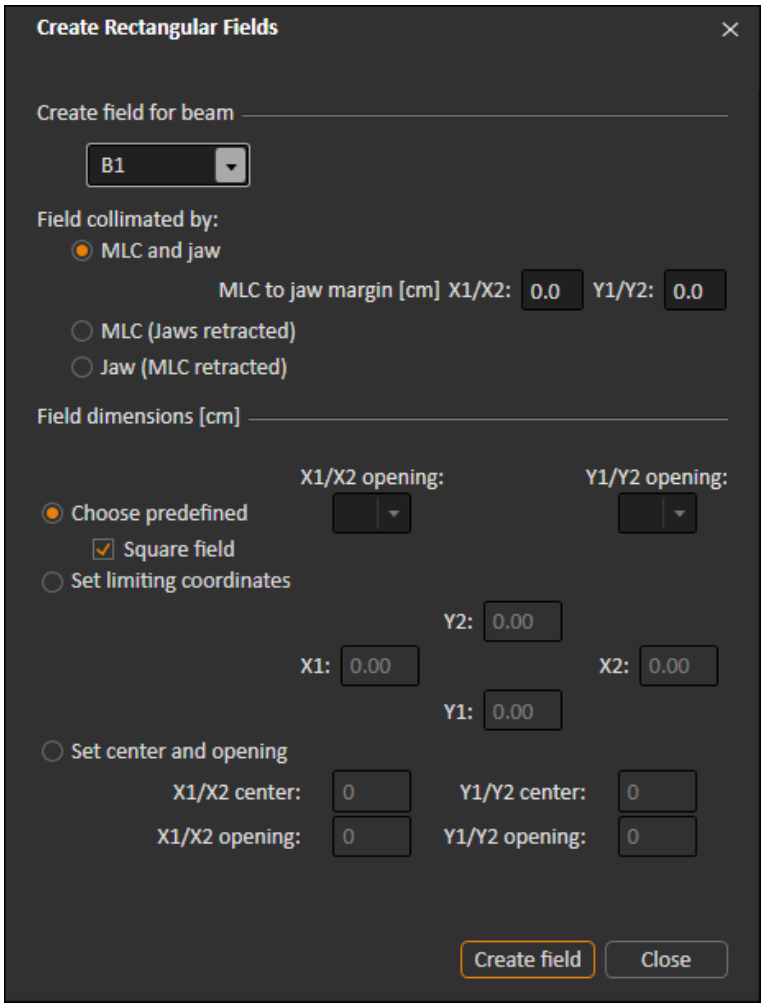


Figure 248. The **Create Rectangular Fields** dialog.

2. Select the beam to create the field for in the **Create field for beam** list.

3. Select if the field should be collimated by; MLC and jaw, MLC (Jaws retracted) or Jaw (MLC retracted).
4. Set **Field dimensions**. The options are: Choose predefined, Set limiting coordinates and Set center and opening.
5. Click **Create field**. This creates a rectangular field that will be visible in the BEV.

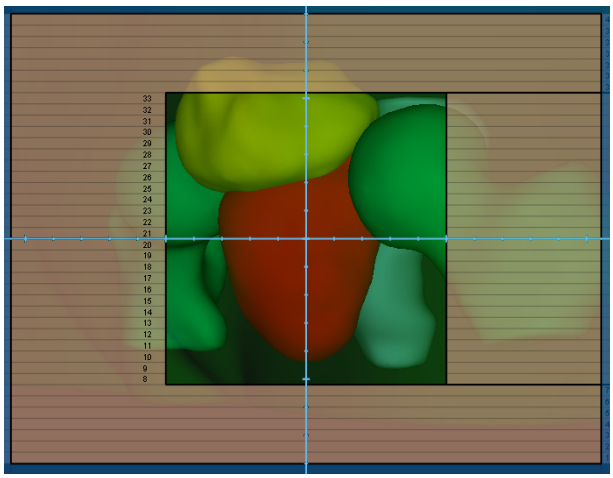


Figure 249. A rectangular field has been created based on the settings in the Create rectangular fields dialog.

Note: *It is possible to continue working with the rectangular shape, by drawing an aperture shape of protect type around areas to protect and reconform.*

6.4 THE ELECTRON BEAM DESIGN MODULE

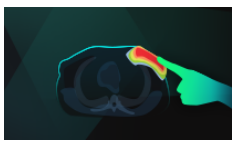
Before entering the Electron Beam Design module, an electron plan has to be created in the Plan Setup module and a dose grid must be defined.

In electron planning, beam orientations and cutout contours are designed by the user in order to manually optimize the plan. The Electron Beam Design module provides tools that make it possible to, with just a few clicks, compute:

- cutout contours based on the projection of the target ROIs that are to be treated and the OAR ROIs that are to be protected. These ROI choices are denoted as Treat and Protect settings. The user can also define beam margins.
- MU as to fulfill the prescription.

In addition to this the user can also:

- define a prescription.
- edit parameters such as isocenter position, gantry angle, cutout contour, couch angle and collimator angle.
- perform manual beam weighting.



In this section

This section contains the following sub-sections:

6.4.1	The Electron Beam Design module user interface	p. 462
6.4.2	Define or modify prescription	p. 464
6.4.3	Specify settings in the Treat and Protect tab	p. 465
6.4.4	Conform field openings	p. 467
6.4.5	Edit beam properties	p. 468
6.4.6	Calculate dose	p. 470
6.4.7	Scale dose	p. 472
6.4.8	Beam weighting	p. 473
6.4.9	Cutouts	p. 474

Precautions

WARNING!

Block/cutout verification. Always verify that the blocks and electron beam cutouts created in the Beam design modules are physically realizable. It is not possible to define any block manufacturing constraints in RayStation.

For proton blocks, the size of the block milling tool is taken into consideration in the automatic block generation tools. However, it is possible to obtain a block that cannot be manufactured using the manual block editing/creation tools. It is then possible to run the milling tool algorithm manually after the block editing. However, since it is not done automatically, the responsibility that the block is physically realizable still lies with the user.

Always check the created block against the block aperture printout. (27064)

WARNING!

Maximum allowed statistical uncertainty does not affect already computed clinical Monte Carlo dose. When changing the Maximum allowed statistical uncertainty for clinical Monte Carlo electron dose, be aware that already computed doses are not affected. Doses computed prior to the change may therefore be marked as clinical although they have a statistical uncertainty that would not result in clinical dose if they were recomputed. (98834)

6.4.1 The Electron Beam Design module user interface

Workspace

The Electron Beam Design module workspace contains several views showing the Beam's Eye View (**BEV**), **2D** and **3D** patient views and **DVH**s.

The workspace also contains three sub-windows showing 2D image data in a specific patient plane, making it possible to simultaneously work in three dimensions. One of the two sub-windows to the right shows **Dose Statistics** and **Clinical Goals**.

The lower part of the workspace displays the beam list, which contains the tabs **Beams**, **Treat and protect** and **Beam weighting**. At the borders between the different views are handles which can be dragged to adjust the size of the workspace as desired.

The Electron Beam Design workspace has two tool tabs: **General** and **Cutout**.

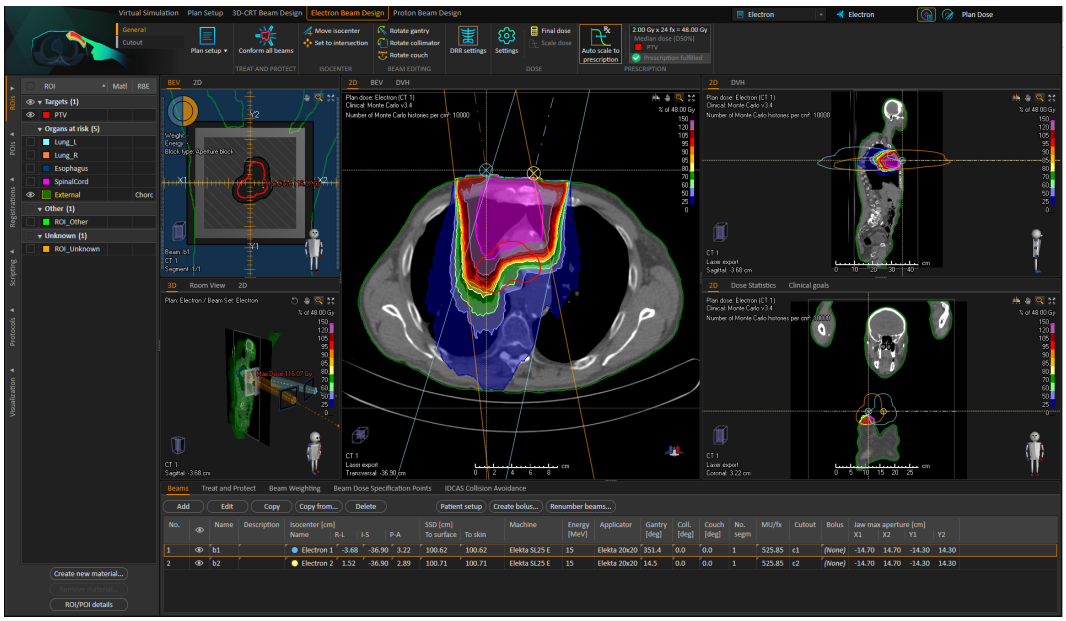


Figure 250. The Electron Beam Design workspace.

Graphical User Interface

For more information about the tools, operations and various view types in the Graphical User Interface, see *chapter 3 The Graphical User Interface*.

Context menus

Each view has a context menu which is opened by right-clicking in the view. For a description of the general context menu options, see *section 3.9 The context menu on page 102*.

DVHs, Dose statistics and Clinical goals

For detailed information on DVHs, dose statistics and clinical goals, see *section 3.7 Common graphs, tables and tools on page 77*.

Statistical uncertainty from Monte Carlo dose engines

The mean relative statistical uncertainty (MRSU) is computed for each electron beam dose and is shown in the patient 2D views when the dose view selection is set to **Beam dose**. It is not visible for **Plan dose** or **Beam set dose**. The MRSU is computed as the RMS of the relative uncertainty for all voxels with a dose exceeding 50% of the maximum dose from the beam.

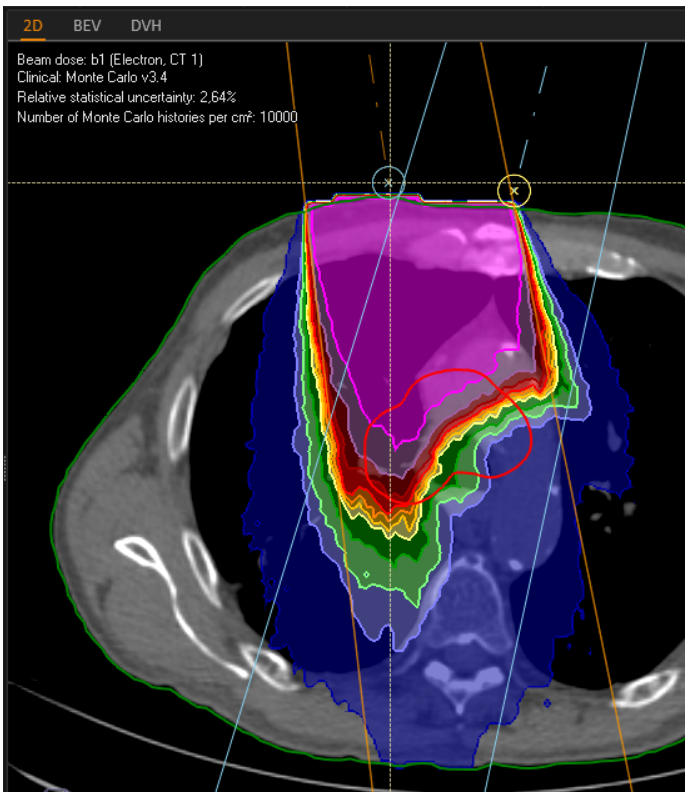


Figure 251. The relative statistical uncertainty shown in the 2D patient view.

The value shown is the same number as the one used by the system to check if a beam dose should be considered clinical. The threshold value is set in Clinic settings. See *section D.2 The Clinic Settings application on page 920* for more information.

Note: *Since the MRSU is computed only for voxels in high-dose regions, it gives no information about how accurate the dose is in low-dose regions.*

The MRSU value is not included in the reports.

6.4.2 Define or modify prescription

For instructions on how to to define or modify a dose prescription, see *section 6.1.12 Define or modify prescription on page 343*.

6.4.3 Specify settings in the Treat and Protect tab

To specify the treat and protect settings, use the **Treat and Protect** tab at the bottom of the workspace.

Note: *Adding treat and protect aperture shapes are done from the tool panel.*

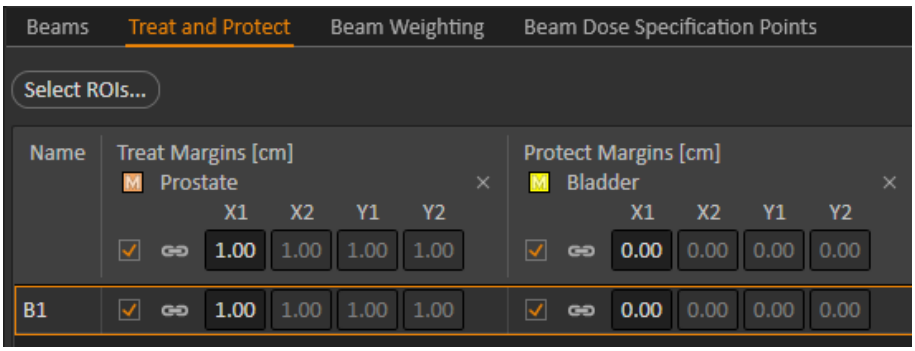


Figure 252. The **Treat and Protect** tab.

ROI usage

The header list in the **Treat and Protect** tab contains all the ROIs that are selected to use for planning. For conformal treatments, the list is default populated by all ROIs classified as Target or OAR. For primarily optimized treatment techniques, the list is empty per default.

To add or remove ROIs from the presented list in the **Treat and Protect** tab, click the **Select ROIs...** button. This opens the **Select ROIs** dialog. It is also possible to click the x next to the ROI's name in the column head to remove that ROI from the list.

Select ROIs to treat or protect

The outlines of ROIs selected as treat or protect will be input to the automatic aperture generation. An ROI will be classified as being treated or protected based on its type. All ROIs classified as Unknown/Other will be classified as ROIs to protect.

To select to treat or protect an ROI for a beam, check the checkbox for that ROI in the row for that beam.

To simultaneously select to treat or protect an ROI for all current beams in the beam set, click the checkbox in the header section for the ROI.

Margins used when conforming to Treat and Protect ROIs

A margin to use around a treat or protect ROI can be set. The margin recipe can be set as either a uniform margin or individual margins in all beam directions. The selection can be done per each beam by clicking the icon for that beam, or for all beams simultaneously by clicking the link icon in the header.

Uniform margins: the margins are all set to the first/X1 margin value.

Non uniform margins: the margins can be edited separately.

Margin values can be entered per ROI for each individual beam, or edited in the header to apply the margin values for the ROI for all beams in the beam set.

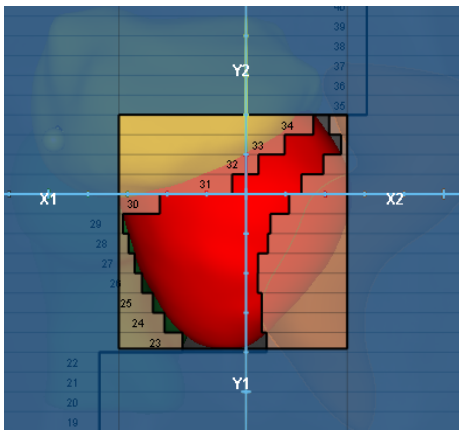


Figure 253. Apertures generated without margins. Rectum and bladder (blue and yellow) are protected. PTV (red) is treated.

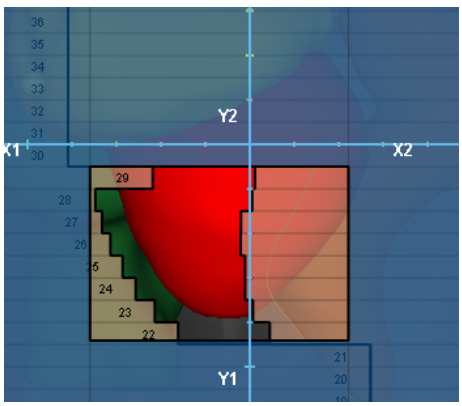


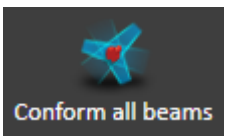
Figure 254. Apertures generated with a 0.5 cm margin. The field is broadened where this does not harm the protected ROIs.

6.4.4 Conform field openings

The conform cutout contours tool is used to shape the field openings based on the ROIs selected for treat and protect, and using the margins defined. For each beam the generated cutout will conform to the ROI(s) selected for treatment while shielding ROI(s) selected for protection.

Conform cutout contours for all beams

To conform cutout contours for all beams according to the treat and protect settings, click the **Conform all beams** button.



Conform cutouts

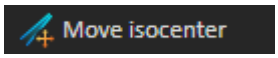
Cutouts can be created using the conform cutout tool, see *section 6.4.9 Cutouts on page 474* for more information.

6.4.5 Edit beam properties

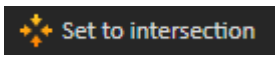
The beams can be manually optimized by changing the isocenter positions, beam angles and segment shapes.

Edit beam positions

The table below describes the **Isocenter** tools:



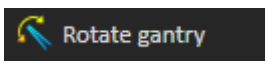
Move isocenter: Move the isocenter to the desired position by click and drag in the BEV.



Set to intersection: Move the isocenter to the slice intersection.

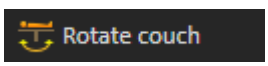
Edit beam angles

The beam angles for gantry, couch and collimator can be edited manually directly from the BEV or a 2D patient view.



Click the **Rotate gantry** button in the toolbar. Click and drag to left/right in the lower part of the BEV or in a 2D patient view to adjust the gantry angle.

Click the **Rotate collimator** button in the toolbar. Click and drag up/down in the BEV to adjust the collimator angle.



Click the **Rotate couch** button in the toolbar. Click and drag up/down in the right part of the BEV to adjust the couch angle.

Edit beams directly in the beam list

The **Beams** tab contains buttons for adding, editing, copying and deleting beams. For more information, see *section 6.1.6 Add, edit, copy or delete beams on page 316*.

The **Beams** tab contains the beam list and includes columns for **Name**, **Description**, **Isocenter**, **SSD**, **Treatment machine**, **Energy**, **Applicator**, **Gantry angle**, **Coll. angle** (Collimator angle), **Rotate aperture**, **Couch angle**, **No. segm** (Number of segments), **MU/fx** (MU/fraction), **Cutout**, **Bolus** and **Jaw max aperture**.

If the **Rotate aperture** option is selected for a beam, the cutout shape is rotated together with the collimator. If unselected, the cutout's exposure and protect areas on the patient remain.

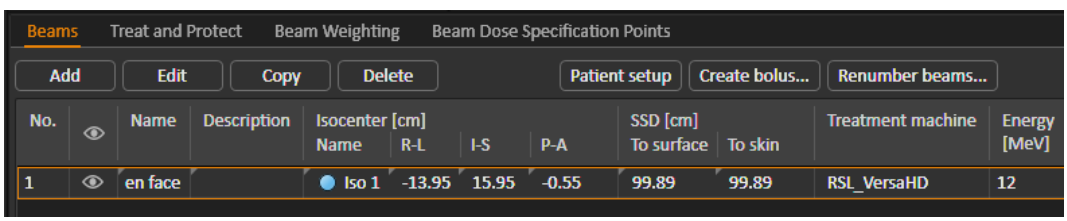


Figure 255. The **Beams** tab in the Electron Beam Design module.

Copy to all or Copy to selected

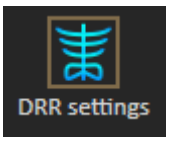
Properties that are editable in the beam list can be copied to all beams or to a sub-selection of beams. Right-click in the cell which property shall be copied and select **Copy to all** or **Copy to selected**. Multiple beams are selected by Shift or Ctrl mouse click. For electron beams, it is not possible to copy energy between beams.

Renumber beams

The beams will be delivered in ascending order. To renumber the beams, click the **Renumber beams** button.

Edit DRR settings

To edit DRR settings, click the **DRR settings** icon. For more information, see section *section 6.1.8 The DRR views and settings on page 330*.



6.4.6 Calculate dose

Dose computation can be performed using the buttons in the **Dose** toolbar in the Plan Setup module.

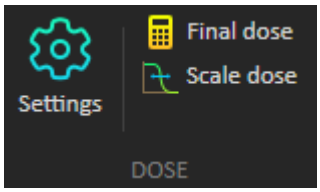
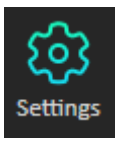


Figure 256. The Dose toolbar.

Dose computation settings

To edit the dose computation settings:

1. Click the **Settings** button.



2. This opens the Dose Computation Settings dialog.

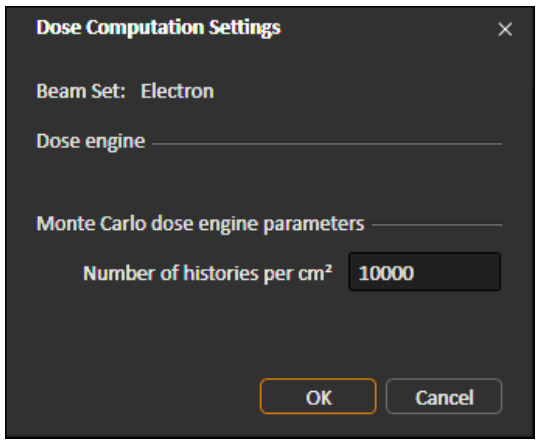


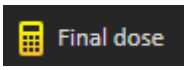
Figure 257. The Dose Computation Settings dialog.

3. Enter **Number of histories per cm²** to be used per beam for the electron beams in the beam set. The lower limit is 1000 per cm^2.
4. Click **OK**.

Note: *Changing the number of histories does not invalidate calculated dose. If the number of histories is changed after a clinical dose has already been computed, it will not be possible to re-calculate dose based on the updated number of histories without first invalidating the dose manually. If a non-clinical dose exists, changing the number of histories and re-calculating dose will result in a new dose being calculated based on the changed number of histories.*

Calculate final dose

A final dose can be calculated using the electron Monte Carlo dose engine. Click the **Final dose** button or type Ctrl + D to calculate the clinical dose.



The electron Monte Carlo dose engine is described in detail in the *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual*.

6.4.7 Scale dose

The dose can be scaled to fulfill the prescription or to fulfill an arbitrary dose-volume relation for a selected ROI or POI. For instructions on how to scale dose, see *section 6.1.15 Scale dose on page 356*.

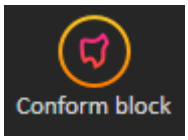
6.4.8 Beam weighting

Beam weighting is described in detail in *section 6.3.12 Beam weighting on page 445*.

6.4.9 Cutouts

Conform cutout contour

To conform the cutout contour according to the treat and protect settings, click the **Conform cutout** button.



Edit the cutout contour

The cutout contour can be edited in the BEV using the **Brush** tool or the **Polygon** tool.

- **Brush**: The size of the ball can be adjusted using the slider in the **Block editing** toolbar, by pressing the + and - keys on the numerical keyboard, or by using the mouse wheel while pressing the ALT key. The smallest diameter of the brush is set to the milling tool diameter for the block.
- **Polygon**: A new contour is added to the original contour if the starting point is inside a contour on its edge, and finish point is inside the same contour. A new contour is subtracted from the original contour if the starting point is outside a contour on its edge, and the finish point is outside the same contour. If defining a two point polygon with both points outside the current aperture shape, and the line intersecting it twice, the smaller half will be cut off. Crossing contours are not allowed.

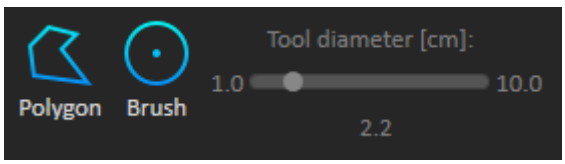
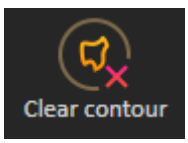


Figure 258. The Cutout editing tools.

Remove cutout contour

To clear the cutout contour, click the **Clear cutout** button.



Print cutout contour

A cutout contour can be printed in its actual size on an office printer. This is done by first creating a cutout report in PDF format and then printing the PDF file using an office printer.

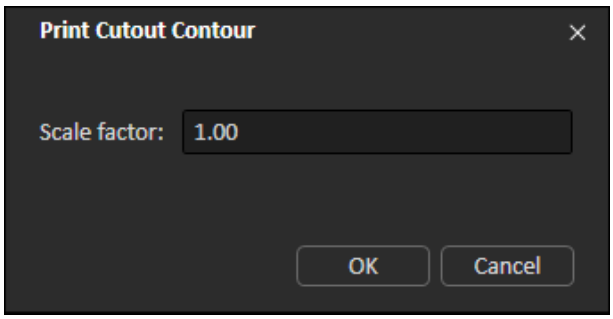
WARNING!

Verify the scale of the block/cutout printout. The printer settings will affect the actual size of the block/cutout in the printout. Before using the block/cutout printout for block/cutout manufacturing or verification, always check that the scale of the x- and y-axes are equal and that 1 cm on the verification scale corresponds to 1 cm using a ruler. (54970)

To print a cutout contour:

1. Click the **Print cutout contour** button.

2. Select a **Scale factor** in the **Print Cutout Contour** dialog. Default scale factor value is 1.

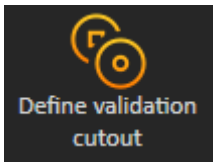


3. Click **OK**. A cutout report will be created in the PDF format.

Define validation cutout

To define a validation cutout:

1. Click the **Define validation cutout** button.



This opens the Define validation cutout dialog.

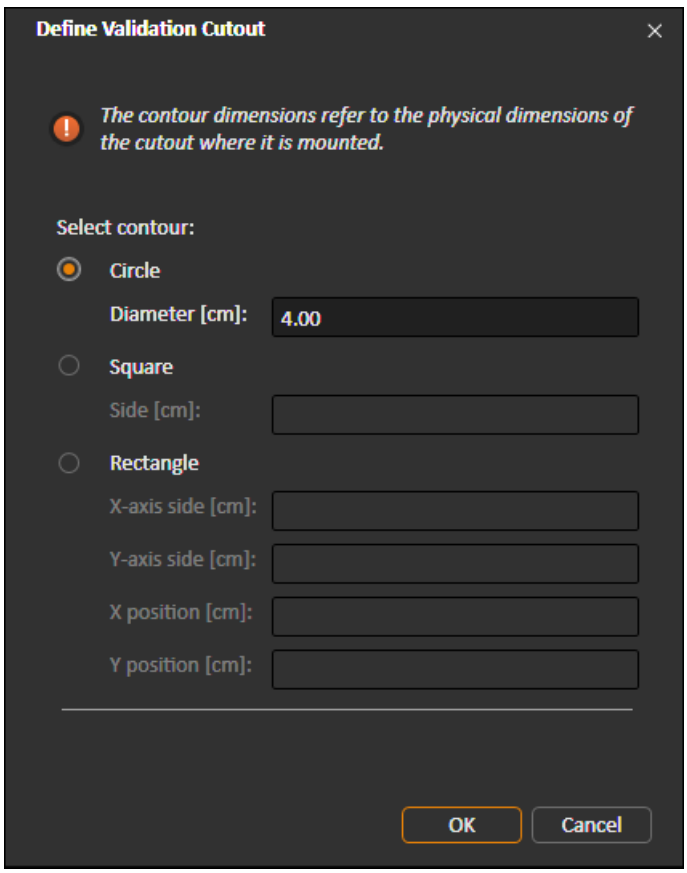


Figure 259. The Define validation cutout dialog.

2. Select contour. Available block contour shapes are:
   - **Circle** – centered around the isocenter.
   - **Square** – centered around the isocenter.
   - **Rectangle** – the X and Y positions refer to the lower left corner of the rectangle, where the X and Y axes are aligned with those of the Beam limiting device coordinate system.

   Note: *The contour dimensions here are defined in the physical downstream plane of the cutout, i.e. not in the isocenter plane.*

   Note: *The rectangle is defined in the IEC 61217 beam limiting device coordinate system and is not affected by the jaw labeling standard selected in RayPhysics.*

3. Click **OK**.

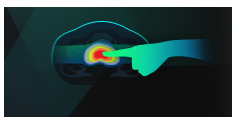
6.5 THE PROTON BEAM DESIGN MODULE

The Proton Beam Design can be used to create proton plans for the broad beam techniques Uniform Scanning, Double Scattering and Wobbling. The module can be used also to conform aperture openings for Pencil Beam Scanning and Line Scanning techniques for machines that support blocks or MLC.

For US/DS/Wobbling, the Proton Beam Design module provides tools that make it possible to compute aperture openings, compensator shapes, spread out Bragg peak (SOBP) ranges and widths and the corresponding nozzle settings based on the target ROIs that are to be treated and the OAR ROIs that are to be protected. These ROI choices are denoted as Treat and Protect settings. The user can also define margins for the selected Treat and Protect ROIs for each beam.

In addition to this the user can also:

- edit parameters such as isocenter position, gantry angle, collimator angle and couch angle.
- edit snout positions, block openings, MLC openings, compensator shape and SOBP range and width.
- perform manual beam weighting.



In this section

This section contains the following sub-sections:

6.5.1	The Proton Beam Design module user interface	p. 486
6.5.2	Define or modify prescription	p. 488
6.5.3	Specify treat and protect settings	p. 489
6.5.4	Compute beam set parameters (US/DS/Wobbling)	p. 494
6.5.5	Calculate dose	p. 496
6.5.6	Scale dose	p. 498
6.5.7	Edit beam properties	p. 499
6.5.8	Edit Nozzle settings	p. 501
6.5.9	MLC, block and compensator properties	p. 503
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6.5.11	Edit block aperture	p. 506
6.5.12	Edit MLC aperture	p. 510
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Prerequisites

The treatment plan must have at least one beam defined. For US/DS/Wobbling, see *Add proton beams for Uniform Scanning/Double Scattering/Wobbling on page 320*. For active scanning techniques the machine must support MLC or there must be at least one beam with a block. See *Add proton beams for Pencil Beam Scanning/Line Scanning or add carbon ion beams for Pencil Beam Scanning on page 323* for more information.

Precautions

WARNING!

Block/cutout verification. Always verify that the blocks and electron beam cutouts created in the Beam design modules are physically realizable. It is not possible to define any block manufacturing constraints in RayStation.

For proton blocks, the size of the block milling tool is taken into consideration in the automatic block generation tools. However, it is possible to obtain a block that cannot be manufactured using the manual block editing/creation tools. It is then possible to run the milling tool algorithm manually after the block editing. However, since it is not done automatically, the responsibility that the block is physically realizable still lies with the user.

Always check the created block against the block aperture printout. (27064)

WARNING!

US/DS/Wobbling beam monitor units. The beam monitor units value in RayStation is not expected to be dosimetrically correct and shall only be used as a means to control the dose level displayed in RayStation. (370010)

WARNING!

Physical/effective dose for protons. Be careful when mixing proton beam sets with other modalities. The prescription dose for protons relates to the physical dose, i.e., the biological effectiveness has not been taken into account. This can be handled either by including the RBE scaling factor in the proton beam model or by taking this fact into account when setting dose levels when mixing with doses of other modalities. (371601)

WARNING!

CT to density calibration for proton and carbon ion plans. In RayStation, the same CT to mass density calibration curve is used for proton and carbon ion dose calculations as for photon dose calculations. Note that the requirement on a correct CT calibration is considerably higher for proton and carbon ion dose calculations than for photon dose calculations. CT calibration validated for photon or electron use may not be sufficient for ion dose calculation. (371600)

WARNING!

Anisotropic lateral beam spread for US/DS/Wobbling. RayStation does not consider anisotropic lateral scattering in the dose calculation of Uniform Scanning, Double Scattering or Wobbling beams. In the dose engine validation of the Sumitomo Wobbling delivery system, it was found that the error in lateral penumbra is significant (> 2 mm for 80%-20% penumbra width) for fields using the largest fixed field size setting of the treatment machine and an aperture with a physical opening of 15 cm in combination with a large air gap (25 cm).

Be aware of this limitation in the dose calculation and be extra careful in the patient specific QA process for fields that employ a combination of large field sizes and large air gaps. (261663)

WARNING!

Apertures mounted downstream of the compensator for DS/US/Wobbling. In the RayStation proton dose engine for delivery systems where the aperture is mounted downstream of the range compensator, there is an algorithm intended for reproducing the sharpening effect of the lateral dose penumbra that this setup provides. An artifact of this algorithm is that the scattering caused by the range compensator in the central parts of the field (away from the aperture edge) is underestimated. This artifact can give significant errors in the computed dose for compensator geometries that host large gradients in the interior of the compensator. A more detailed description of this artifact is given in the *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual*.

Be aware of this limitation in the dose calculation and be extra careful in the patient specific QA process for delivery systems where the aperture is mounted downstream of the range compensator. (150310)

WARNING!

Aperture edge scatter effect for DS/US/Wobbling. Scatter from the edges of the MLC and block aperture are not included in the RayStation US/DS/Wobbling proton dose calculation algorithm.

The effect of the edge scatter is to add characteristic "ears" to the edges of the lateral dose profiles. These "ears" are most pronounced in the surface region, but will also affect the dose deeper into the patient. The shape and magnitude of the edge scatter "ears" depend on factors such as:

- the depth of the measured profiles, where the "ears" are sharper at shallow depths, get more diffused at greater depths, to eventually disappear at some distal depth.
- the air gap, where the "ears" get more diffused for larger air gaps.
- the field size, where more edge scatter is expected for larger fields, since more of the inner aperture edge is exposed to the beam.

The effect of the omission of the edge scatter in the dose calculation can lead to discrepancies between delivered and computed dose, especially in the surface region, and sometimes deeper into the patient.

Be aware of this limitation in the dose calculation and be extra careful in the patient specific QA process to be able to determine if the omission of the edge scatter in the dose calculation is acceptable or not for each individual patient case. (261664)

WARNING!

Flat fluence for DS/US/Wobbling. The RayStation US/DS/Wobbling pencil beam proton dose calculation algorithm assumes a flat fluence. It is the user responsibility to assure that this assumption is acceptable for their delivery system. (372132)

WARNING!

Lateral penumbra at large air gap for US/DS/Wobbling. The lateral penumbra is sometimes significantly underestimated at shallow depths and in a few cases overestimated at the end of the SOBP range for beams with a large air gap between the aperture and the patient. This effect has primarily been observed for beams with a thick range shifter and/or a range modulator with a high-Z material.

The user shall be aware of this limitation in the pencil beam dose algorithm and is recommended to always minimize the air gap for US/DS/Wobbling beams. (372143)

WARNING!

Surface dose overestimation for Wobbling. A systematic overestimation of the computed dose in the surface region has been found for a few beam configurations of the Sumitomo Wobbling delivery system. The error may become significant for beam configurations that combine a high beam energy with a large modulation ridge filter and a thick compensator. The error becomes more pronounced for large field sizes, although the effect is also present for smaller field sizes.

Be aware of this limitation in the dose calculation and be extra careful in the patient specific QA process for fields that involve a combination of high beam energy, large modulation ridge filter and a thick compensator. (261665)

WARNING!

Accuracy of Pencil Beam dose engine for proton US/DS/Wobbling beams with thick beam line components. In the RayStation 7 US/DS/Wobbling pencil beam dose engine validation, a few deviations from the dose accuracy requirements were noted for doses in water, especially at shallow depths, for setups where the protons pass through a thick beam-line component (e.g. range shifter, range modulator, or compensator). These deviations have been linked to the handling of secondary proton transport over the air gap, resulting mainly in an overestimation of the dose in the surface region. The effect increases with thickness of the component. When a compensator is used the effect is larger for increasing air gaps. For components mounted in the non-moveable part of the nozzle the effect is not primarily dependent on the air gap.

The user shall be aware of these limitations in the pencil beam dose engine, and is recommended to minimize the air gap when a compensator is used. (370009)

WARNING!

The effect of the infinite slab approximation on proton DS/US/Wobbling. The DS/US/Wobbling Pencil Beam dose engine is based on the so-called infinite slab approximation. This approximation disregards lateral inhomogeneities for individual ray traces, which will see the patient as a stack of semi-infinite layers. The effect of this approximation is more severe for patients with large lateral inhomogeneities, especially closer to the target area. This situation is common for many lung cases with the effect of significant loss of target coverage. It should be noted that also other treatment sites may be affected.

Be aware that the dose computation may not be accurate for patients with large lateral inhomogeneities relative the beam direction. (370003)

WARNING!

Range compensator effect in proton DS/US/Wobbling Pencil Beam dose calculation. The proton DS/US/Wobbling Pencil Beam dose engine treats any range compensator device as an extension of the patient and the pencil beam tracing will start at the entrance of the range compensator. This means that the broadening of each pencil beam ray trace may have become significant when reaching the patient surface and the dose error caused by the infinite slab approximation in the presence of any lateral inhomogeneity may be large. It is important to point out that the patient outline here becomes a large lateral inhomogeneity when it is angled to the ray traces. This error will thus increase with:

- Magnitude of air gap
- Angle between beam and surface normal
- Shallowness of target
- Internal lateral inhomogeneities

The user shall be aware of this limitation in the pencil beam dose engine. (383008)

WARNING!

Lateral penumbra for beams using block aperture in combination with compensator for Mitsubishi Electric Co SELECT BEAM NOZZLE in US mode. In the dose engine validation of RayStation 7, a systematic deviation has been found in the computed lateral dose for beams delivered with the Mitsubishi SELECT BEAM NOZZLE in US mode (Mitsubishi US) using a block aperture in combination with a range compensator. The studied fields used an 8x8 cm^2 squared block aperture opening in combination with a 3 cm or 6 cm homogenously thick range compensator, and were delivered to a water phantom. The measured lateral profiles exhibit more rounded shoulders (high dose field edges) than observed in the calculated profiles, while the low dose part of the calculated profiles (dose levels<50%) is in excellent agreement with the measurements. Consequently, the calculated profiles can be significantly broader than the measured profiles at for example the D95% level, and the difference in 20-80% lateral penumbra has been observed to exceed 2 mm in several cases. The fail rate in Gamma (3 mm, 3%) analysis of the profiles, has also been seen to exceed 5% relatively frequently.

These deviations were not found for Mitsubishi US fields employing the MLC as primary collimator or for fields that used a block aperture without a range compensator.

Refer to *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual* for more details.

Be aware of this limitation in the pencil beam dose engine and be extra careful in examining this behavior in the commissioning of RayStation and in the subsequent patient specific QA. (372150)

6.5.1 The Proton Beam Design module user interface

Workspace

The Proton Beam Design workspace contains several views showing the Beam's Eye View (**BEV**), **2D** and **3D** views and **DVH**s.

The workspace also contains three sub-windows showing 2D image data in a specific patient plane, making it possible to simultaneously work in three dimensions. One of the two sub-windows to the right shows **Dose Statistics** and **Clinical Goals**.

The beam list at the bottom of the workspace contains the tabs **Beams**, **Treat and protect**, **Block & Compensator** (for US/DS/Wobbling), **Block** (for PBS/LS with block), **Nozzle settings** (for US/DS/Wobbling), **Beam weighting**, **Beam dose specification points** and **MLC** (for machines with MLC).

The Proton Beam Design workspace has three tool tabs: **General**, **Aperture** (for Block and/or MLC) and **Compensator** (for US/DS/Wobbling).

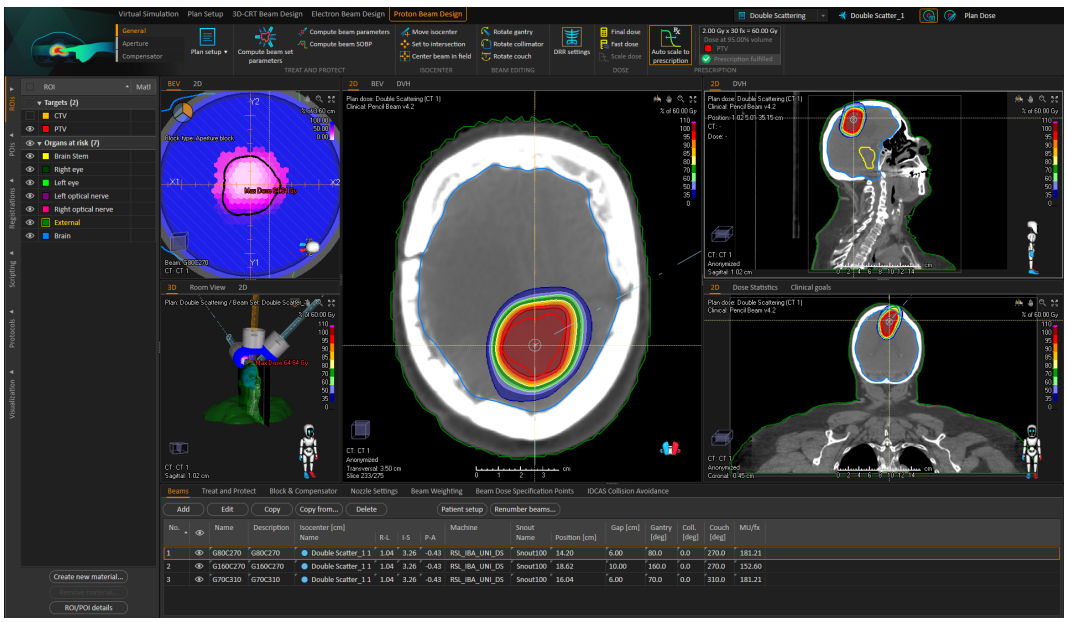


Figure 260. The Proton Beam Design workspace.

Graphical User Interface

For more information about the tools, operations and various view types in the Graphical User Interface, see *chapter 3 The Graphical User Interface*.

Context menus

Each view has a context menu which is opened by right-clicking in the view. For a description of the general context menu options, see *section 3.9 The context menu on page 102*.

DVHs, dose statistics and clinical goals

For detailed information on DVHs, dose statistics and clinical goals, see *section 3.7 Common graphs, tables and tools on page 77*.

6.5.2 Define or modify prescription

For instructions on how to to define or modify a dose prescription, see *section 6.1.12 Define or modify prescription on page 343*.

6.5.3 Specify treat and protect settings

When planning a proton treatment, the user must specify some plan computation settings that will be used as input to the plan computation. These are:

- **ROI usage**: Specify Treat and Protect ROIs.
- **Lateral margins**: Specify lateral margins for each treat and protect ROI for aperture (block or MLC) contour generation.
- **US/DS/Wobbling specific computation settings** (not applicable for PBS/LS): distal and proximal margins, distal protect, density uncertainty, air gap, smearing radius and maximum gradient.

Treat and Protect tab

To use the treat and protect tab the machine must support blocks and/or MLC aperture. Specify the **Treat and Protect** settings at the bottom of the workspace.

For beams with a compensator, the Protect ROIs can be protected either by a **Compensator** or an **Aperture** that can be selected from a drop-down list.

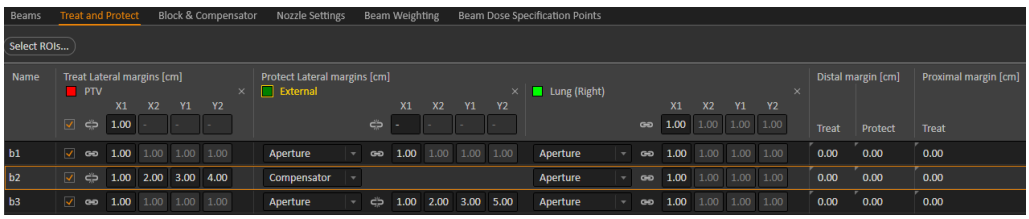


Figure 261. The **Treat and Protect** tab for beams with a compensator.

For beams without a compensator, the Protect ROIs can only be protected by an **Aperture**.

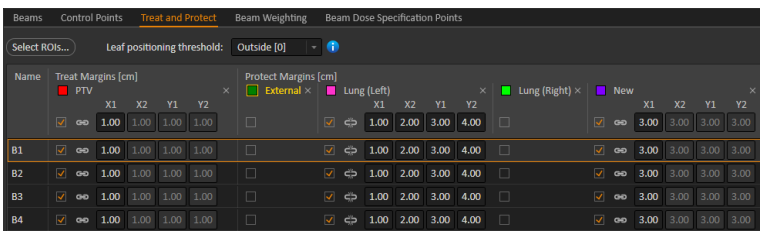


Figure 262. The **Treat and Protect** tab for beams without a compensator.

ROI usage

The header list in the **Treat and Protect** tab contains all the ROIs that are selected to use for planning.

To add or remove ROIs from the presented list in the **Treat and Protect** tab, click the **Select ROIs...** button. This opens the **Select ROIs** dialog. It is also possible to click the "x" next to the ROI's name in the column head to remove that ROI from the list.

Select ROIs to treat or protect

The outlines of ROIs selected as treat or protect will be input to the automatic aperture generation. An ROI will be classified as being treated or protected based on its type. All ROIs classified as Unknown/Other will be classified as ROIs to protect.

To select to treat or protect an ROI for a beam, check the checkbox for that ROI in the row for that beam.

To simultaneously select to treat or protect an ROI for all current beams in the beam set, click the checkbox in the header section for the ROI.

Leaf positioning threshold

The leaf positioning threshold represents the amount of relative area of the target that a leaf shall overlap at the target boundary. It is only visible for machines with MLC.

To add leaf positioning threshold, click the drop-down list and select:

- Outside: If the threshold is set to 0, leaves are positioned to barely touch the target boundary.
- Inside: If the threshold is set to 1, the leaves are moved inwards such that there is no non-target area exposed between the leaf and the target.
- Mid: Set the threshold value to 0.5. An intermediate threshold value implies that a leaf is positioned such that the ratio of the covered target area, and the covered target area had the threshold been set to 1, equals the threshold value.
- Custom: For old plans or plans edited from scripting a custom leaf positioning threshold can be set.

Note: *Leaf positioning threshold is applied to polygon drawn MLC openings and Treat ROIs. Protect shapes and protect ROIs are always fully protected.*

Margins used when conforming to Treat and Protect ROIs

A margin to use around a treat or protect ROI can be set. The margin recipe can be set as either a uniform margin or individual margins in all beam directions. The selection can be done per each beam by clicking the icon for that beam, or for all beams simultaneously by clicking the link icon in the header.

Uniform margins: the margins are all set to the first/X1 margin value.

Non uniform margins: the margins can be edited separately.

Margin values can be entered per ROI for each individual beam, or edited in the header to apply the margin values for the ROI for all beams in the beam set.

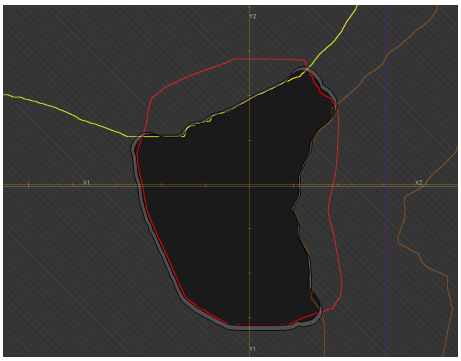


Figure 263. Apertures generated without margins. Rectum and bladder (brown and yellow) are protected. PTV (red) is treated.

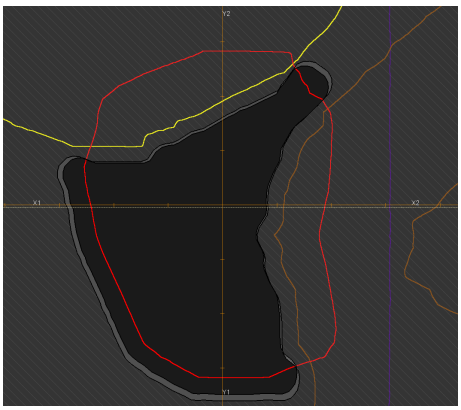


Figure 264. Apertures generated with a 0.5 cm margin. The field is broadened where this does not harm the protected ROIs.

Beam specific computation parameters

The beam specific computation settings are located in the **Treat and protect** tab and can be edited directly in the list. Click on the desired settings field to enable editing. Certain settings are not applicable for PBS/LS machines and beams without compensator.

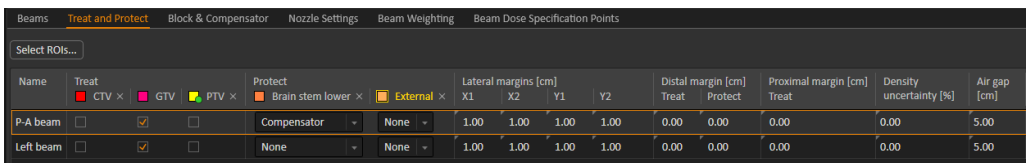


Figure 265. The **Treat and Protect** tab contains all the computation parameters.

Table 6.1: The plan computation parameters.

Parameter	Applicable for	Description
Lateral margins		Lateral margins are set for ROIs and beams with block or MLC in the **Treat and protect** tab. The lateral margins specify the distance from the aperture contour to the projected target ROIs in the isocentric plane.
Distal and **Proximal** treat margins	US/DS/Wobbling	The target margins are used for SOBP range and width and compensator shape computation. RayStation will aim at finding an SOBP range so that the 95% isodose will match the distal target edge, including the distal target margin. The SOBP width is set as the maximum target width including the distal and proximal margins. It is possible to increase and or decrease the margins in order to obtain the desired dose distribution. Only applicable for US/DS/Wobbling.
Distal protect margin	Beams with compensator	If an ROI has been set to as Protect using the compensator, the distal protect margin will set the distance from the 95% isodose line to the ROI edge.
Density uncertainty	US/DS/Wobbling	Specifies the uncertainty in the actual beam range. This results in distal and proximal dose margins which depends on their water equivalent depth, i.e. the margin will be larger for the distal edge, which has a greater depth.
Air gap	US/DS/Wobbling	This is the prescribed minimum distance (gap) between the most downstream object in the beam line (compensator or snout tip) and the patient outline. For machines with the compensator downstream of the snout tip, the snout's outer dimensions are used as the outer dimension of the compensator. ***Note:*** *The air gap refers to the intended air gap when computing beam parameters, i.e. it may not correspond to the actual air gap if any beam parameters (e.g. the snout position) have been changed. The actual air gap is displayed in the beam list.*
Smearing radius	Beams with compensator	Each compensator thickness value is set to the thinnest value among its neighbors that lie within the smearing radius. This will have the effect that a shift in the patient position of the same magnitude as the smearing radius will not result in an undershoot. ***Note:*** *Using a smearing radius smaller than or equal to the compensator matrix resolution will not smear the compensator.*

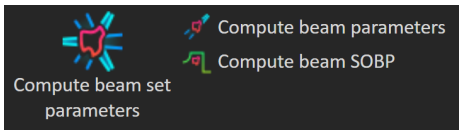
Parameter	Applicable for	Description
Maximum gradient	Beams with compensator	The compensator is computed so that there are no gradients larger than the specified maximum gradient (degrees) in the thickness values matrix. If the target and patient geometry requires high compensator gradients in order to obtain a conform dose, this may result in an overshoot. However, since the compensator values are never set to thicker values in the algorithm, it will never result in an undershoot.

6.5.4 Compute beam set parameters (US/DS/Wobbling)

The Compute beam set parameters tool can be used for US/DS/Wobbling to shape all fields in the beam set based on the ROIs selected for treat and protect using the defined margins and other user-defined plan computation settings.

Compute beam set parameters for US/DS/Wobbling by clicking:

- **Compute beam set parameters** button - computes parameters for **all** beams according to the defined treat and protect settings.
- **Compute beam parameters** button - computes parameters for **current** beam according to the defined treat and protect settings.
- **Compute beam SOBP** button - computes SOBP range and width according to the defined density uncertainty and distal and proximal treat-margins and corresponding nozzle settings.



The RayStation 7 system automatically computes:

- Range and width of the SOBP field and the corresponding nozzle settings.
- Aperture openings.
- Compensator geometry (if beam has a compensator).
- Snout position (according to air gap).
- Beam MU. The beam MU is always set to 1.

After manual editing of the block or MLC contour and/or compensator shape, the present field may not be adequate to get the expected target coverage as expressed by the treat and protect settings. By clicking the **Compute beam SOBP** parameters button, the SOBP range and width for the beam is updated to reflect the current status of the aperture openings, compensator and treat and protect settings.

Note: *The dose will be invalidated after successful change of the SOBP range and width.*

Note: *An aperture contour (block or MLC) must be present in order to compute new SOBP range and width values.*

Compute block contours (PBS/LS)

To compute block contours for all PBS/LS beams with blocks, click the **Compute block contours** button.

Compute block
contours

6.5.5 Calculate dose

Dose computation can be performed using the buttons in the **Dose** toolbar located in the **General**, **Aperture** and **Compensator** tabs in the workspace.

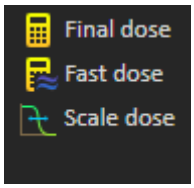


Figure 266. The Dose toolbar for US/DS/Wobbling.

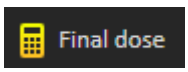
Calculate fast dose for US/DS/Wobbling

An approximate dose can be computed using the Fast Pencil Beam dose engine. Click the **Fast dose** button to quickly get an approximate non clinical dose.

The Fast Pencil Beam dose engine is described in detail in the *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual*.

Calculate final dose for US/DS/Wobbling

A final dose can be calculated using the Pencil Beam dose engine. Click the **Final dose** button or type Ctrl + D to calculate the clinical dose.



Calculate final dose for PBS/LS

A final dose can be calculated by selecting the dose engine Pencil Beam or Monte Carlo from a drop-down list. Click the **Final dose** button or type Ctrl + D to calculate the clinical dose.

For further information, see *section 7.2.15 Dose computation options on page 604*.

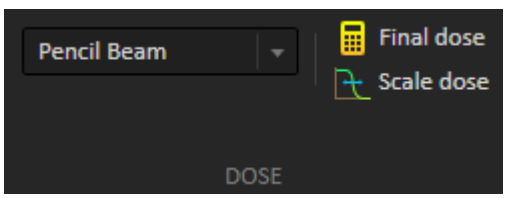


Figure 267. Final dose for dose engine Pencil Beam.

Figure 268. Final dose for dose engine Monte Carlo where ions/spot is selected.

Figure 269. Final dose for dose engine Monte Carlo where statistical uncertainty is selected.

The Monte Carlo and the Pencil Beam dose engine are described in detail in the *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual*.

6.5.6 Scale dose

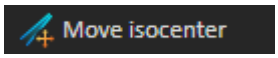
The dose can be scaled to fulfill the prescription or to fulfill an arbitrary dose-volume relation for a selected ROI or POI. For instructions on how to scale dose, see *section 6.1.15 Scale dose on page 356*.

6.5.7 Edit beam properties

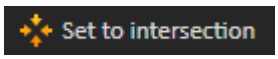
It is possible to manually change beam properties, such as the the isocenter positions, beam angles and block, MLC and compensator shapes.

Edit beam positions

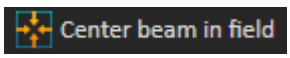
The table below describes the **Isocenter** tools:



Move isocenter: Move the isocenter to the desired position by click and drag in the BEV.



Set to intersection: Move the isocenter to the slice intersection.

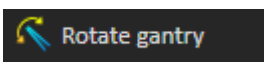


Center beam in field: Move the isocenter to the center of the field opening (not applicable for MLC fields).

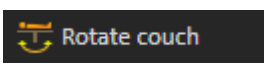
Edit beam angles

The beam angles for gantry and couch can be edited manually directly from the BEV or a 2D patient view.

To rotate the gantry, click the **Rotate gantry** button in the toolbar. Click and drag to left/right in the lower part of the BEV or in a 2D patient view to adjust the gantry angle.



To rotate the couch, click the **Rotate couch** button in the toolbar. Click and drag up/down in the right part of the BEV to adjust the couch angle.



Edit beams directly in the beam list

The **Beams** tab contains buttons for adding, editing, copying and deleting beams. For more information, see *section 6.1.6 Add, edit, copy or delete beams on page 316*.

The **Beams** tab contains the beam list and includes columns for (where applicable): **Name**, **Description**, **Isocenter**, **Treatment Machine**, **Snout Name**, **Snout Position**, **Gap**, **Gantry angle**, **Collector angle**,**Couch angle**, **Range shifter**, **Spot Tune ID**, **Number of energy layers**, **MU/fx** (MU/fraction), **Spot weight** (Min/Max)

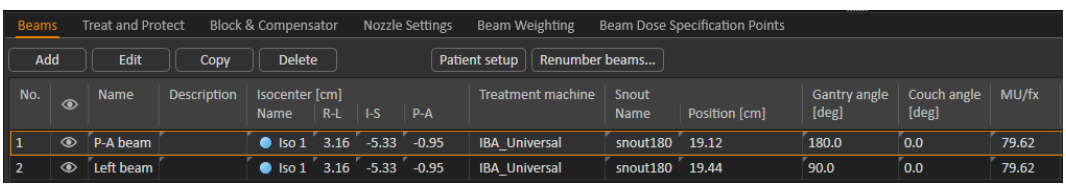


Figure 270. The **Beams** tab in the Proton Beam Design module.

The snout position and the air gap can be edited manually in the beam list. When editing the air gap in the beam list, the snout position is adjusted to achieve the desired air gap. For more information regarding air gap, see Table 6.1.

The block contour and compensator geometry are defined in the isocentric plane. This means that if the snout position is changed, directly or by editing the air gap, the size of the physical block contour and compensator geometry will change, in accordance with the beam divergence (which may be different in X and Y).

As an effect, the block contour may no longer fit inside the snout inner dimensions when changing the snout position. This is checked during dose computation.

Note: *The aperture contour at the isocenter may not be preserved after editing of the snout position.*

For ion beams collimated by block and a collimator angle different from zero, and all beams collimated by MLC, the aperture contour at the isocenter is not preserved after editing of the snout position. The user must always review the dose distribution after editing of the snout position, and if necessary, re-conform the block or MLC.

Copy to all or Copy to selected

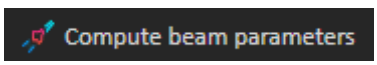
Properties that are editable in the beam list can be copied to all beams or to a sub-selection of beams. Right-click in the cell which property shall be copied and select **Copy to all** or **Copy to selected**. Multiple beams are selected by Shift or Ctrl mouse click.

Renumber beams

The beams will be delivered in ascending order. To renumber the beams, click the **Renumber beams** button.

Compute beam parameters for a selected beam after modifying the treatment plan

To compute beam parameters for the current beam according to the treat and protect settings, click the **Compute beam parameters** button.



6.5.8 Edit Nozzle settings

The **Nozzle settings** tab lists the nozzle settings for a selected beam.

IBA US/DS

The following parameters are editable for IBA US/DS beams:

- SOBP range.
- SOBP width.

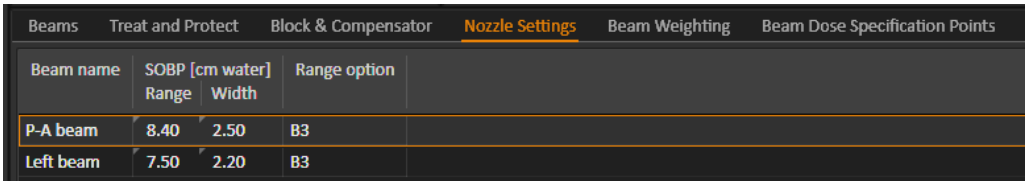


Figure 271. The Nozzle settings tab for an IBA US/DS beam.

Mevion DS

For Mevion Double Scattering beams the **Nozzle settings** tab includes the parameters **SOPB range** (editable), **SOPB width** (editable), **Maximum collimated field diameter**, **Range option**, **First scatterer name** and **Second scatterer name**.

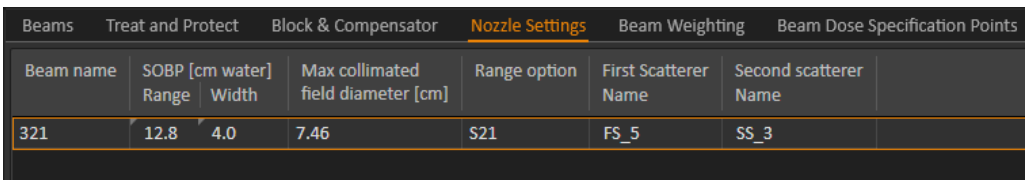


Figure 272. The Nozzle settings tab for a Mevion DS beam.

Sumitomi Wobbling

For Sumitomo Wobbling beams the **Nozzle settings** tab includes the parameters **SOBP range** (editable), **Nominal energy**, **Maximum collimated field diameter Scatterer name**, **Scatterer setting**, **Scatterer physical thickness**, **Scatterer thickness** and **Ridge filter name**. The **Ridge filter name** is editable and is used instead of the **SOBP width**.

Note: *The Maximum collimated field diameter can be changed when editing the aperture opening or snout position. RayStation automatically updates the nozzle settings to maintain the closest possible range and width.*

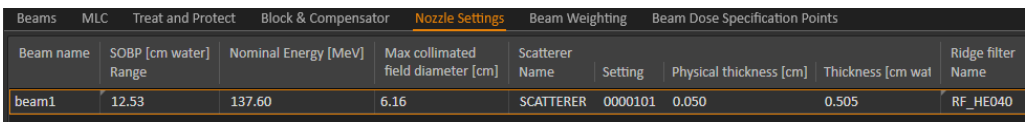


Figure 273. The Nozzle settings tab for a Sumitomo Wobbling beam.

Mitsubishi Electric Co

For Mitsubishi Electric Co SELECT BEAM NOZZLE in US mode beams the **Nozzle settings** tab includes the parameters **SOPB range option**, **SOPB range** (editable), **SOPB width** (editable), **Nominal energy**, **Maximum collimated field diameter**, **Scatterer name**, **Scatterer physical thickness**, **Ridge filter** and **Range shifter**.

Note: *The Maximum collimated field diameter can be changed when editing the aperture opening or snout position. RayStation automatically updates the nozzle settings to maintain the closest possible range and width.*

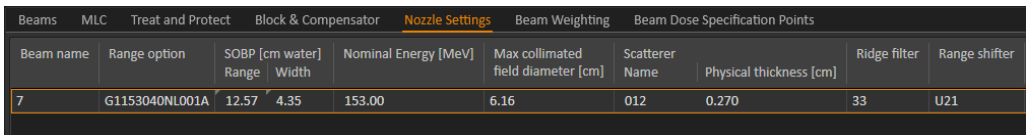


Figure 274. The Nozzle settings tab for a Mitsubishi Electric Co SELECT BEAM NOZZLE in US mode beam.

6.5.9 MLC, block and compensator properties

MLC

The **MLC** tab is visible for plans using machines with MLC. The tab displays the MLC leaf geometry and positions given at the MLC virtual tray plane for the selected beam.

The leaves for the selected beam are listed in the MLC table, and can be set to a desired position.

1. Select the leaf pairs to modify. Multiple rows are selected by Shift or Ctrl mouse click.
2. Add either new positions for **X1** and/or **X2**, or the distances (positive or negative) to push **X1** and/or **X2**. (Naming of positions is for an MLCX machine according to the Jaw labeling standard IEC 61217.)
3. Click **Apply**.

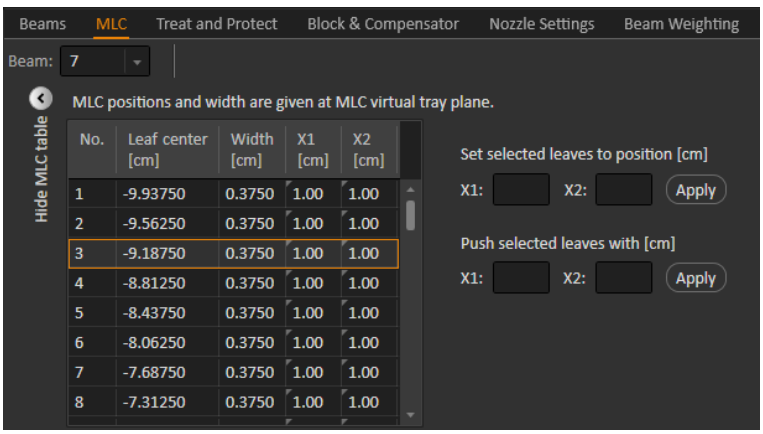


Figure 275. The **MLC** tab.

Block and compensator

The **Block & Compensator** tab presents the block and compensator settings per beam (for US/DS/Wobbling).

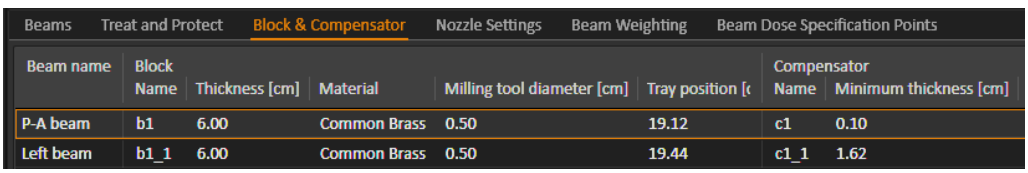


Figure 276. The **Block & Compensator** tab.

Block

The **Block** tab presents the block settings per beam (for PBS/LS with blocks).

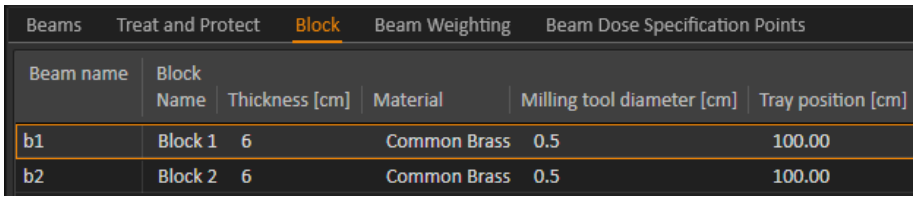


Figure 277. The **Block** tab.

Note: *For Mevion Hyperscan with adaptive aperture and Hyperscan PBS, the milling tool diameter is 0 cm.*

6.5.10 Beam weighting

Beam weighting is described in detail in *section 6.3.12 Beam weighting on page 445*.

6.5.11 Edit block aperture

For a beam with a block, the block can be edited using the tools located in the **Aperture** tab in the toolbar.

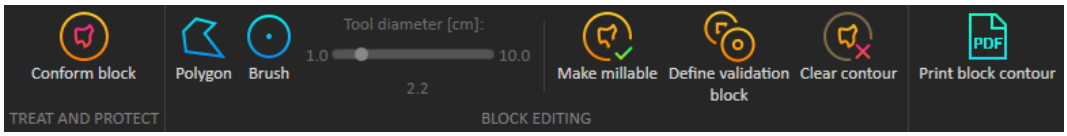
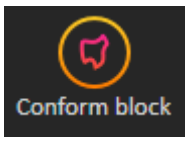


Figure 278. The block editing tools

Conform block for a single beam

The block parameters for a selected beam can be computed according to the specified treat and protect settings and margins by clicking the **Conform block** button.



The calculation will yield the block contour, defined at the isocentric plane, along with a corresponding SAD, separate in X and Y (IEC Gantry coordinate system). The SAD is used to scale the contour to the physical position of the block. If the calculation would have resulted in multiple openings, only the largest opening is kept. The selected milling tool is applied after the block contour is generated. To ensure target coverage, this step may make the block contour larger, but never smaller, and thus the resulting block contour may violate protect margins.

Note: *The SAD is exported in DICOM as [300A,030A] Virtual Source-Axis Distance (VSAD).*

Note: *The dose will be invalidated after a new block contour has been calculated.*

Note: *Sub-optimal aperture openings may be computed for DS and Wobbling.*

If conform MLC or block contour is performed before a range option is populated on the beam, suboptimal aperture openings may be created for machines with SAD dependent on field size. This is because SADs depends on the range option for the beam, which in turn depends on the max collimated field diamater. To be able to conform aperture opening for beams without a range option, RayStation will use the mean value of the SADs in all range options.

Edit the block shape

The block shape can be edited in the BEV using the **Polygon** or **Brush** tool.

- **Brush**: The size of the ball can be adjusted using the slider in the **Block editing** toolbar, by pressing the + and - keys on the numerical keyboard, or by using the mouse wheel while pressing the ALT key. The smallest diameter of the brush is set to the milling tool diameter for the block.

- **Polygon**: A new contour is added to the original contour if the starting point is inside a contour on its edge, and finish point is inside the same contour. A new contour is subtracted from the original contour if the starting point is outside a contour on its edge, and the finish point is outside the same contour. If defining a two point polygon with both points outside the current aperture shape, and the line intersecting it twice, the smaller half will be cut off. If a polygon is drawn entirely outside an original block, fully inside or is fully containing the old block shape, the old block shape will be replaced by the new contour. Crossing contours are not allowed.

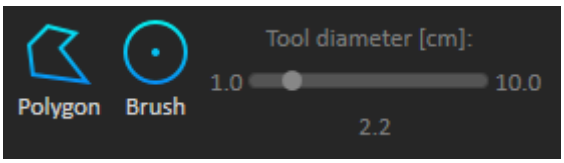
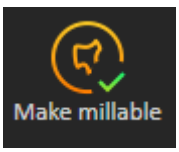


Figure 279. The block editing tools

Make block millable

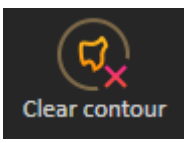
The Make millable function can be used to ensure that the block can be realized using the specified milling tool dimension. It is recommended to click the **Make millable** button after manual editing of the block opening.



Note: *The Make millable function has no meaning for Mevion Hyperscan with adaptive aperture.*

Clear block contour

To clear the block contour, click the **Clear contour** button.



Print block contour

A block contour can be printed in its actual size on an office printer. This is done by first creating a block report in PDF format and then printing the PDF file using an office printer.

WARNING!

Verify the scale of the block/cutout printout. The printer settings will affect the actual size of the block/cutout in the printout. Before using the block/cutout printout for block/cutout manufacturing or verification, always check that the scale of the x- and y-axes are equal and that 1 cm on the verification scale corresponds to 1 cm using a ruler. (54970)

To print a block contour:

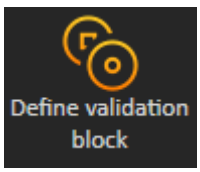
1. Click the **Print block contour** button.

2. Select a **Scale factor** in the Print Block Contour dialog. Default scale factor value is 1.
3. Click **OK**. A block report will be created in pdf format.

Define validation block

To define a validation block:

1. Click the **Define validation block** button.



This opens the **Specify Validation Block** dialog.

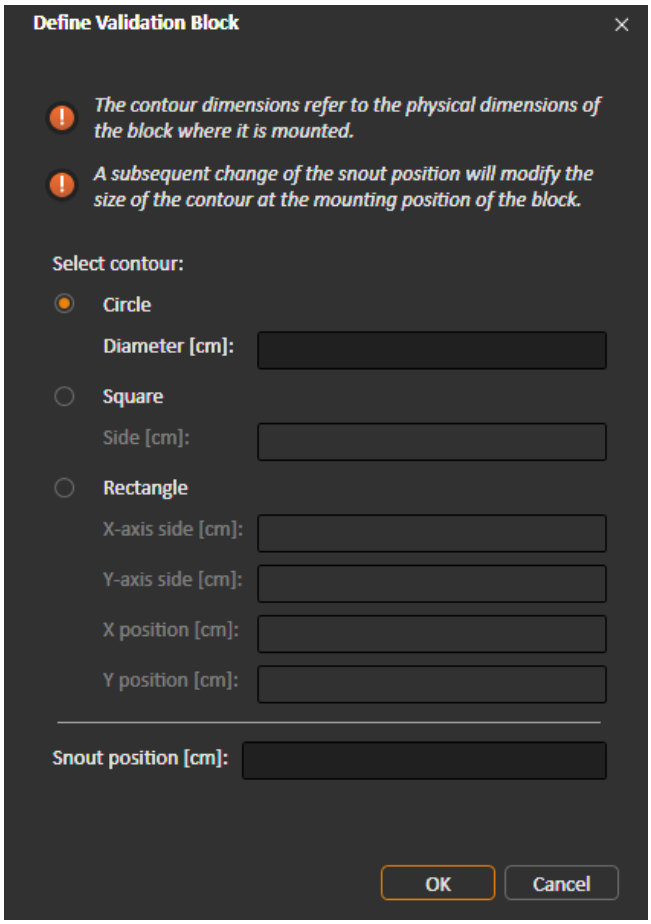

Define Validation Block
The contour dimensions refer to the physical dimensions of the block where it is mounted.
A subsequent change of the snout position will modify the size of the contour at the mounting position of the block.
Select contour:
Circle
Diameter [cm]:
Square
Side [cm]:
Rectangle
X-axis side [cm]:
Y-axis side [cm]:
X position [cm]:
Y position [cm]:
Snout position [cm]:
OK
Cancel

Figure 280. The Define Validation Block dialog.

2. Select contour. Available block contour shapes are:
   - **Circle** – centered around the isocenter.
   - **Square** – centered around the isocenter.
   - **Rectangle** – the X and Y positions refer to the lower left corner of the rectangle, where the X and Y axes are aligned with those of the Beam limiting device coordinate system.

   Note: *The contour dimensions here are defined in the physical downstream plane of the block, i.e. not in the isocenter plane.*
3. Specify **Snout position**.
4. Click **OK**.

6.5.12 Edit MLC aperture

For a beam with an MLC , the MLC can be edited using the tools located in the **Aperture** tab in the toolbar.

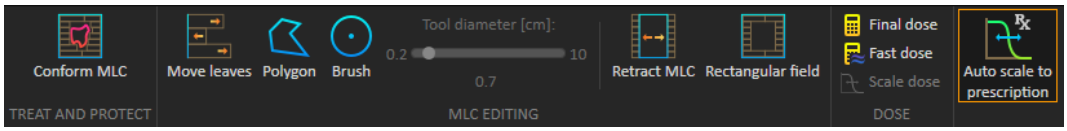


Figure 281. The MLC editing tools.

Conform MLC for a single beam

The MLC parameters for a selected beam can be computed according to the specified treat and protect settings and margins by clicking the **Conform MLC** button. If the calculation would have resulted in multiple openings, only the largest opening is kept.

Note: *The dose will be invalidated after a new MLC opening has been calculated.*

Note: *Sub-optimal aperture openings may be computed for DS and Wobbling.*

If conform MLC or block contour is performed before a range option is populated on the beam, suboptimal aperture openings may be created for machines with SAD dependent on field size. This is because SAD depends on the range option for the beam, which in turn depends on the max collimated field diamater. To be able to conform aperture opening for beams without a range option, RayStation will use the mean value of the SADs in all range options.

Move leaves

Use the **Move leaves** button to manually pull the leaves to a desired position. Left-click and press SHIFT/CTRL to select multiple leaves. Left-click and press ALT to align the selected leaves.

Edit the MLC contour

The MLC contour can be edited in the BEV using the **Polygon** or **Brush** tool.

- **Brush**: The size of the ball can be adjusted using the slider in the **MLC editing** toolbar, by pressing the + and - keys on the numerical keyboard, or by using the mouse wheel while pressing the ALT key.
- **Polygon**: A new MLC opening is conformed around the polygon of points. Right click to to end the polygon. Crossing contours are not allowed.

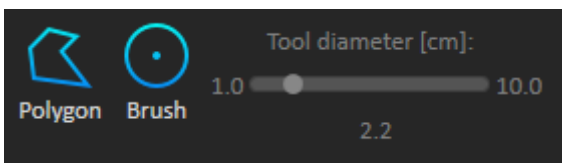


Figure 282. The MLC editing tools

Retract MLC

The **Retract MLC** button sets the MLC- leaves in the most open allowed position supported by the machine. The property is symmetric for the two leaf banks.

Create rectangular MLC field

1. Click the **Rectangular field** button.

This opens the **Create Rectangular Fields** dialog.

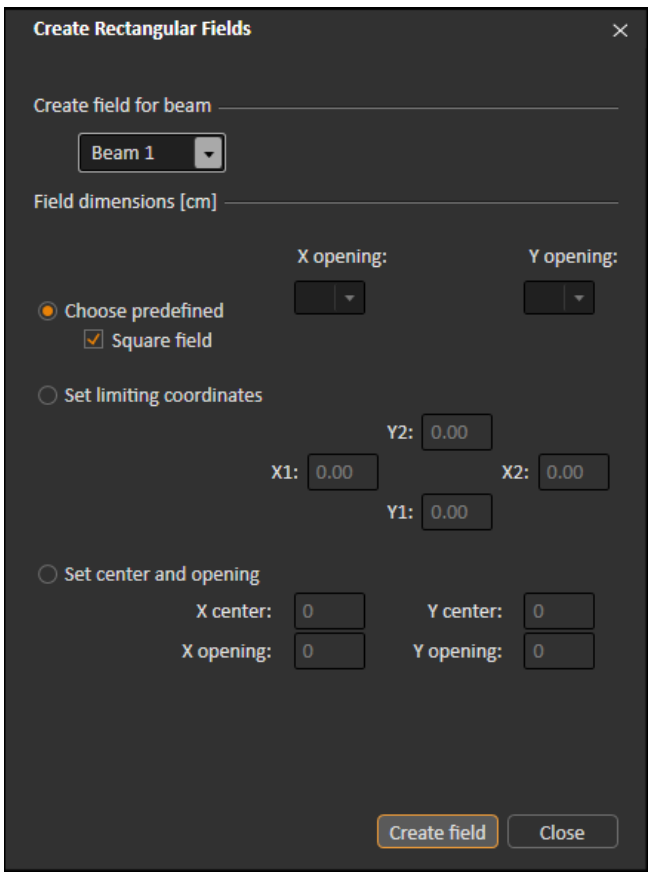


Figure 283. The Create Rectangular Fields dialog.

2. Select the beam to create the field for in the **Create field for beam** list.

3. Enter values for the opening.

   Note: *The positions are defined in the physical plane.*

4. Click **Create field**.

   Note: *The resulting field size will be as close as possible to, but not smaller than, the entered values. The result is shown in the dialog.*

6.5.13 Edit Compensator

For a beam with a compensator, the compensator can be edited using the tools located in the **Compensator** tab in the toolbar.

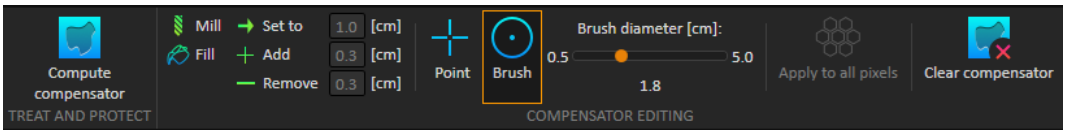
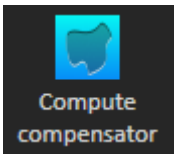


Figure 284. The Compensator editing tools.

Compute compensator geometry for a single beam

The compensator for a selected beam can be computed according to the treat and protect settings, selected margins, smearing radius and gradient values by clicking the **Compute compensator** button.

Note: *A block or MLC contour must have been computed in order to compute a compensator.*



The calculation will yield the compensator geometry, defined at the isocentric plane, using the milling pattern as given in the machine (regular or hexagonal) and a pixel spacing as given in the Add/Edit beam dialog. The snout position is modified to maintain the expected air gap for the beam.

The **Compute compensator** button will set up the active compensator area as a rectangular bounding box with 1 cm margin around the aperture (block or MLC) contour at isocenter. Each pixel in the active compensator area is assigned a thickness according to the details found in the *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual*.

The active compensator area is editable using the compensator editing tools and will be exported in the DICOM RT Ion plan. The active compensator pixels will be indicated with their corresponding thickness value in the BEV, while non-active compensator pixels will be indicated with thickness value "-".

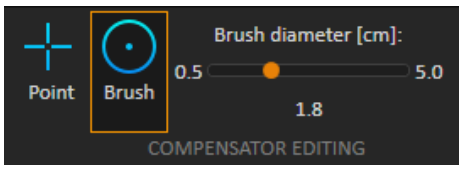
Dose computation is only allowed for beams where the aperture contour is inside the active compensator area, which means that the compensator may have to be re-conformed in order to compute dose, if the aperture contour has been edited so that it is outside the compensator active area. There is no relation between the active compensator area and the snout inner dimensions.

Note: *The dose will be invalidated after a new compensator has been calculated.*

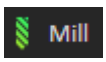
Note: *The compensator geometry is calculated at the isocenter plane, and the geometry at the physical plane is obtained by projection using the machine SAD in X and Y. For machines supporting only collimator angle zero, the SAD in the machine (which might be different in X and Y) will be used. For machines supporting collimator angles different from zero the mean value of SAD in X and Y is instead used to project the compensator geometry to its physical plane, which means the result of compute compensator will be different compared to machines only allowing collimator angle zero, and possibly sub-optimal, for such machines. The user must verify that the computed compensator gives an acceptable dose distribution.*

Edit the compensator shape

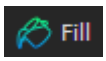
The compensator thickness can be manually edited using the mouse in the Beam's Eye View (BEV). The BEV pointer tools are either a variable sized **Brush** or a **Point**. The diameter of the **Brush** tool can be changed with a slider. The smallest diameter of the brush is set to the milling tool diameter for the compensator.



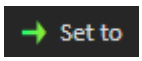
The **Point** and **Brush** tools can be used with the editing tools described below.



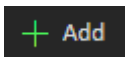
Mill. Mills out the compensator to the depth at a specific position. Click at a position with the desired thickness, keep the mouse button pressed down and move the mouse to mill. Only pixels with a thicker value than the start value are addressed.



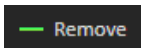
Fill. Fills out the compensator to the thickness at a specific position. Click at a position with the desired thickness, keep the mouse button pressed down and move the mouse to fill. Only pixels with a thinner value than the start value are addressed.



Set to. Sets the pixel values to a defined value. Click at a position, keep the mouse button pressed down and move the mouse to set the desired thickness.

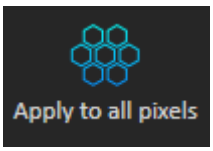


Add. Adds a layer of a specified thickness. Click at a position, keep the mouse button pressed down and move the mouse where the compensator thickness should increase. Pixels are only addressed once within a click-release motion.



Remove. Removes a layer of a specified thickness. Click at a position, keep the mouse button pressed down and move the mouse where the compensator thickness should decrease. Pixels are only addressed once within a click-release motion.

The **Set to**, **Add**, and **Remove** tools can also be applied to all compensator pixels in the current compensator, by clicking the **Apply to all pixels** button.



Compensator filters

To finalize the manual editing, sharp edges of the compensator shape can be softened using the **Gradient limit** filter. The compensator can also be expanded by changing the **Smearing radius**. For a description of these filters, see *Beam specific computation parameters on page 491*.

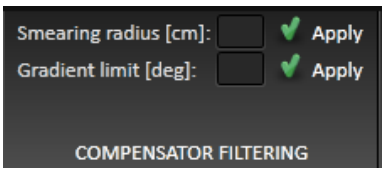
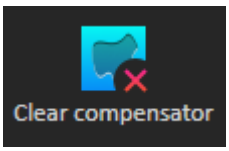


Figure 285. The Compensator filtering tools.

Note: *These parameters are for post processing of the compensator and will not affect the Treat and Protect computations.*

Clear compensator

To completely remove the compensator definition, click the **Clear compensator** button.

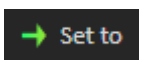


Define validation compensator

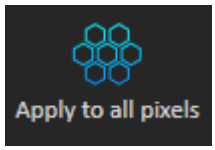
To create a validation compensator, the use of a compensator must be specified when the beam is created (See *Add proton beams for Uniform Scanning/Double Scattering/Wobbling on page 320*), and an aperture with contour must be present.

To create a validation compensator:

1. Make a note of the **Snout Position** for the beam (in the **Beams** tab).
2. Click the **Set to** button and fill in the thickness value in the corresponding edit box.



3. Click **Apply to all pixels**.



The compensator will be created with the specified settings. For beams with compensator closest to the patient the snout position is retraced a distance corresponding to the thickness of the compensator: for beams with the compensator closest to the patient.

7 PLAN OPTIMIZATION

The Plan Optimization planning activity contains the Plan Optimization module and the Multi Criteria Optimization module. Biological optimization and robust optimization can be performed in the Plan Optimization module but these features are described in separate sections.

In this chapter

This chapter contains the following sections:

7.1	The Plan Optimization module - photons	p. 518
7.2	The Plan Optimization module - protons	p. 565
7.3	The Plan Optimization module - carbon ions	p. 610
7.4	The Multi Criteria Optimization module	p. 653
7.5	Biological optimization	p. 689
7.6	Robust optimization	p. 711

7.1 THE PLAN OPTIMIZATION MODULE - PHOTONS

The Plan Optimization module can be used to generate optimized SMLC, DMLC, VMAT, 3D-CRT, Conformal Arc and TomoHelical photon treatment plans through optimization with respect to user-defined treatment objectives and constraints.

It is also possible to co-optimize two beam sets. See *section 7.1.19 Multiple beam set optimization on page 557* for more information.

In this section

This section contains the following sub-sections:

7.1.1	The Plan Optimization user interface	p. 520
7.1.2	Plan Optimization workflow	p. 521
7.1.3	Optimization functions – objectives and constraints	p. 524
7.1.4	Optimization function list templates	p. 529
7.1.5	Specify optimization and segmentation settings	p. 530
7.1.6	Beams in the Plan Optimization module	p. 537
7.1.7	Control points and MLC positions	p. 539
7.1.8	Beam weighting	p. 541
7.1.9	Beam optimization settings	p. 542
7.1.10	Treat	p. 547
7.1.11	Protect	p. 548
7.1.12	Running the optimization	p. 549
7.1.13	Evaluating fluence in Beam's Eye View (BEV)	p. 551
7.1.14	Define or modify prescription	p. 552
7.1.15	Compute dose	p. 553
7.1.16	Compute function values	p. 554
7.1.17	Edit segment shapes	p. 555
7.1.18	The evaluation views	p. 556
7.1.19	Multiple beam set optimization	p. 557
7.1.20	Wave arc	p. 563

7.1.1 The Plan Optimization user interface

Workspace

The top left corner shows the result of the optimization process for each visualized ROI in a dose volume histogram (DVH). Behind the DVH are tabs for dose statistics as well as for review of clinical goals.

The bottom view defaults to the **Objectives/constraints** tab – listing the user specified objectives and constraints, with buttons for adding, editing and deleting of such functions. There are also tabs for the beam list, the control point list, the beam optimization settings and beam weighting.

The lower right corner, visualizes the **Optimization Progress** in terms of function values per iteration.

The window in the top right corner shows image set data for the current plan in **2D**, **3D** or Beam's Eye View (**BEV**).

For TomoHelical plans there is a **Leaf Open Times** view that displays a histogram for the leaf open time of all leaves and of all projections.

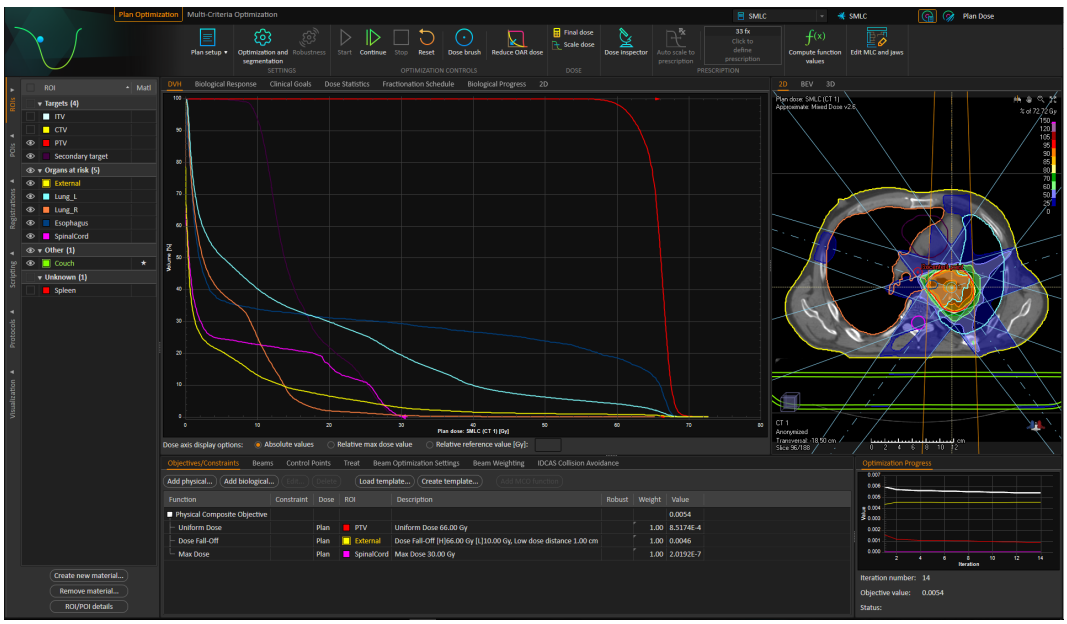


Figure 286. The Plan Optimization module workspace. The view shows a dose volume histogram, dose distribution in the image data, beam list and the progress of optimization.

Graphical User Interface

For more information about the tools, operations and various view types in the Graphical User Interface, see *chapter 3 The Graphical User Interface*.

7.1.2 Plan Optimization workflow

This section describes a suggested workflow for creating an optimized photon plan based on physical parameters.

1. **Create a new plan and add treatment beams.** For standardized treatment plans, it is preferable to set up a new plan via a plan generation protocol in the **Protocols** tab. See *section 6.1.2 Plan generation protocols on page 300* for more details.

   If no plan generation protocol exists, perform the following steps:

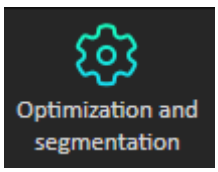
   a. **Create a new plan** in either the Plan Setup module or directly in the Plan Optimization module. Add a prescription if desired. For more information on how to create a plan, see *section 6.1.3 Create a new plan on page 306*.

   b. **Add the treatment beams** by loading a template, or add them manually. For more information on how to add beams, see *section 6.1.6 Add, edit, copy or delete beams on page 316*.

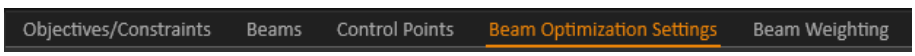
2. **Set up the optimization functions (objectives and constraints).** Define them one by one or by adding a set of pre-defined functions from a function list template (see *section 7.1.4 Optimization function list templates on page 529*).

   Add the objectives and constraints according to the instructions in *Add objectives and constraints on page 524*.

3. **Specify the optimization and segmentation settings** according to the instructions in *section 7.1.5 Specify optimization and segmentation settings on page 530*.

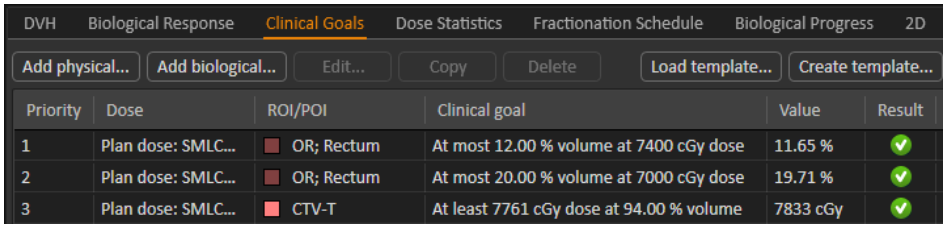
   

4. **Specify the beam optimization settings.** Click the **Beam Optimization Settings** tab and select the settings for each beam as required.

   The available settings will depend on the selected treatment technique. For more information about the available settings, see *section 7.1.9 Beam optimization settings on page 542*.

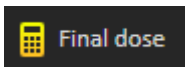
5. **Add the clinical goals.** Define them one by one or by adding a set of pre-defined goals from a clinical goals template.



For information about clinical goals and instructions on how to add them, see *section 3.7.3 Clinical goals on page 81*.

6. **Optimize the plan** according to the instructions in *section 7.1.12 Running the optimization on page 549*.

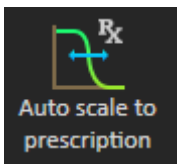
7. **Compute final dose.** If compute final dose was not selected in the Optimization settings, compute final dose.



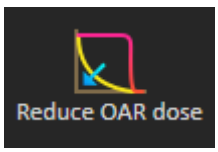
8. **If needed, use the Scale dose and Auto scale to prescription options (optional).**

Use the Scale dose option to fulfill the prescription or to fulfill an arbitrary dose-volume relation for a selected ROI or POI. For more information, see *section 6.1.15 Scale dose on page 356*.

Use the Auto scale to prescription option to fulfil the prescription value regardless of any additional changes. For more information, see *section 6.1.16 Auto scale to prescription on page 358*.



9. **Reduce OAR dose (optional).** If desired, select to reduce the OAR dose by clicking the corresponding button.



This option will continue the optimization, attempting to reduce the dose in the risk organs (OARs) while maintaining dose homogeneity in the target organs. This option is only available if there is at least one control point in every beam.

If the current beam set already has minimal OAR dose, this function will not have any significant effect.

7.1.3 Optimization functions – objectives and constraints

An optimization problem consists of an objective function that is to be minimized and optionally a number of constraints. Constraints are used for requirements that must be fulfilled. The optimal solution to the problem is the one that gives the best value of the objective function without violating any of the constraints.

The user specifies a number of optimization functions. These can either be part of the objective function or used as individual constraints. The optimization functions included in the objective function are assigned weights reflecting their relative importance, i.e. an objective with the weight 10 is 10 times more important than one with weight 1. (Weights are almost only relative. Having all weights at 1 gives almost the same effect as having all weights at 100. The only difference will be in the application of the optimization tolerance and some internal numerical tolerances.)

Note: *For multiple beam sets that have a dependency, the optimization functions in the dependent beam set can relate to either: the combined beam set + background dose (background dose dependency), or the combined dose of the two co-optimized beam sets (co-optimized dose dependency), or the separate beam set dose.*

This is selected per optimization function in the Add Optimization Function dialog, see section 7.1.19 Multiple beam set optimization on page 557.

Add objectives and constraints

Optimization functions can be added in two ways; by defining them one by one or by adding a set of pre-defined functions from a function list template (see *section 7.1.4 Optimization function list templates on page 529*).

To add an optimization function:

1. Click the **Add physical...** button in the **Objectives/constraints** tab to open the **Add Optimization Function** dialog.

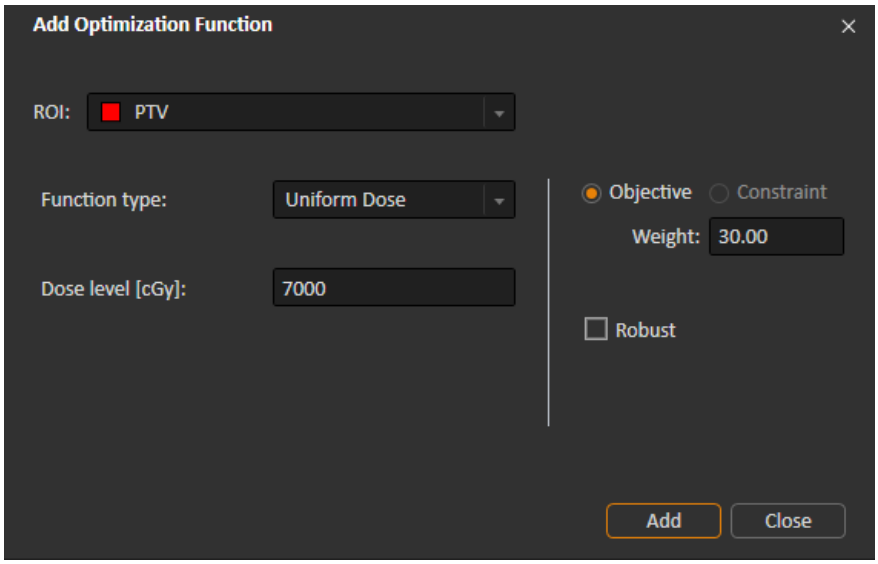


Figure 287. The **Add Optimization Function** dialog.

2. Select the **ROI** for which a function should be added. The function types available depend on the organ type of the ROI.
3. Select **Function type** and specify the function parameters (see *Available objectives and constraints on page 525*).
4. Select if the function is going to be used as an **Objective** or a **Constraint**.
5. Assign a **Weight** to define the relative importance of the objective.
6. Select if the optimization should be **Robust** by checking the corresponding checkbox.

   For more information, see *section 7.6 Robust optimization on page 711*.
7. Click **Add**.

Available objectives and constraints

The table below lists available function types dependent on the ROI organ type.

Function type	Organ type	Parameter(s)	Description
Min Dose	Target	Dose level	The objective/constraint is met when all parts of the ROI has a dose that is greater than or equal to the specified Min Dose.
Max Dose	OAR and target	Dose level	The objective/constraint is met when the ROI has a maximum dose that is less than or equal to the specified Max Dose.

Function type	Organ type	Parameter(s)	Description
Min DVH	Target	Dose level, Volume (%)	The objective/constraint is met when at least the specified % volume of the ROI receives at least the specified Min Dose.
Max DVH	OAR and target	Dose level, Volume (%)	The objective/constraint is met when only the specified % volume of the ROI receives more than the specified Max Dose.
Uniform Dose	Target	Dose level	The objective is met when the entire ROI volume receives a dose equal to the specified dose level.
Min EUD (Equivalent Uniform Dose)	Target	Dose level, Parameter A	A<1: Lower doses are given higher weight so that cold spots influence the EUD to a large extent. A=1: This corresponds to the mean dose. Cold and hot spots are given equal weight. The objective/constraint is met if the EUD value is greater than or equal to the dose level.
Max EUD	OAR and target	Dose level, Parameter A	A>1: Higher doses are given higher weight so that hot spots influence the EUD to a large extent. A=1: This corresponds to the mean dose. Cold and hot spots are given equal weight. The objective/constraint is met if the EUD value is less than or equal to the dose level.
Target EUD	Target	Dose level, Parameter A	The objective/constraint is met if the EUD value is exactly equal to the dose level.

Function type	Organ type	Parameter(s)	Description
Dose Fall-Off	OAR and target	High dose level, Low dose level, Low dose distance, Adapt to target dose levels	This function is a max dose function where the max dose level is a function of the distance to the target. The allowed max dose level falls off linearly from the high dose level at the border of the target to the low dose level at the dose distance from the target. At greater distances, the low dose level is still applied. The objective/constraints is met when all voxel doses within the specified ROI are less than or equal to their respective max dose levels. Note that the function is applied to voxels within the specified ROI. If the dose fall-off function is defined for an ROI of organ type which overlaps a target ROI, then the voxels within the target ROI are disregarded. Likwise, if the dose fall-off function is defined for a target ROI which overlaps other target ROIs, then the voxels within the other target ROIs are disregarded. It is advisable to select **Adapt to target dose levels** for cases with multiple target levels. If **Adapt to target dose levels** is selected, the high dose level is adjusted relative to the highest dose level of each target. ***Note:*** *The high dose level will not be adapted if the target functions are defined on both planned dose and beam set dose.*
Uniformity constraint	OAR and target	Relative standard deviation (Rel. std. dev. (%))	The constraint is met when the variation of dose within the ROI is less than the specified % variation. (The uniformity constraint does not specify the desired dose level – dose level must be specified by applying an additional Min or Max dose objective or constraint for the ROI.)

The optimization functions are described in detail in *RSL-D-RS-7.0-OPT, A guide to optimization in RayStation 7*.

Edit objectives or constraints

It is possible to edit an existing objective/constraint by double-clicking on it in the objectives/constraints list, or by clicking the **Edit...** button, to open the Edit Optimization Function dialog. Another way to modify the objectives/constraints is by dragging the corresponding arrow symbol in the DVH window.

Note: *At least one target function, i.e. Min Dose, Min DVH, Uniform Dose or Min EUD must be included in the optimization problem.*

Delete objectives or constraints

Use the **Delete** button to delete objectives or constraints from the list.

Add MCO functions

This function is described in detail in *section 7.4.11 Add MCO function on page 684*.

The **Add MCO functions** button is:

- only visible in the Plan Optimization module if the user has an MCO license.
- activated when creating a deliverable plan in MCO (using the **Start** or **Continue** buttons).
- inactivated if the navigated state used to create the deliverable plan is changed.

7.1.4 Optimization function list templates

A set of objectives and/or constraints can be stored as an optimization function list template. Using optimization function list templates can simplify the planning process, since standard optimization functions can be re-used as a starting point when optimizing new plans.

Add optimization functions from template

To add optimization functions from an optimization function list template, click the **Load template...** button. Select a template in the drop-down list in the **Select Function List Template** dialog. The objectives and constraints for the selected template are listed in the dialog's function lists. To add the template's functions to the plan, click the **Add** button.

To rename the selected template, click **Rename** and enter a new name for the template. Note that approved templates cannot be renamed. To delete the selected template, click **Delete**.

To approve a template, click **Approve**. Only admin users can approve a template and delete an approved template. Approved templates have a padlock next to the template name. If a non-approved template is loaded, a warning will be displayed. These warnings can be disabled in Clinic Settings (*section D.2.2 The Preferences tab on page 922*).

Create optimization function list template

An optimization function list template can be created from a plan's existing set of optimization functions. To store the current plan's functions as a template, click the **Create template...** button and enter a name for the new template. (The template can later be renamed or deleted from the **Select Function List Template** dialog.)

Note: *In case of multiple beam sets that have a dependency, function list templates cannot be created for co-optimized dose dependencies, or for the second beam set having background dependency if it contains objectives that relate to the beam set dose.*

7.1.5 Specify optimization and segmentation settings

Depending on the treatment technique (VMAT, SMLC, DMLC, 3D-CRT, Conformal Arc or TomoHelical), different optimization and segmentation settings can be entered.

Specify optimization and segmentation settings for SMLC

Click the **Optimization and segmentation** button to open the **Settings** dialog.

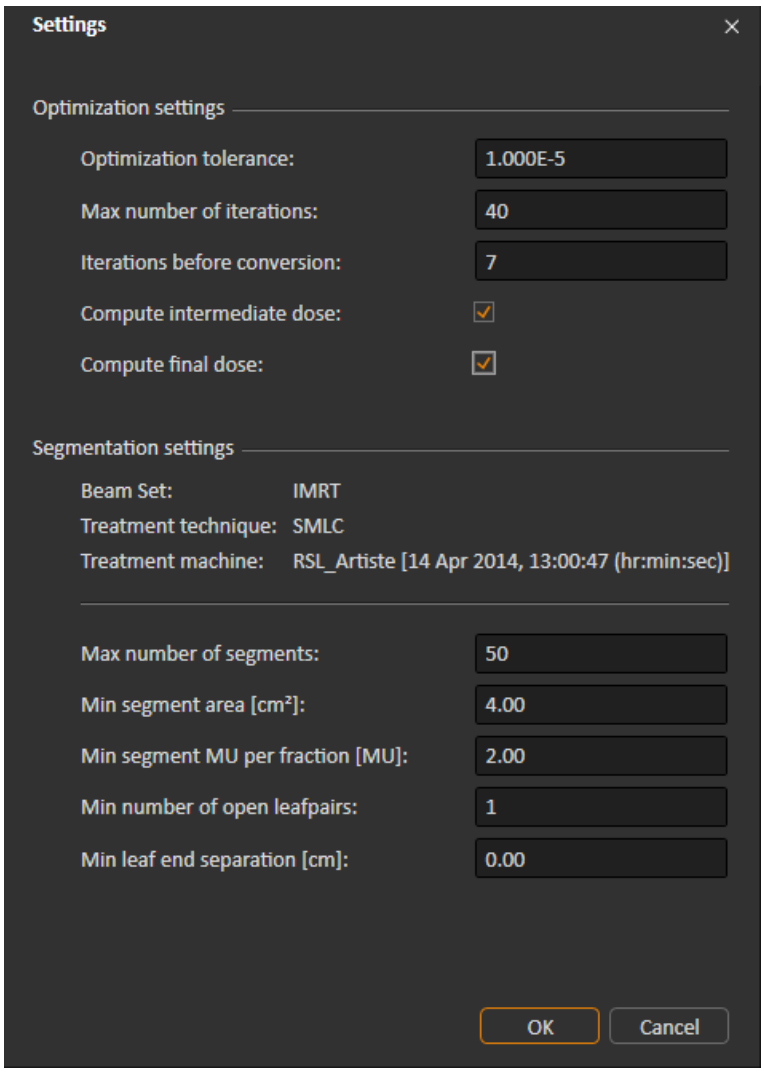


Figure 288. The **Settings** dialog for SMLC optimization.

The user can edit the following optimization settings:

Parameter	Description
Optimization tolerance	The software stops the optimization when the change in the Composite Objective value indicates that an optimal solution has been found. This occurs when the change in objective value is less than the tolerance level. The optimization tolerance should be around 1e-5 or 1e-6.
Max number of iterations	The optimization algorithm can usually find an optimal solution in 25–100 iterations, but by setting maximal number of iterations the optimization can be stopped prior to this if it is believed that the objectives will not be met or whenever the result already is satisfying.
Iterations before conversion	The optimization algorithm has two phases. In the first phase, a fluence map from each beam direction is optimized. In the next phase, this fluence map is converted to segments. The segments are then optimized until an optimal solution is found or the max number of iterations is reached. The iterations before conversion determine how many iterations the first phase of the optimization shall last. This parameter also determines at which point an intermediate dose shall be calculated if that option is selected. For a continuation of the optimization, this parameter is not applicable.
Compute intermediate dose	If this box is checked, the clinical dose engine will be used to compute the dose directly after the conversion. This dose will be used by the optimizer as background dose using the optimization dose engine only to compute the delta contribution in each consecutive iteration. This option is recommended for increased dose accuracy but it may be omitted during exploratory optimization runs or in benign geometries (homogeneous densities, non-oblique beam incidence).
Compute final dose	With this option selected, a final dose will be computed for the current beam parameters after the optimization is finished. The clinical dose engine used is the collapsed cone dose engine.
Max number of segments	This parameter defines the maximum number of segments the optimizer shall create for the plan. In some cases fewer segments are created by the optimizer because the specified number was found not necessary for the plan. This may happen for a very smooth target or if the number of iterations before conversion is set too low.
Min segment area	This parameter defines a constraint on the minimum segment area for a segment allowed during optimization. This parameter may be used to avoid small segments which may be undesirable from a dosimetric point of view.
Min segment MU per fraction	This parameter defines a constraint on the minimum segment MU per fraction allowed during optimization.
Min number of open leafpairs	The minimum allowed number of leafpairs allowed in a contiguous sequence of open leafpairs.

Parameter	Description
Min leaf end separation	Specifies the minimum allowed leaf end separation allowed in leafpairs that are open on purpose. It is similar to the minimum leaf gap required by the machine, but it does not apply to leaf pairs that are intended to be closed. ***Note:*** *This parameter only has an impact on the "interior parts" of a segment opening. This means that the lowermost and uppermost leafpairs of a segment opening can have a leaf gap smaller than the value of the Min leaf end separation parameter.*

Specify optimization and segmentation settings for DMLC

Click the **Optimization and segmentation** button to open the **Settings** dialog.

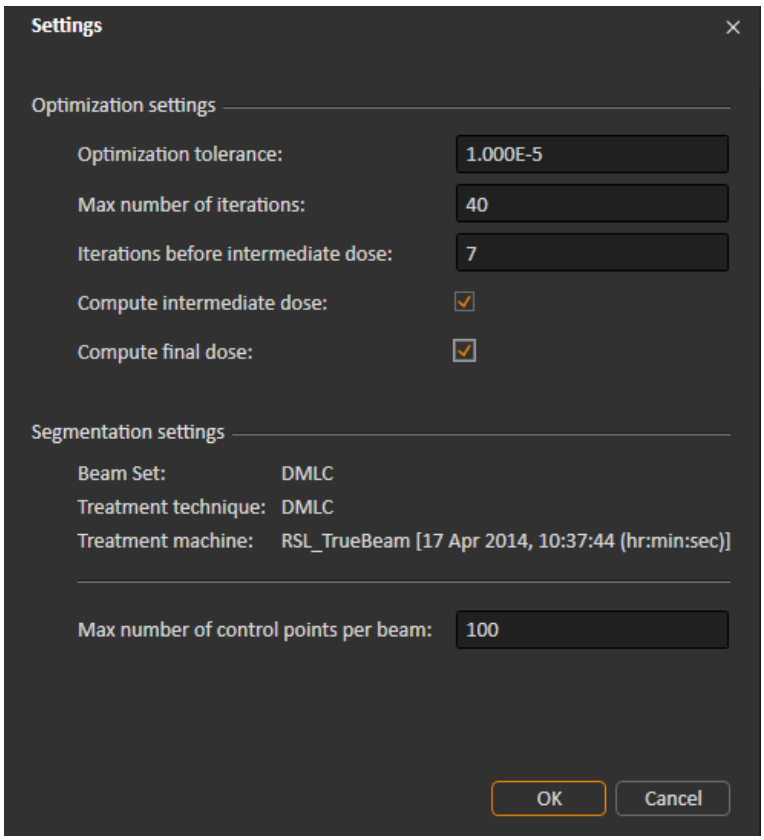


Figure 289. The **Settings** dialog for DMLC optimization.

The optimization settings for DMLC (Sliding Window) are the same as for SMLC. For more information, see *Specify optimization and segmentation settings for SMLC on page 530*.

The only segmentation setting is **Max number of control points per beam** which specifies the maximum number of control points that the optimizer shall create for each beam.

When a DMLC optimization is started a fluence map from each beam direction is optimized. When the optimization has finished the fluence maps are converted to control points.

From this state it is possible to optimize the leaf positions further, that is, to continue the previous optimization.

Note: *The DMLC plans created in RayStation are of 'sliding window type'. For machines that have backup jaw, the jaw will not be moved during "beam on" irrespective of the selected jaw movement rule of the machine.*

Specify optimization and segmentation settings for VMAT

Click the **Optimization and segmentation** button to open the **Settings** dialog.

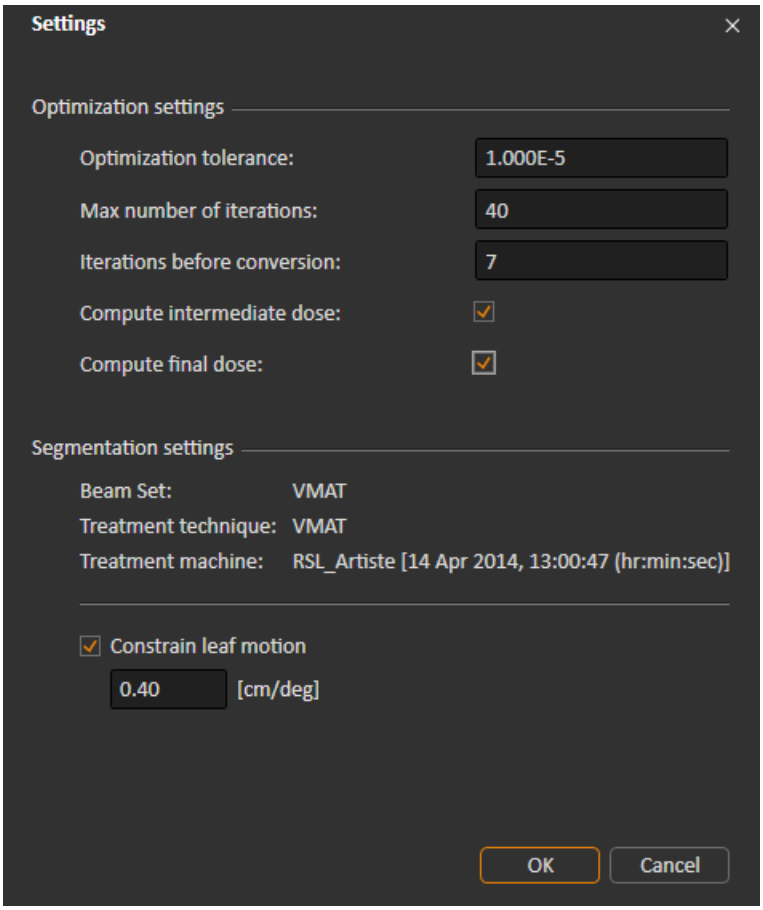


Figure 290. The **Settings** dialog for VMAT optimization.

Most of the settings for VMAT are the same as for SMLC. For more information, see *Specify optimization and segmentation settings for SMLC on page 530*.

For VMAT, the leaf motion may optionally be limited to a specified leaf travel distance per degree of gantry motion by checking the **Constrain leaf motion** checkbox. Using this limit may have a negative impact on plan quality, but the plans may become less complex to deliver more accurately.

Note: *For VMAT plans large differences in MLC positions between consecutive control points may affect the accuracy of the dose computation. One way to limit the leaf travel is to use the parameter Constrain leaf motion. Another way is to decrease the maximum leaf speed when the machine is commissioned. The accuracy of the dose computation may also be improved by selecting a shorter gantry spacing.*

Specify optimization and segmentation settings for 3D-CRT

Click the **Optimization and segmentation** button to open the **Settings** dialog.

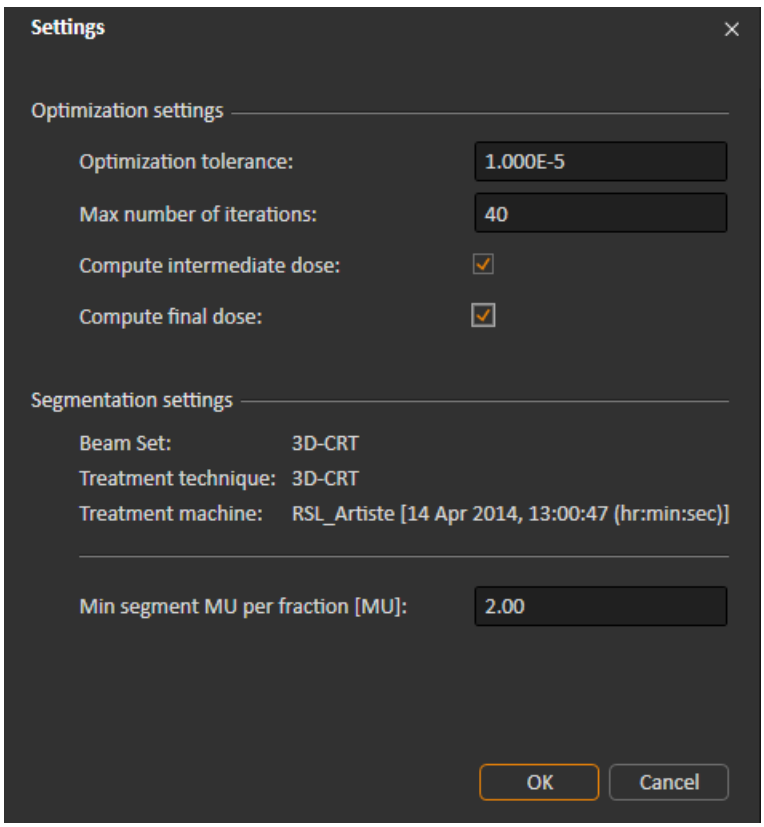


Figure 291. The **Settings** dialog for 3D-CRT optimization.

Most of the settings for 3D-CRT are the same as for SMLC. For more information, see *Specify optimization and segmentation settings for SMLC on page 530*.

For 3D-CRT, it is possible to **Compute intermediate dose**. If this box is checked, the final dose engine will be used to compute the dose directly after the segments have been created, i.e., before the optimization has started. This dose will be used by the optimizer as background dose using the optimization dose engine only to compute the delta contribution in each consecutive iteration. This option may be used for very heterogeneous geometries in which the objective function values changes a lot after final dose computation.

Note: *The intermediate dose cannot be used in combination with beam angle optimization (gantry, collimator and couch). This is because the concept of delta contributions becomes invalid when the beam orientation changes.*

For beams where at least one angle is optimized, the intermediate dose is discarded and the end result is an optimization dose without the additional accuracy from the intermediate calculation.

Specify optimization settings for TomoHelical

Click the **Optimization and segmentation** button to open the **Settings** dialog.

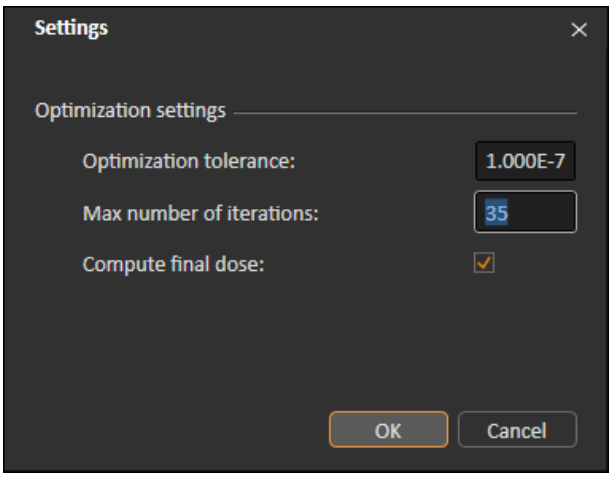


Figure 292. The **Settings** dialog for TomoHelical optimization.

The user can edit the following optimization settings:

Parameter	Description
Optimization tolerance	The software stops the optimization when the change in the Composite Objective value indicates that an optimal solution has been found. This occurs when the change in objective value is less than the tolerance level. The optimization tolerance should be around 1e-5 or 1e-6.

Parameter	Description
Max number of iterations	The optimization algorithm can usually find an optimal solution in 25–100 iterations, but by setting maximal number of iterations the optimization can be stopped prior to this if it is believed that the objectives will not be met or whenever the result already is satisfying.
Compute final dose	With this option selected, a final dose will be computed for the current beam parameters after the optimization is finished. The clinical dose engine used is the collapsed cone dose engine.

For the TomoHelical treatment technique there are no segmentation settings.

7.1.6 Beams in the Plan Optimization module

The **Beams** tab contains buttons for adding, editing, copying, deleting and renumbering beams. For more information, see *section 6.1.6 Add, edit, copy or delete beams on page 316*. There are also buttons for creating and loading beam list templates, see *section 6.1.7 Beam list templates on page 328* for more information.

For the treatment techniques SMLC, DMLC and 3D-CRT the beam list contains columns for beam number, beam name, beam description, isocenter, SSD (Source to skin distance), treatment machine, energy, gantry angle, collimator angle, couch angle, number of segments, MU/fraction, bolus and Jaw max aperture (the smallest rectangle that covers the jaw openings of all segments of the beam).

WARNING!

Collimator angle for VMAT, Conformal Arc and Static Arc. Collimator angles 0, 90, 180 and 270 degrees should if possible be avoided for arc beams as this may lead to accumulated dose leakage. The collimator angles should preferably be shifted at least 10 degrees from the above values. The accumulated dose leakage due to interleaf transmission is not reproduced by the clinical dose computation which may lead to faulty clinical decisions. Closed leaf pairs are likely to be positioned in the middle of the target projection which may accumulate the leakage to the center of the target at these collimator angles. (110570)

For 3D-CRT plans only: If a Treatment machine that supports wedges is selected, there is a choice of wedge angles and orientations in the list. When optimizing with respect to wedge angle for a machine that has several wedge types, the wedge angle will be optimized if there is no wedge or a dynamic/virtual wedge selected. If a standard wedge is selected, the wedge angle will not be optimized.

For information on how to create bolus, see *section 6.1.11 Create bolus on page 341*.

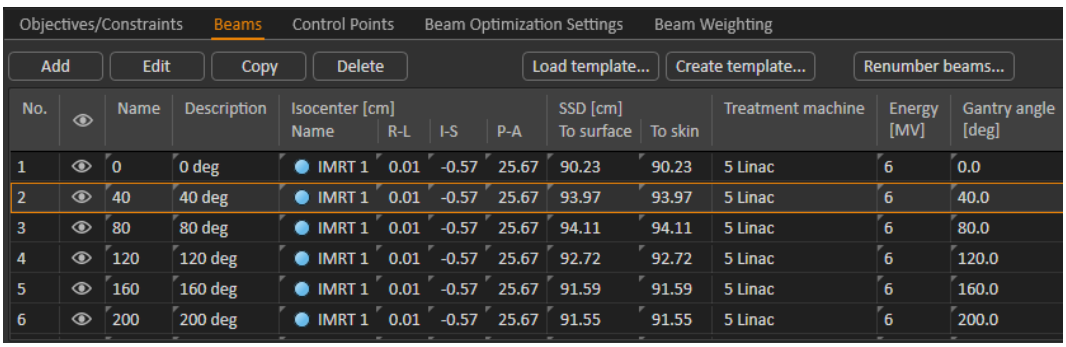

Objectives/Constraints
Beams
Control Points
Beam Optimization Settings
Beam Weighting
Add
Edit
Copy
Delete
Load template...
Create template...
Renumber beams...
No.
Name
Description
Isocenter [cm]
Name
R-L
I-S
P-A
SSD [cm]
To surface
To skin
Treatment machine
Energy [MV]
Gantry angle [deg]
1 0 0 deg IMRT 1 0.01 -0.57 25.67 90.23 90.23 5 Linac 6 0.0
2 40 40 deg IMRT 1 0.01 -0.57 25.67 93.97 93.97 5 Linac 6 40.0
3 80 80 deg IMRT 1 0.01 -0.57 25.67 94.11 94.11 5 Linac 6 80.0
4 120 120 deg IMRT 1 0.01 -0.57 25.67 92.72 92.72 5 Linac 6 120.0
5 160 160 deg IMRT 1 0.01 -0.57 25.67 91.59 91.59 5 Linac 6 160.0
6 200 200 deg IMRT 1 0.01 -0.57 25.67 91.55 91.55 5 Linac 6 200.0

Figure 293. The **Beams** tab, with treatment technique SMLC selected.

For VMAT and Conformal Arc, some additional columns are displayed in the list. These are: Gantry start angle, Gantry stop angle, Rotation direction, Estimated delivery time and Max gantry spacing.

For TomoHelical the following additional columns are displayed: Number of projections, Projection time, Gantry period, Couch speed, Delivery time, Modulation factor, Pitch factor and Planned field width.

7.1.7 Control points and MLC positions

The **Control points** tab lists all segments and corresponding MLC positions for a selected beam.

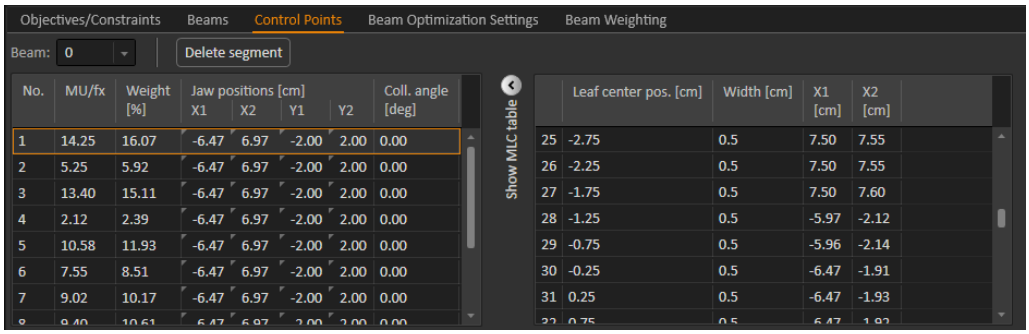


Figure 294. The **Control points** tab for SMLC and 3D-CRT.

The **Delete segment** button will delete the current segment for a selected beam.

Note: *Segments can only be deleted for SMLC and 3D-CRT plans. However, the last control point cannot be deleted.*

Note: *For VMAT and Conformal Arc plans the machine may use other delivery times and dose rates than the ones presented in the user interface. However, the machine will always deliver the specified MU.*

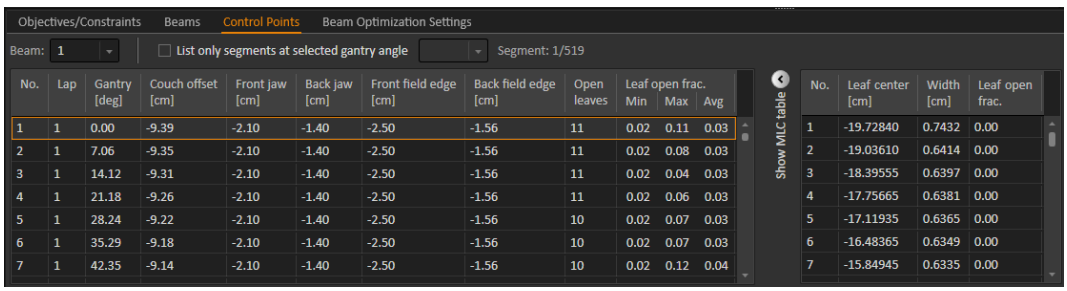
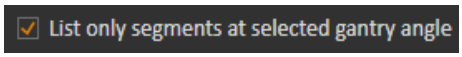


Figure 295. The **Control points** tab for TomoHelical.

Note: *Front and back jaw positions are stored in the database and sent to the machine. For usability, the front and back field edges are also presented. They represent the edges of the full width at half maximum (FWHM) of the resulting dose on the isocenter plane. The conversion between jaw positions and field edges are done using the conversion table stored in the machine model.*

The field edges are also used for jaw presentation in the graphical patient views (e.g., BEV).

For TomoHelical plans it is possible to select to only list the segments that are located at a certain gantry angle by checking the corresponding checkbox.



Edit jaw positions in the Control points tab

The Jaw positions for the selected segment are listed in the **Control points** tab and can be set to a desired position.

Note: *If there are several segments present and the machine demands the same jaw positions for all segments, all segments will be updated when one of the rows are edited.*

Edit the segment shapes in the Control points tab

Click the **Control points** tab at the bottom of the workspace. The leaves for the selected segment are listed in the MLC table, and can be set to a desired position.

1. Select the leaf pairs to modify. Multiple rows are selected by Shift or Ctrl mouse click.
2. Add new positions for X1 and/or X2 directly in the table, or Y1 and/or Y2 for YMLC.

For 3D-CRT, the leaves can be set to a desired position or pushed a certain distance. See *section 6.3.9 Control points and MLC positions on page 442* for more information.

7.1.8 Beam weighting

Beam weighting is described in detail in *section 6.3.12 Beam weighting on page 445*.

7.1.9 Beam optimization settings

The beam optimization settings are defined per beam and can be edited in the **Beam Optimization Settings** tab.

Note: *It is not possible to simultaneously optimize beams that have segments and beams that lack segments.*

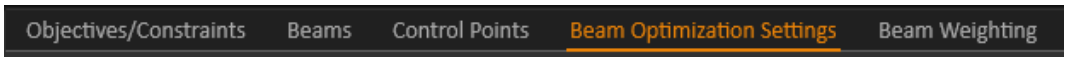


Figure 296. The **Beam Optimization Settings** tab.

The Beam Optimization Settings tab for different treatment techniques

The **Beam Optimization Settings** tab contains different columns depending on the treatment technique:

- **The tab for SMLC** contains columns for Number, Name, Exclude, Segment shapes, Segment MU, Beam MU, Split if necessary, Jaw assignment and Jaw limits.
- **The tab for DMLC** contains columns for Number, Name, Split if necessary, Jaw assignment and Jaw limits.
- **The tab for 3D-CRT** contains columns for Number, Name, Exclude, Segment shapes, Segment MU, Gantry, Collimator and Couch. There is an additional column Wedge if the treatment machine supports wedges.
- **The tab for VMAT** contains columns for Number, Name, Exclude, Segment shapes, Segment MU, Jaw assignment, Jaw limits, Create dual arcs, Gantry spacing, Max del. Time and Limit MU (Apply and Max MU/fx).

  Note: *If the machine is commissioned so that "Use maximum gantry angle speed or maximum dose rate for each control point" is true, then the Maximum delivery time (Max del. Time) cannot be specified by the user.*

  If the VMAT treatment machine is commissioned for burst mode (mArc) an additional column, Beam on interval, is presented in tab for VMAT.
- **The tab for Conformal Arc** contains columns for Number, Name, Exclude and Segment MU.
- **The tab for TomoHelical** contains columns for Number, Name, Jaw mode, Field width, Pitch factor, Delivery time factor (Apply and Max), Delivery time (Apply and Max) and Gantry period (Apply and Max).

The beam optimization variables

The table below describes the beam optimization variables.

Optimization variables	Subject to optimization
Segment shapes	The shape of the segments
Segment MU	The MU of the segments
Beam MU	The MU of the beam
Gantry	The gantry angle of the beam
Collimator	The collimator angle of the beam
Couch	The couch angle of the beam
Wedge	The angle of the wedge (if wedges are supported)

Note: *It is possible to optimize wedge angle for the following wedge types: Siemens virtual, Varian enhanced dynamic and Elekta motorized. Optimization of standard wedges is not supported.*

Supported variable combinations for SMLC

The table below lists supported combinations of optimization variables for SMLC.

Optimization variables	Description
Segment shapes and **Segment MU**	This is the only combination of variables that can be selected for beams without segments. It can also be used for beams that have segments.
Segment MU	This option can be selected for beams that have segments. Before the actual optimization starts, a clinical dose is computed for all segments using the CC dose engine.
Beam MU	This option can be selected for beams that have segments. The beams are required to have a clinical dose before the optimization is started.

Supported variable combinations for DMLC

It is not possible to select the variables that are optimized for DMLC.

Supported variable combinations for 3D-CRT

The table below lists supported combinations of optimization variables for 3D-CRT.

Optimization variables	Description
Segment shapes, **Segment MU** and any combination of the variables **Gantry**, **Collimator**, **Couch** and **Wedge**	These combinations of variables are supported irrespective if segments exist or not.
Segment MU	This option can only be selected for beams that have segments.

Supported variable combinations for VMAT

The table below lists supported combinations of optimization variables for VMAT.

Optimization variables	Description
Segment shapes and **Segment MU**	This is the only combination of variables that can be selected for beams without segments. It can also be used for beams that have segments.
Segment MU	This option can be selected for beams that have segments. Before the actual optimization starts, a clinical dose is computed for all segments using the collapsed cone dose engine.

Supported variable combinations for Conformal Arc

The table below lists supported combinations of optimization variables for Conformal Arc.

Optimization variables	Description
Segment MU	This is the only option for Conformal Arc. The segments are created using the Treat feature in the 3D-CRT Beam Design module, see *section 6.3.6 Specify settings in the Treat and Protect tab on page 437*.

Beam optimization settings for TomoHelical

Beam optimization settings	Description
Jaw mode	This setting determines if the jaws are allowed to move or not. In **Fixed** mode the jaws are not allowed to move. In **Dynamic** mode the jaws are allowed to move.
Field width	The longitudinal distance thickness of the treatment field at the machine isocenter.
Pitch factor	Each gantry rotation, the couch moves a distance which is the **Field width** times the **Pitch factor**.

Beam optimization settings	Description
Delivery time factor	The delivery time will be limited by the shortest possible delivery time multiplied by this factor. Check the **Apply** checkbox to enter a value for this setting.
Delivery time [sec]	An upper limit for the delivery time. Check the **Apply** checkbox to enter a value for this setting.
Gantry period [sec]	An upper limit for the gantry period. Check the **Apply** checkbox to enter a value for this setting.

Other beam optimization settings

The table below describes other beam optimization settings.

Beam optimization settings	Description
Exclude	A beam containing segments can be excluded from the optimization. By default all beams are included. Beams that are excluded from the optimization are not affected by the optimization, but the dose is a part of the beam set dose.
Split if necessary	Supported for SMLC and DMLC only. If the machine has a carriage and the jaw assignment is not set to 'Lock to limits', the beam is split during optimization if the target is too wide for the treatment machine to avoid open leaves in the field. A beam created during split will inherit its angles, isocenter and SSD from the original beam. Split beams are removed when the optimization is reset.
Jaw assignment and Jaw limits	Supported for SMLC, DMLC and VMAT if the treatment machine has non-fixed jaws. There are three different modes: • **Automatic**: after the optimization the jaws are positioned as close as possible to the openings formed by the leaf pairs, either per beam or per segment. • **Use limits as max**: the jaw limits will serve as an outer limit for the jaw positions. The system will thus try to position the jaws closer to the openings formed by the leaf pairs if possible, but the jaws will never be positioned outside the limits. • **Lock to limits**: only supported for machines that are set up to position jaws 'per-beam'. Here the jaws will be locked to the entered limits.

Beam optimization settings	Description
Create dual arcs	A second arc beam moving in the opposite direction to the original arc beam will be created during optimization. Using the dual arc feature generally improves plan quality. The second arc beam is removed when the optimization is reset.
Gantry spacing	The spacing between the arc control points.
Beam on interval (only applicable for burst mode)	A burst mode arc consists of a sequence of 'beam on' and 'beam off' intervals. Leaves are only moved in the beam off intervals. The length of the beam on interval is defined by the **Beam on interval** parameter. The total length of one beam on and one beam off interval is defined by the **Gantry spacing** parameter.
Max del. time	The maximum delivery time for VMAT optimization is a soft upper limit on the delivery time, which means that the limit may be violated at the end of an optimization in favor of plan quality. The value may also be overridden in case it violates machine constraints.
Limit MU	Supported for VMAT only. The parameter **Max MU/fx** is a soft upper limit on the MU for the arc beam, that is, the value can be violated at the end of the optimization in favor of plan quality. If a too low value is chosen, the plan quality will be poor. It is possible to use this function both before starting and continuing an optimization. However, it is difficult to set a reasonable limit before an optimization has been run. When the **Apply** checkbox is checked, the current MU will be selected by default. This value can then be modified by the user. Note that the actual value of MU/fx after an optimization is displayed in the **Beams** list.

7.1.10 Treat

The treat workflow is only supported for the VMAT, SMLC, and DMLC treatment techniques. When a new plan is created the **Treat** tab contains no ROIs. To populate the **Treat** tab with ROIs, click the **Select ROI** button. This opens the **Select ROI** dialog where it is possible to select which ROIs to use for planning. Only ROIs with organ type Target can be selected. To remove an ROI from the **Treat** tab, click the 'x' symbol beside the ROI name.

The **Treat** tab exists in the following modules: Plan Optimization, Multi-Criteria Optimization and Adaptive Replanning.

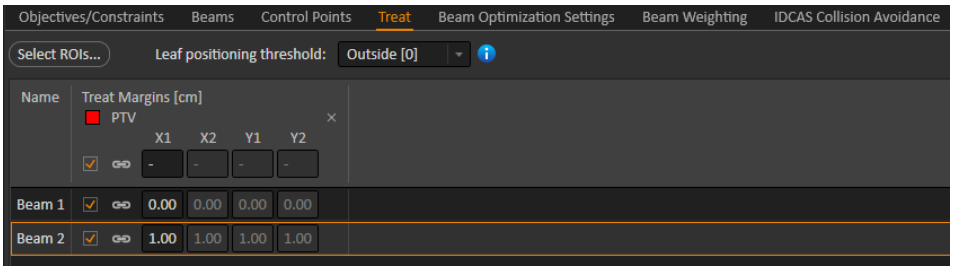


Figure 297. The **Treat** tab in the Plan Optimization module.

For each **Treat** ROI it is possible to select whether the ROI should be treated by a given beam.

For each ROI in each beam, it is possible to select **Margins** in the X1, X2, Y1, and Y2 directions. For further information, see *Margins used when conforming to Treat and Protect ROIs on page 438*.

It is also possible to set the boundary on how a leaf shall be positioned in relation the ROI plus margin projections using the Leaf positioning threshold, see *Leaf positioning threshold on page 415*.

Optimization can only be started if there are dose objectives of type Min Dose, Min DVH, Uniform Dose, Min EUD or Target EUD for all ROIs that are selected for treat. The optimization will aim to achieve MLC leaf positions that are within the target projections of the selected ROIs combined with the specified margins. If no ROI is selected, the optimization will use its usual leaf position bounds, which is the target projection of all target ROIs with a margin.

After optimization, when segments have been created, it is not possible to modify the treat settings. The optimization first needs to be reset.

7.1.11 Protect

The protect workflow is only supported for the TomoHelical treatment technique. When a new plan is created the **Protect** tab contains no ROIs. To populate the **Protect** tab with ROIs, click the **Select ROI** button. This opens the **Select ROI** dialog where it is possible to select which ROIs to use for planning. Only ROIs with different organ type than the target organ type can be selected. To remove an ROI from the **Protect** tab, click the 'x' symbol beside the ROI name.

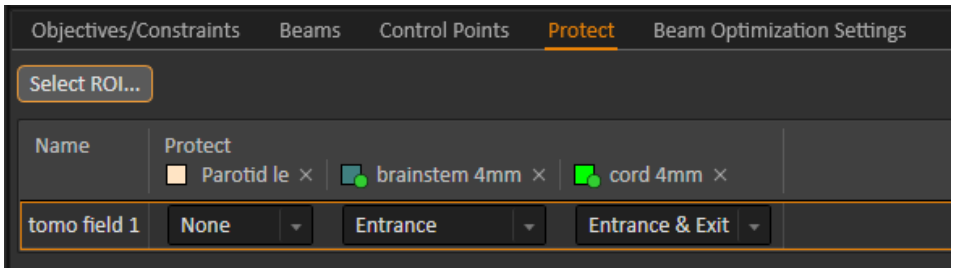


Figure 298. The **Protect** tab in the Plan Optimization module.

The **Protect** tab exists in the following modules: Plan Optimization, Multi-Criteria Optimization and Adaptive Replanning.

The table below describes the different protect modes that can be set for each ROI in the **Protect** tab.

Protect mode	Description
None	no protection
Entrance	protection against entrance radiation
Entrance & Exit	protection against entrance and exit radiation

After optimization, when segments have been created, it is not possible to modify the protect settings. The optimization first needs to be reset.

Note: *After optimization, the user is recommended to study the segments in the BEV to verify that the protection of the ROIs is sufficient.*

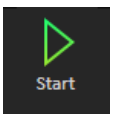
7.1.12 Running the optimization

The optimization process is controlled by the optimization control buttons in the toolbar.

Note: *The optimization control buttons (Start, Continue, Reset and Reduce OAR dose) will only operate on the beams included in the optimization. Beams that are set as 'Excluded' in the Beam optimization settings tab will not be affected.*

Note: *For co-optimized beam sets, the optimization control buttons will affect both beam sets.*

The optimization control buttons

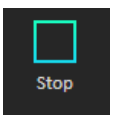


The **Start** button starts a new optimization. Only active if the beams are empty (no control points, wedges or blocks).

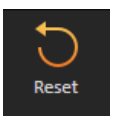
The **Continue** button starts an optimization from the current state. The optimization will continue using the user-defined optimization functions. Only active if there is at least one control point in every beam.

Note: *If there is a wedge but no control point, the Start button and the Continue button are disabled. In order to start with a specified wedge angle, a segment must be created in the 3D-CRT Beam Design module. This enables the Continue button.*

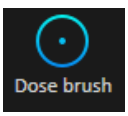
Note: *If the irradiated volume after an optimization is too small or too large, the target volume (as defined through the optimization functions) may need to be modified. After such a modification, it is strongly advised to reset and start a new optimization instead of continuing.*



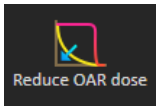
The **Stop** button stops the optimization after the current iteration is finished.



The **Reset** button resets the beams, i.e. removes all control points, blocks and wedges, sets all beam MUs to zero and removes all beams created by the optimization through beam splits or dual arcs.



Use the dose brush tool in a 2D view to modify the dose distribution within the dose brush sphere. Hold down left mouse button and drag up or down to increase or decrease dose. The magnitude depends on the distance that the mouse is moved.
The optimization starts when the mouse button is released. Click **Stop** to exit the tool, or **Cancel** to ignore the dose brush result. The size of the sphere is adjusted using Alt + mouse wheel.



The **Reduce OAR dose** button starts an optimization from the current state. Auto-generated reference dose functions are used to reduce the dose in the risk organs (OARs), while maintaining dose homogeneity in the target organs. Only active if there is at least one control point in every beam. If the current beam set already has minimal OAR dose, this function will not have any significant effect.

Optimization Progress

The lower right window of the workspace shows the result of the optimization progress. A graph plots the values of the objective functions as a function of the number of iterations. All values are plotted separately but also the sum of the objectives (bold white line) which the optimization tries to minimize. The objective function curves are colored in the same color as the corresponding ROIs.

When using the Reduce OAR dose function, the displayed objective functions are those specfied by the user, not the auto-generated ones.

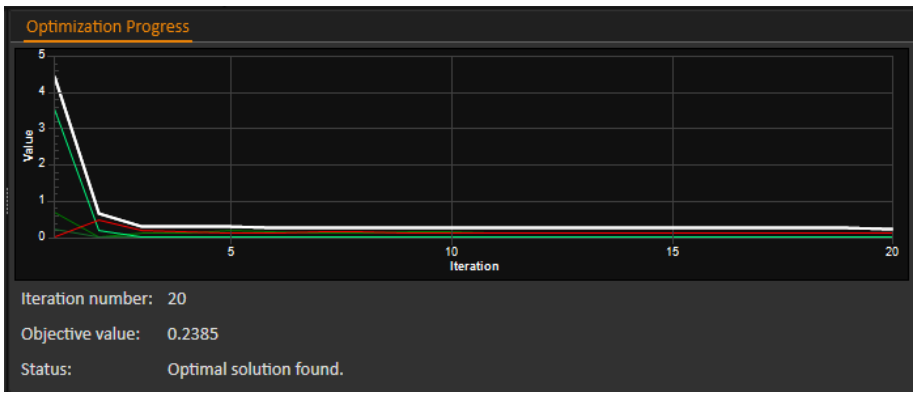


Figure 299. The Optimization progress graph.

7.1.13 Evaluating fluence in Beam's Eye View (BEV)

The **BEV** can be used to inspect fluence (only for non-VMAT/Conformal Arc photon plans) and individual beam segments. Use the pie chart in the upper left corner to navigate among the beams and beam segments. For more information, see *Navigation options on page 103*. The current beam and segment can also be selected in the **Beams** list and **Control points** list respectively.

Edit beam angles in BEV

As in the Plan Setup module the user can edit beam angles (gantry, collimator and couch angles) visually in the BEV. These tools are activated from the BEV context menu. For more information, see *section 6.2.6 Edit beam properties on page 402* and *Edit beam angles in patient views on page 327*.

Editing beam angles invalidates the dose and requires re-computation of the dose distribution.

Retract MLC

Right-click in the BEV to open the context menu and select **Retract MLC**.

Evaluating Leaf Open Times in BEV

The leaf open times are visualized using transparency, where complete transparency represents an opening time of 100% per projection, and completely opaque an opening time of 0% respectively. This representation is disabled if the user starts the **Beam animation**, and is instead animated using the actual leaf open times, opening and closing the leaves according to the values presented in the **Control points** list.

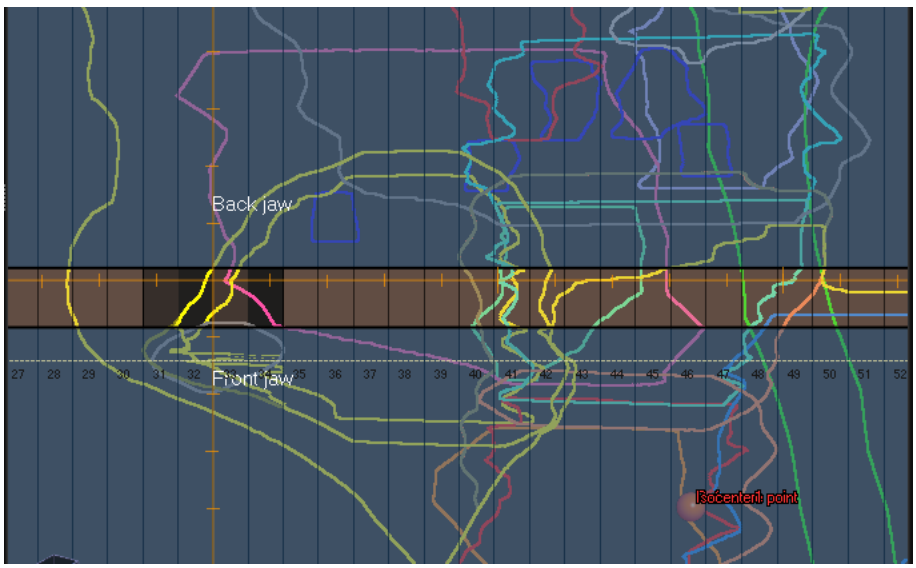


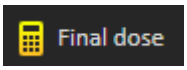
Figure 300. Leaf open times visualized in the BEV.

7.1.14 Define or modify prescription

For instructions on how to to define or modify a dose prescription, see *section 6.1.12 Define or modify prescription on page 343*.

7.1.15 Compute dose

Click the **Final dose** button in the toolbar or type Ctrl + D to compute the dose using the clinical dose engine of the current treatment modality.



Note: *If there already is a valid clinical dose, it will not be recomputed.*

When the computation is completed, the dose will show up in the patient views. Click **Cancel** to abort a started dose computation.

The dose engine is described in detail in *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual*.

WARNING!

Dose computation region. Radiation transport and dose is computed only inside a region consisting of ROIs of type External, Bolus for beam, Support and Fixation. Image data not included in this region will be omitted from dose computation and is regarded as a vacuum (no interactions).

If the beam Field Of View covers part of the patient not inside the External ROI or any equipment not defined by Bolus, Support or Fixation ROIs, the dose computation will be incorrect.

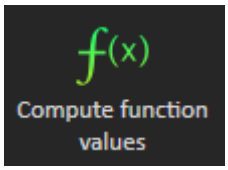
Note also that the computation is limited to the dose grid. There is no warning if the dose grid does not cover the appropriate region. (7285)

WARNING!

Approximate dose is only intended for intermediate treatment planning steps. Approximate dose has lower accuracy compared to the dose displayed as "Clinical" and it must not be used for clinical decisions. A plan with approximate dose cannot be approved or exported. (126034)

7.1.16 Compute function values

If an optimization function is altered after an optimization is run the value for the changed function can be updated by clicking the **Compute function values** button in the toolbar.



7.1.17 Edit segment shapes

Click the **Edit MLC and jaws** button.

This opens the Edit MLC and jaws dialog which provides tools to manually edit the segment shape.

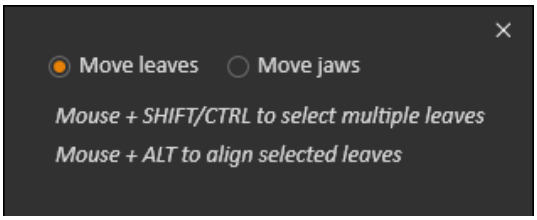


Figure 301. The Edit MLC and jaws dialog in the Plan Optimization module.

- Use the **Move leaves** tool to manually pull the leaves to a desired position. Left-click and press SHIFT/CTRL to select multiple leaves. Left-click and press ALT to align the selected leaves.
- Use the **Move jaws** tool to manually pull the jaws in the BEV to desired positions. Click with the mouse on the (blue) jaw to move it.

Note: *Although it is possible to manually move a jaw and thereby collimate using the jaws also inside a field, this is not advisable. E.g., for an Elekta machine where the x-jaw is relatively thin compared with an MLC leaf, the jaw collimation will not be very effective.*

7.1.18 The evaluation views

Dose Volume Histogram (DVH)

The DVH view presents the cumulative dose volume histograms of the ROIs selected in the ROI List. The dose can be displayed as **absolute** or **relative [%]**. It is also possible to manually set the reference value for the relative scale. For a further description of the DVH view, see *section 3.7.1 Dose Volume Histogram (DVH) on page 78*.

Dose statistics

The dose statistics view lists ROI dose information. For more information, see *section 3.7.2 Dose statistics table on page 79*.

Dose difference

The dose difference view displays the dose difference between two treatment plans. See *The Dose difference view on page 75* for more information.

Clinical goals

The clinical goals functionality makes it possible to define evaluation criteria for specific ROIs and POIs. The result (pass/fail) is easy-to-read in a single column. For more information about the clinical goals functionality, see *section 3.7.3 Clinical goals on page 81*.

Note: *The clinical goals will not affect the optimization.*

7.1.19 Multiple beam set optimization

Multiple beam set planning and how to create beam set dependencies are described in detail in *section 6.1.20 Multiple beam set planning on page 372*. This section describes optimization of multiple beam sets.

Independent beam sets

For independent beam sets the objectives/constraints always apply to the beam set dose. This means that, if the additional beam set is set as independent, the optimization will be carried out looking only at the dose of the separate beam set.

Dependent beam sets

For multiple beam sets that have a dependency, they can either have a background dose dependency or a co-optimized dose dependency.

When having dependent beam sets, the objectives/constraints can be defined to either relate to the separate beam set dose, or to the combined beam set + background dose (background dose dependency), or to the combined dose of the two co-optimized beam sets (co-optimized dose dependency).

Background dose dependency

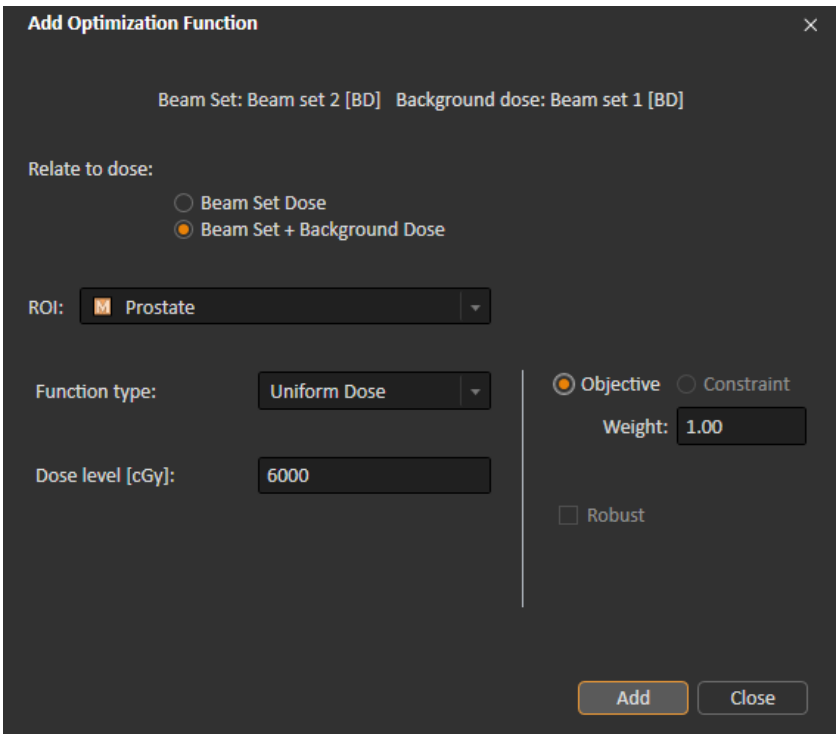


Figure 302. The Add Optimization Function dialog where the objective function is defined to relate to the beam set + background dose.

If the objective is set to relate to the beam set + background dose, the selected beam set will try to create whatever dose is needed to reach the specified objectives/constraint for the combined dose from this beam set and the background dose that this beam set is dependent on. The background dose for a dependent beam set is the dose from the beam set it is dependent on plus, if applicable, the background dose for that beam set. For an adapted plan, the background dose also includes delivered dose. For instance, if the background beam set has an underdosage of a corner of the target, the other beam set will try to create a higher dose in that area in order to compensate and achieve a homogenous beam set + background dose. There has to be a computed dose for the background beam set before the other dependent beam set can be optimized.

It is possible to define a composite objective function consisting of some objectives that relate to the beam set + background dose and other objectives that relate to the beam set dose.

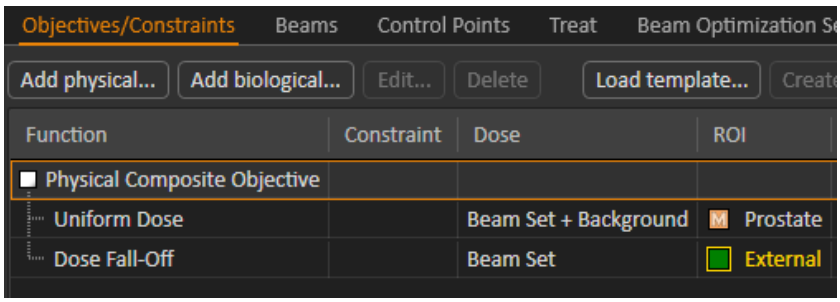


Figure 303. In the Dose column in the Objectives/Constraints tab it is possible to see if an objective/constraint relates to the beam set + background dose or only the beam set dose.

Note: *If the objectives/constraints for the dependent beam set applies to the beam set + background dose, the requested dose level must be reasonably higher than the background dose.*

Note: *Making the additional beam set dependent or independent will clear all existing prescriptions and objectives/constraints, since the dose levels will no longer be relevant.*

When planning with dependent beam sets, the DVHs will include checkboxes for dose presentation to allow simultaneous studying of the different planning doses. The dose presentation buttons are described further in *Dose presentation for multiple beam sets on page 374*.

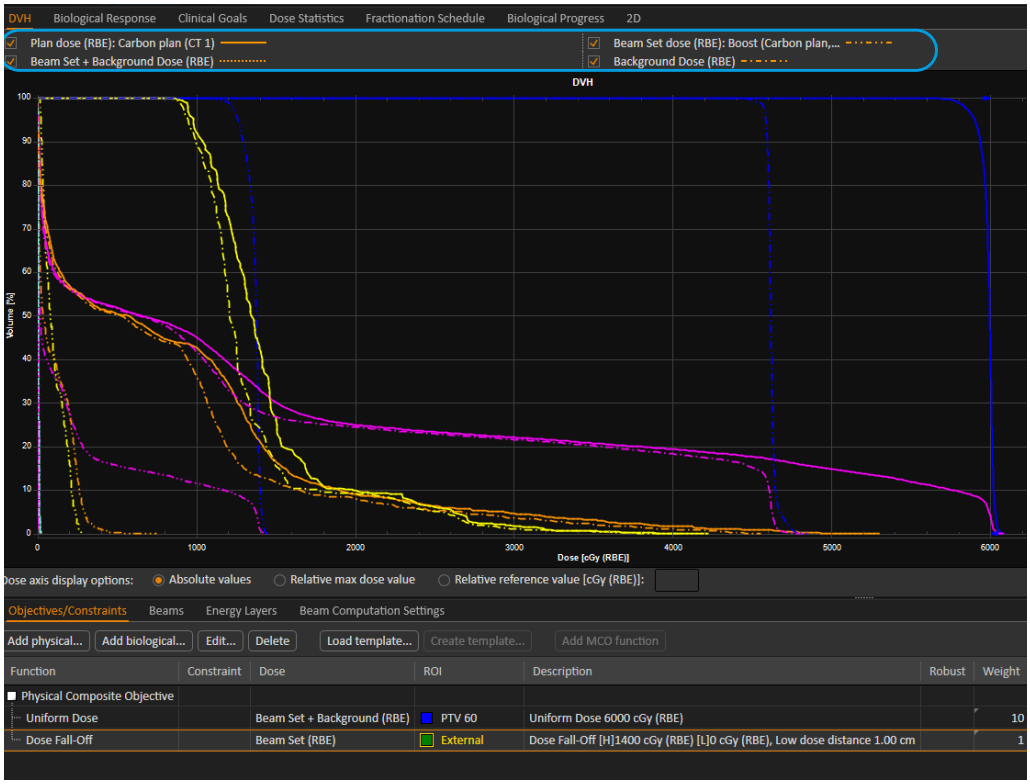


Figure 304. In the DVH view it is possible to study plan dose, beam set dose, beam set + background dose and background dose by checking the corresponding checkbox.

Co-optimized dose dependency

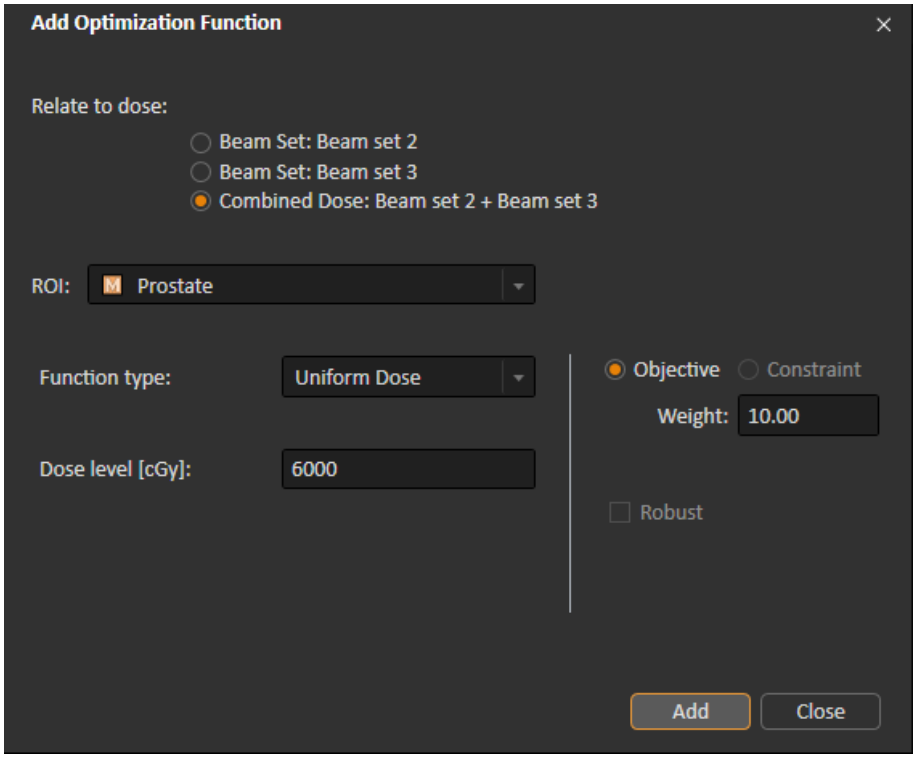


Figure 305. The Add Optimization Function dialog where the objective function is defined to relate to the combined dose for both co-optimized beam sets.

If the objective is set to relate to the combined dose, the optimization problem will try to distribute the dose given by this objective to the two beam sets according to their respectively defined beam set objectives. For instance, if the combined dose objective is to have 6000 cGy uniformly in the PTV, and for beam set 1 an objective is to spare a risk organ to the right of the PTV, then the dose to the PTV in beam set 1 will most likely contribute to the left side of the PTV.

Combined dose = Dose for beam set 1 + Dose for beam set 2

It is possible to define a composite objective function consisting of some objectives that relate to the combined dose and other objectives that relate to the individual beam set doses.

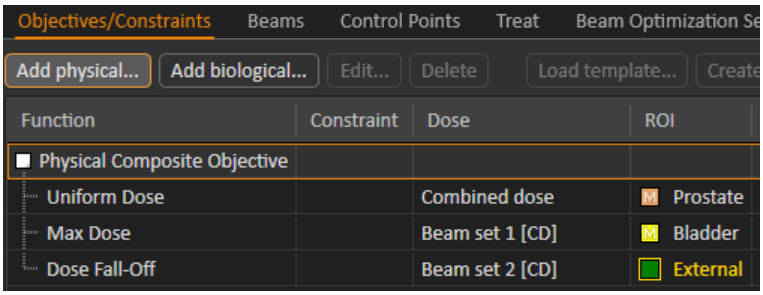


Figure 306. In the Dose column in the Objectives/Constraints tab it is possible to see if an objective/constraint relates to the combined dose for both co-optimized beam sets or only an individual beam set dose.

Note: *Changing the co-optimized dose dependency will clear all existing prescriptions and objectives/constraints for the involved beam sets, since the dose levels will no longer be relevant.*

When planning with dependent beam sets, the DVHs will include checkboxes for dose presentation to allow simultaneous studying of the different planning doses. The dose presentation buttons are described further in *Dose presentation for multiple beam sets on page 374*.

Figure 307. In the DVH view it is possible to study plan dose, combined dose and the individual beam set doses for the co-optimized beam sets by checking the corresponding checkbox.

Note: *If the combined dose is equal to the plan dose (e.g., when only two beam sets exist with co-optimized dose dependency), then the combined dose will be omitted in the DVH.*

7.1.20 Wave arc

For a machine that is set up to support variable couch angles (dynamic wave arcs) in RayPhysics, it is possible to define a VMAT beam based on a wave arc template. When VMAT is selected as treatment technique, a **Wave arcs** checkbox will be available in the Add beam dialog. If that checkbox is checked, the arc beam is defined by selecting a wave arc template from a number of predefined templates. It is also possible to reverse the template.

If the beam set contains at least one wave arc beam, there will be a **Wave Arc** tab. In the **Wave Arc** tab it is possible to perform the same operations as in the **Add beam** dialog, namely to load and to reverse a template. It is also possible to edit a wave arc and to save it as a new template. Wave arc templates may be renamed or deleted.

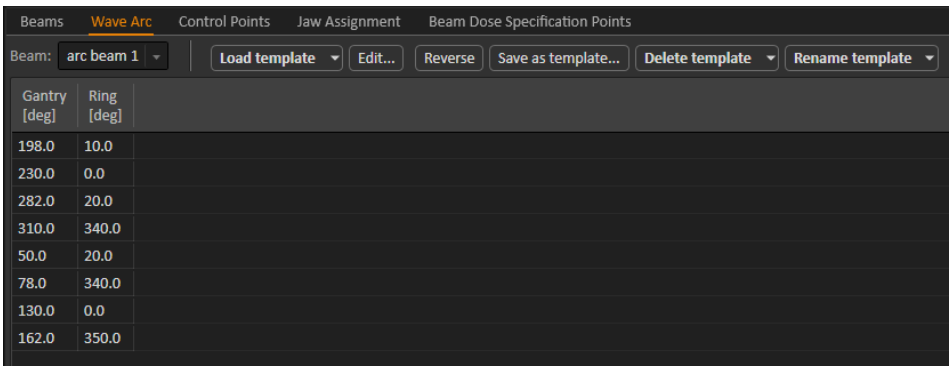


Figure 308. The Wave Arc tab.

In RayStation 7 there are several predefined wave arc templates. A wave arc template is defined as a set of pairs of gantry and ring angle values. The first pair defines the starting point of the trajectory and the last pair defines the end point. In between there are a number of turning points.

When the edit button is pressed, the **Edit Wave Arc Trajectory** dialog is opened where the gantry and ring angle values can be edited and new turning points can be inserted or deleted. When the Apply or OK button is pressed, the wave arc is updated and the feasibility is tested. If the wave arc is in conflict with any machine constraint, the user is informed and the wave arc is not accepted. The shape of the wave arc can be studied in the 3D window.

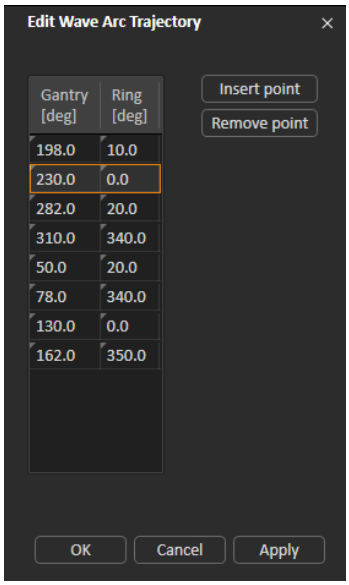


Figure 309. The **Edit Wave Arc Trajectory** dialog

In the GUI, the term ring is used instead of couch if the flag "Replace couch rotation by ring rotation" has been set in RayPhysics.

Note: *After a wave arc template has been selected, it is important to study the wave arc trajectory in the 3D view and deduce if the template is a reasonable choice. In particular, make sure that the arc will not fail the beam entry validation,* *section 6.1.13 Beam entry validation on page 349.*

7.2 THE PLAN OPTIMIZATION MODULE - PROTONS

This section describes how to generate optimized proton plans for the treatment techniques Pencil Beam Scanning (PBS) and Line Scanning (LS) in the Plan Optimization module through optimization with respect to user-defined treatment objectives and constraints. The result for a PBS plan is a hexagonal spot position pattern with optimized spot weights. The result for a Line Scanning plan is a contiguous line pattern in a regular Cartesian grid with optimized line weights.

In this section, the term proton PBS includes both step-and-shoot PBS and quasi-discrete PBS.

In this section

This section contains the following sub-sections:

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7.2.3	Beam list	p. 576
7.2.4	Treat and Protect tab	p. 577
7.2.5	Beam Computation Settings	p. 578
7.2.6	MLC settings	p. 582
7.2.7	Specify optimization settings	p. 583
7.2.8	Running the proton PBS and Line Scanning optimization	p. 589
7.2.9	Energy layers	p. 591
7.2.10	Spot editing	p. 594
7.2.11	Bragg peak visualization	p. 599
7.2.12	Blocks	p. 601
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7.2.14	Define or modify prescription	p. 603
7.2.15	Dose computation options	p. 604
7.2.16	Compute function values	p. 607
7.2.17	The evaluation views	p. 608
7.2.18	Evaluation of proton PBS and Line Scanning plans	p. 609

Precautions

WARNING!

Accuracy of Pencil Beam dose engine for proton PBS and Line Scanning beams with range shifters. In the RayStation 7 PBS Pencil Beam dose engine validation, a few deviations from the dose accuracy requirements were noted for doses in water, especially at shallow depth, when a range shifter with a relatively large air gap was used. These deviations have been linked to the handling of secondary proton transport over the air gap, resulting mainly in an overestimation of the dose in the surface region, but the spot to sub-spot discretization may also contribute to the dose error when spots at the patient surface become very large.

The user shall be aware of these limitations in the pencil beam dose engine. It is strongly recommended to use the RayStation Monte-Carlo dose engine for computation of final dose for any beam including a range shifter. (369527)

WARNING!

Scanned field size limitations for Proton PBS PB dose engine. The PBS Pencil Beam dose engine validation of RayStation 7 only covers scanned field sizes down to 4 x 4 cm^2. Be extra careful when creating PBS and Line Scanning plans with scanned field sizes smaller than 4 x 4 cm^2. (369529)

WARNING!

Sub-spot limitations for Proton PBS PB dose engine. In the RayStation PBS pencil beam dose calculation, the Gaussian spot fluence is discretized into 19 sub-spots. This is done to minimize the errors introduced by the inherent infinite slab approximation of the pencil beam algorithm. The choice of 19 is a compromise between the accurate representation of the initial Gaussian fluence and the sufficiently course sampling of the patient geometry for typical spot sizes on the one hand, and the calculation speed on the other. The user should be aware about two consequences of the sub-spot discretization:

1. Rapid wiggles may appear in the dose distribution. This problem has mainly been observed for beams employing a range shifter, where the wiggles are especially prolific in the entrance region, but may extend also deeper into the patient. The wiggles have also been observed for beams without a range shifter, but then mostly for plans with the spots organized in a regular pattern rather than the hexagonal pattern, which is default in RayStation. This numerical artifact can potentially have a degrading effect on plans created in RayStation, but is likely more important in the QA process where measured and calculated doses in single points are compared. If comparison is performed at a point where the dose wiggles have a significant amplitude, a false negative, or positive result could be achieved.
2. The distance between the sub-spots is ~0.85 times the spot size. For a 5 mm spot, this translates to a sub-spot distance of ~4 mm. For very large spots, it may be that the distance between the sub spots becomes larger than some geometrical variations of the patient. This could for example be the case when a range shifter with a large air gap is used in combination with low beam energies.

Refer to *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual* for more details.

The user shall be aware of this limitation in the PBS dose calculation and it is strongly recommended to use the RayStation Monte-Carlo dose engine for computation of final dose for any beam including a range shifter. (369528)

WARNING!

Quasi-discrete spill dose is not computed in RayStation. A quasi-discrete PBS plan is computed as a step-and-shoot PBS plan and the spill dose between spots will not be considered. The dose difference between the computed plan and the delivered plan needs to be assessed by the user in the commissioning of RayStation as well as during patient specific QA. (123711)

WARNING!

Ensure that spot selection rules will result in an appropriate dose distribution. The choices in the Beam Computation Settings tab (spot pattern, target margin, OAR range margin, minimum radiological depth, and distal edge margin) will influence the number of spots (or line segments for Line Scanning) in the plan and where they are positioned. The user needs to ensure that the resulting spot pattern gives a dose that corresponds to the goals of the treatment. (370108)

WARNING!

CT to density calibration for proton and carbon ion plans. In RayStation, the same CT to mass density calibration curve is used for proton and carbon ion dose calculations as for photon dose calculations. Note that the requirement on a correct CT calibration is considerably higher for proton and carbon ion dose calculations than for photon dose calculations. CT calibration validated for photon or electron use may not be sufficient for ion dose calculation. (371600)

WARNING!

Physical/effective dose for protons. Be careful when mixing proton beam sets with other modalities. The prescription dose for protons relates to the physical dose, i.e., the biological effectiveness has not been taken into account. This can be handled either by including the RBE scaling factor in the proton beam model or by taking this fact into account when setting dose levels when mixing with doses of other modalities. (371601)

WARNING!

Line Scanning: Recompute dose after changing number of paintings using scripting. If the number of paintings for each segment is changed using scripting for a Line Scanning plan, there might be a slight mismatch between the planned and delivered dose. The reason for this is that the dose is not invalidated when changing the number of paintings. However, it will affect the MU rounding in the Sumitomo treatment Control system. To correctly account for this, the dose should be invalidated by the user (e.g., by changing the dose grid to a new value and then changing it back to the previous value) and then recomputed. (150000)

WARNING!

Dose grid effects for ion PBS plans. The proton and carbon Pencil Beam dose engines in RayStation calculates the average dose to a voxel along the Integrated depth dose (IDD) and the dose to the center point of each voxel laterally and lets this dose value represent the dose in the entire voxel, while the RayStation Monte Carlo dose engine calculates the average dose deposited to a voxel. This means that any variation in dose that occurs on a resolution that is finer than that of the current dose grid may be lost in the dose calculation. The user has the responsibility to choose a dose grid resolution that is suitable for each plan, however, for low energy proton fields, and carbon ion fields without a ripple filter, the Bragg peak may be so sharp that even the highest dose grid resolution in RayStation (1 mm) is insufficient to resolve the Bragg peak, leading to a systematic underestimation of the maximum delivered dose.

Be aware of this limitation in the dose calculation. To determine if the potential loss of dose is on a significant level, be extra careful in the patient specific QA process. (261660)

WARNING!

Too high spot weights outside block and MLC aperture contour. Be aware that too high spot weights outside the aperture contour could lead to mistreatment if the aperture is misaligned in the machine or if the aperture is unintentionally left out during treatment. (252691)

WARNING!

Robust optimization in combination with PBS block and MLC apertures. If robust optimization is used in combination with a aperture for proton PBS plans, make sure that the margins for the aperture are large enough so that the resulting plan is robust. (252705)

WARNING!

Field size limitations for Proton PBS MC dose engine. The Monte Carlo PBS dose engine validation of RayStation 7 only covers the following setups related to field size:

- Scanned field sizes down to 4 x 4 cm^2.
- MLC aperture openings down to 2 x 2 cm^2
- Block aperture openings down to 4 x 4 cm^2

Be extra careful when creating PBS and Line Scanning plans with scanned field sizes or aperture openings smaller than the setups covered in the dose engine validation. (369532)

WARNING!

Mevion Spot Map Converter (SMC) is used for Mevion Hyperscan. During final dose computation with the Ion Monte Carlo dose engine, beam data such as energy layer details, spot positions, spot MU, number of paintings and collimator contour is passed through the Mevion Spot Map Converter (SMC) which optimizes spot delivery and individual pulse collimation. The output from the SMC is then used during dose computation in order to include the actual positions of the collimator leaves for each spot. This may result in unexpected difference between the optimized non-clinical dose and the final clinical dose.

Refer to *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual* for more details. (369117)

WARNING!

The effect of the infinite slab approximation in the PB dose engine on proton PBS/Line Scanning. The proton PBS/Line Scanning Pencil Beam dose engine is based on the so-called infinite slab approximation. This approximation disregards lateral inhomogeneities for individual ray traces, which will see the patient as a stack of semi-infinite layers. The effect of this approximation is more severe for patients with large lateral inhomogeneities, especially closer to the target area. This situation is common for many lung cases, but other treatment sites may also be affected. For lung cases with range shifters, dose to tumors in lung tissue has been shown to be overestimated by up to 10% in the PTV center, with significant loss of target coverage even after dose rescaling.

Be aware that the dose computation may not be accurate for patients with large lateral inhomogeneities relative the beam direction. It is strongly recommended to use the RayStation Monte Carlo dose engine for computation of final dose for any patient where the beam will see large lateral inhomogeneities. (369533)

Note: *The proton and carbon ion PBS module in RayStation includes the possibility to set the minimum and maximum spot weight limits in the Optimization settings (default values are set in the beam model). It is the responsibility of the user to ensure that the PBS plan produced in RayStation is deliverable with respect to these parameters. The filtering of low and high weight spots is performed after a user defined number of iterations. Spot sorting and creation of islands with beam off (for quasi-discrete scanning) is performed in conjunction with spot filtering, or if the optimization is stopped before the spot filtering iteration number. Note that no filtering is performed if the optimization is stopped before the spot filtering iteration number.*

7.2.1 The Plan Optimization user interface

Workspace

The top left corner shows the result of the optimization process for each visualized ROI in a dose volume histogram (DVH). Behind the DVH are tabs for dose statistics as well as for review of clinical goals.

The bottom view defaults to the **Objectives/constraints** tab – listing the user specified objectives and constraints, with buttons for adding, editing and deleting of such functions. There are also tabs for the beam list, the energy layers, beam computation settings and MLC positions (for machines with MLC).

The lower right corner, visualizes the **Optimization Progress** in terms of function values per iteration.

The window at the top right corner shows image set data for the current plan in **2D**, **3D** or Beam's Eye View (**BEV**).

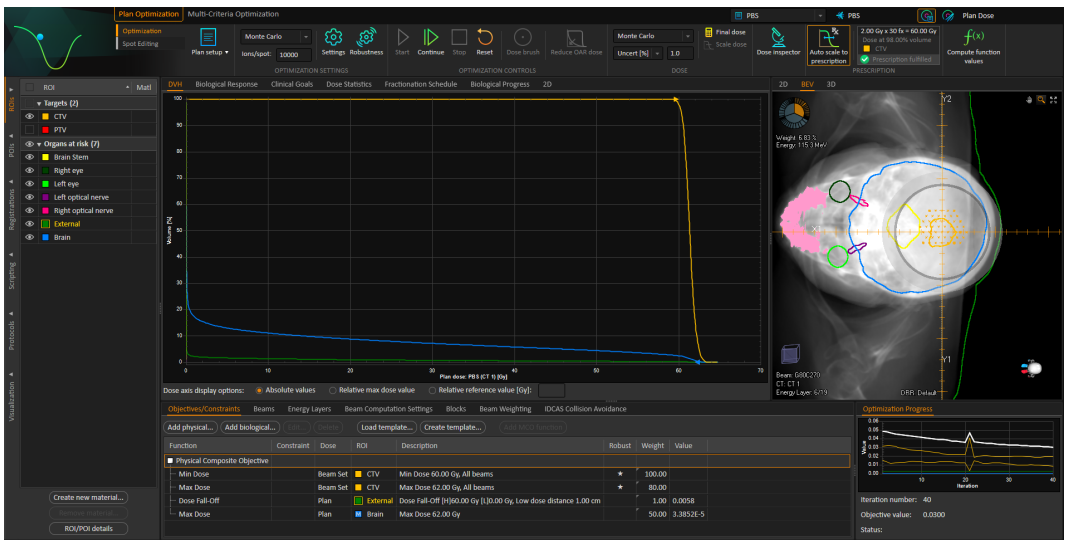


Figure 310. The Plan optimization workspace for proton PBS.

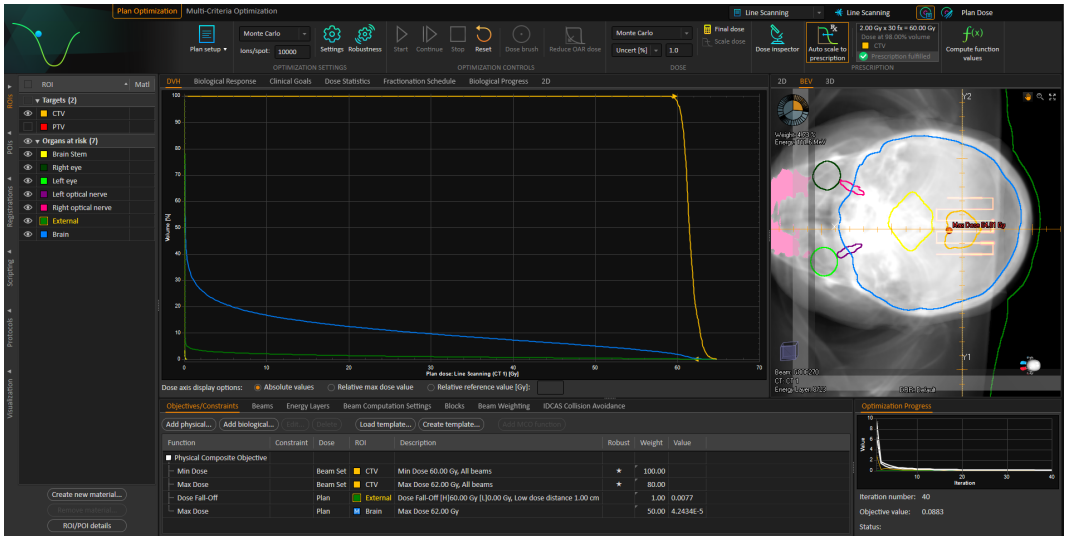


Figure 311. The Plan optimization workspace for Line Scanning.

7.2.2 Objectives and constraints

The available optimization functions and how to add them to the optimization problem are described in *section 7.1.3 Optimization functions – objectives and constraints on page 524*. Optimization functions can also be loaded from templates, see *section 7.1.4 Optimization function list templates on page 529* for more information.

Note: *The MLC and Treat and Protect tabs are visible for machines with MLC. The Blocks tab is visible for machines with block.*

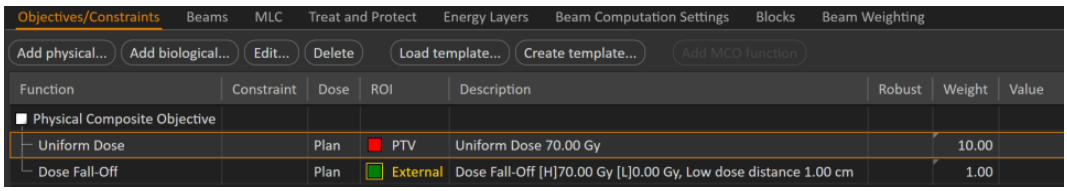


Figure 312. The objectives and constraints tab.

Beam specific objectives

An objective function or constraint does normally relate to the total dose of the beam set. However, it is also possible to let an objective relate to the dose of a selected beam. If a beam has been assigned to one beam specific target objective/constraint, the target projection in the spot selection, prior to the optimization, will only cover the ROI of that beam specific objective. If an additional target volume is covered by that beam, a beam specific target objective/constraint must also be defined for that volume. This is useful for example when working with single field uniform dose or patch plans.

To restrict the optimization function to a selected beam, check the **Restrict function to beam** checkbox in the **Add Optimization Function** dialog and select the desired beam in the drop-down list.

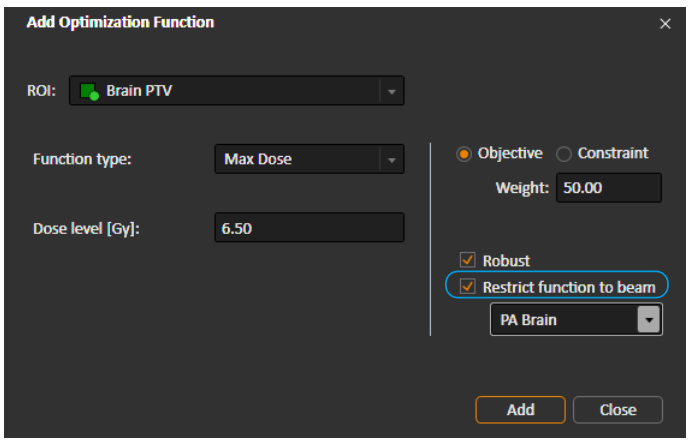


Figure 313. The **Add Optimization Function** dialog where the **Restrict function to beam** option has been selected.

In addition to selecting individual beams in the **Restrict function to beam** drop-down list, it is also possible to select **All beams individually**. With this option, one beam specific objective per beam is created automatically, with the dose values set to the given dose values divided by the number of beams.

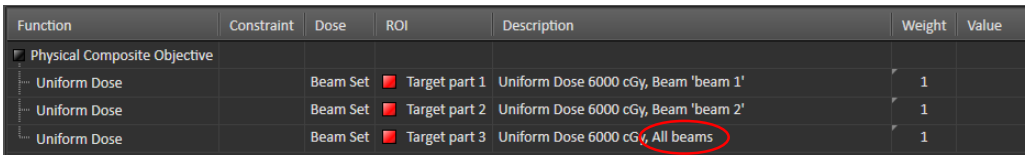


Figure 314. The Objectives/Constraints tab where the optimization function has been set to operate on all beams individually.

7.2.3 Beam list

The **Beams** tab contains the beam list and includes columns for **Isocenter**, **Machine**, **Snout Name**, **Snout Position**, **Gap**, **Gantry angle**, **Collimator angle**, **Couch angle**, **Range Shifter**, **Block** (if applicable), **Spot Tune ID**, **Number of energy layers**, **MU or NP/fx** (depending on primary dosimeter unit in machine) and **Spot weight**. For more information, see *section 6.1.6 Add, edit, copy or delete beams on page 316*.

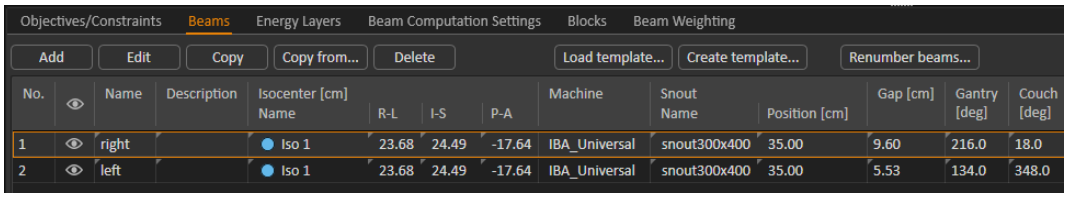


Figure 315. The **Beams** tab in the proton PBS/Line Scanning workspace.

When editing the **Gap** in the beam list, the snout position (moveable snouts) or the patient position (fixed snouts) is adjusted to achieve the desired gap. See *Air gap for proton beams on page 325* for more information.

The Spot tune ID name will be DICOM exported. The Spot tune id is selected in the Add beam dialog, but the Spot tune id column will not be populated until after the optimization. In RayStation 7 only one spot tune id is supported.

Note: *For Line Scanning only: Due to MU rounding, the dose will be approximate (non-clinical) if any of the MU/fx values are edited. Therefore, a clinical dose (final dose) needs to be computed after editing any MU/fx values in the Beam list.*

For Mevion Hyperscan only: Due to the spot map conversion, any change in MU/fx will set the dose to approximate (non-clinical). A clinical dose needs to be computed before the plan can be approved or exported.

For more information about MU rounding or spot map conversion, refer to RSL-D-RS-7.0-REF, RayStation 7 Reference Manual.

7.2.4 Treat and Protect tab

For machines with MLC the **Treat and Protect** tab will be visible. If Treat and protect settings are set for a beam without a block, an MLC aperture will be created during optimization. For further information, see *Treat and Protect tab on page 489*.

7.2.5 Beam Computation Settings

The **Beam Computation Settings** tab contains the following columns: **Number**, **Name**, **Automatic selection of range shifter** (visible for Mitsubishi Electric Co machines), **Spot pattern**, **Target margins** (**Proximal**, **Distal** and **Lateral**), **Min** and **Max Radiol. Depth**, **OAR range margin**, **Distal edge Margin**, **Spot Tune ID** and **Layer repainting**. These are described further in the *Define spot selection and layer repainting settings* below.

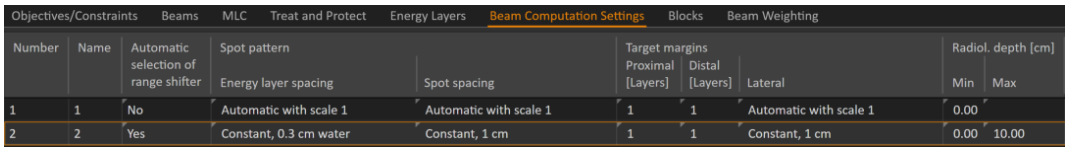


Figure 316. The **Beam Computation Settings** tab for protons. The **MLC** and **Treat and Protect** tabs are visible for machines with MLC. The **Blocks** tab is visible for machines with block.

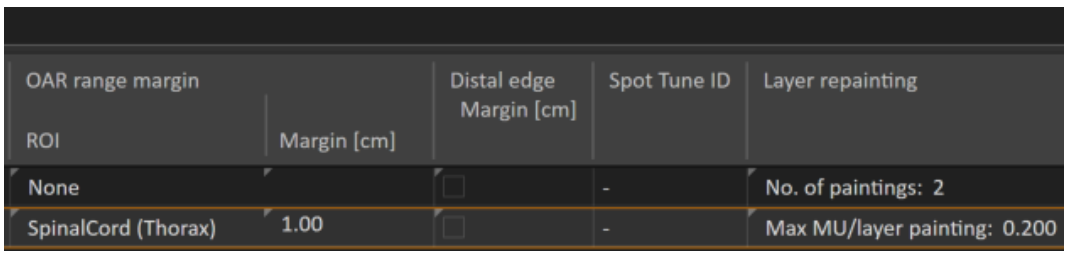


Figure 317. The **Beam Computation Settings** tab for protons (continued).

Define spot selection and layer repainting settings

The table below lists the parameters that are used during the initial spot selection when starting a new optimization and the parameters that are used when setting layer repaintings at the end of an optimization.

Parameter	Description
Automatic selection of range shifter	Available for Mitsubishi Electric Co SELECT BEAM NOZZLE in PBS mode only. If set to yes, the range shifter will automatically be selected from the available range shifters in the machine. For more details regarding automatic range shifter selection for Mitsubishi, refer to the *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual*.

Parameter	Description
Spot pattern, **Energy layer spacing**	The **Energy layer spacing** can be either a constant water equivalent distance or an automatic distance with a scaling factor: • **Automatic with scale**: This option is a variable distance that depends on the Bragg peak width. The energy separation between two adjacent energy layers equals the energy loss over the width (80% dose level) of the most distal Bragg peak in the pair. This means that each Bragg peak will intersect the following Bragg peak at approximately 80% of the dose maximum for a scaling factor of 1. The distance will decrease with a smaller scaling factor value. The default value for this variable can be defined in Clinic Settings. • **Constant [cm water]**: This option is a constant distance. The energies will be set so that the distance between the Bragg peaks will correspond to the user-defined value (in water). ***Note:*** *For Mevion Hyperscan, selecting an energy layer spacing other than Automatic with scale 1.0 will possibly lead to different fine-tuning tuning plates for different energy layers, which may increase the delivery time.*
Spot pattern, **Spot spacing** (PBS only) or **Spot pattern**, **Line spacing** (LS only)	**Spot spacing**/**Line spacing** can be either a constant distance or an automatic distance with a scaling factor: • **Automatic with scale**: This option is a variable distance that depends on the radial spread in the Bragg peak for a specific energy. The spot/line distance is determined as 1.06 times the average projected sigma multiplied by a scaling factor chosen by the user. The spot/line distance is constant within an energy layer but can deviate between different energy layers. The distance will increase with a larger scaling factor value. The default value for this variable can be defined in Clinic Settings. • **Constant [cm]**: This option is a constant distance.

Parameter	Description
Target margins: **Proximal**, **Distal** and **Lateral**	It is possible to set target margins during spot selection in the proximal, distal and lateral directions: • **Proximal [Layers]** - The selected number of energy layers will be added as a proximal target margin. The default value for this variable can be defined in Clinic Settings. • **Distal [Layers]** - The selected number of energy layers will be added as a distal target margin. The default value for this variable can be defined in Clinic Settings. • **Lateral** - If the **Automatic with scale** option is selected, the lateral target margin is determined as a function of the average spot size at the Bragg peak maximum for the highest energy. It is possible to increase or decrease the automatic margin by entering a scaling factor. If the **Constant [cm]** option is selected, it is possible to set the lateral margin as specified in cm. The default value for this variable can be defined in Clinic Settings.
Radiol. Depth [cm]	Bragg peaks are positioned at radiological depths larger (or smaller) than the specified minimum (or maximum) radiological depth in cm. If no value is specified for the maximum radiological depth, no upper limit will be applied to the radiological depth.
OAR range margin	The OAR range margin (cm water) is applied proximal to the specified organ-at-risk. Bragg peaks are not positioned within or distal to the specified organ-at-risk including this margin.
Distal edge Margin [cm]	A distal edge margin of 0.0 cm aims at setting the spots at the distal target edge. It is possible to increase and or decrease the margin in order to obtain the desired dose distribution.
Spot Tune ID	The spot tune id selected in the Add/Edit Beam dialog.

Parameter	Description
Layer repainting	The number of paintings for each energy layer of a beam is set at stop and at the end of an optimization. The options for layer repainting are: • **No. of paintings**: The number of paintings of each energy layer is set to the entered number. ***Note:*** *For Line Scanning, Mitsubishi PBS and Mevion Hyperscan, this is the only applicable option. For Line Scanning and Mitubishi PBS, the selected number of paintings will be taken into account in the optimization to ensure that the line segments or spots in each painting will be deliverable with respect to the limitations of the machine.* ***Note:*** *For PBS techniques other than Mitsubishi PBS (including Mevion Hyperscan), the number of paintings are only set after the optimization and it is the responsibility of the machine delivery system to create deliverable paintings for each energy layer in the plan produced in RayStation.* • **Max MU/layer paint** (For PBS techniques other than Mitsubishi PBS or Mevion Hyperscan): The number of paintings of each energy layer is set so that the MU of each layer paint is lower than the specified value. ***Note:*** *If the beam MU or energy layer weight is modified after optimization, the number of paintings of the energy layers are not automatically updated.*

The spot positions are set at the start of the optimization in such a way that all spot centers fit inside the inner dimensions of the selected snout at the specified location.

If a range shifter is used, the region in which spots can be placed is also constrained by the location and shape of the range shifter, with an additional inner margin of 10 mm. The range shifter lateral dimensions are by default determined by the snout outer dimensions, but could optionally be assigned in the machine model to individual shapes and dimensions.

If an aperture block or MLC is used for a PBS or an LS plan, the spot positions will be restricted by the block or MLC aperture contour. Spots are allowed to be placed inside the block or MLC contour and within a margin of one radial sigma in air outside the block contour. For Mevion Hyperscan, spots are only allowed to be placed inside the block contour (without margin).

If the snout, range shifter or aperture block or MLC restricts the spot positions to a too large extent compared to the target projection, the optimizer may try to increase the weights of the spots close to the target border. This will generate a non-uniform dose distribution with cold and hot spots. It is the responsibility of the user to ensure that spots cover the treated volume with adequate margin.

7.2.6 MLC settings

The **MLC** tab lists the energy layers and the MLC positions for the selected beam.

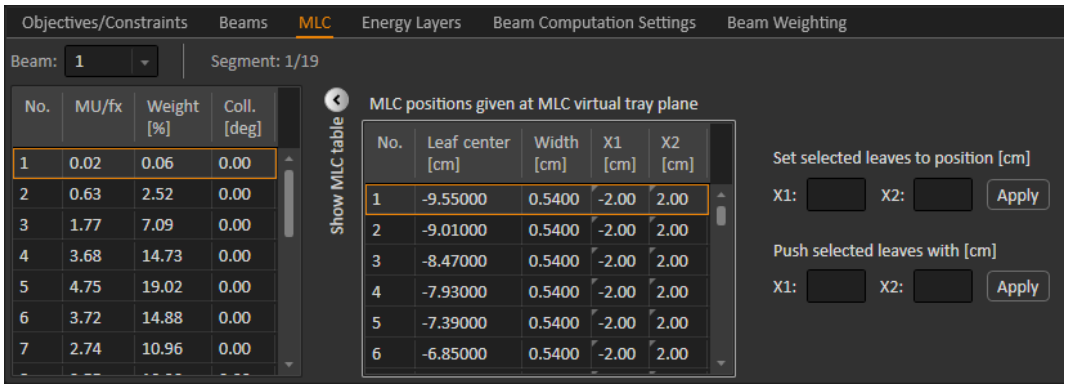

Objectives/Constraints
Beams
MLC
Energy Layers
Beam Computation Settings
Beam Weighting
Beam: 1
Segment: 1/19
No. MU/fx Weight [%] Coll. [deg]
1 0.02 0.06 0.00
2 0.63 2.52 0.00
3 1.77 7.09 0.00
4 3.68 14.73 0.00
5 4.75 19.02 0.00
6 3.72 14.88 0.00
7 2.74 10.96 0.00
Show MLC table
MLC positions given at MLC virtual tray plane
No. Leaf center [cm] Width [cm] X1 [cm] X2 [cm]
1 -9.55000 0.5400 -2.00 2.00
2 -9.01000 0.5400 -2.00 2.00
3 -8.47000 0.5400 -2.00 2.00
4 -7.93000 0.5400 -2.00 2.00
5 -7.39000 0.5400 -2.00 2.00
6 -6.85000 0.5400 -2.00 2.00
Set selected leaves to position [cm]
X1: X2: Apply
Push selected leaves with [cm]
X1: X2: Apply

Figure 318. The **MLC** tab for protons.

Edit MLC positions

Click the **MLC** tab at the bottom of the workspace. The leaves for the selected energy are listed in the **MLC** table, and can be set to a desired position or pushed a certain distance. Each leaf has the same position for all energies.

1. Select the leaf pairs to modify. Multiple rows are selected by Shift or Ctrl mouse click.
2. Add either new positions for **X1** and/or **X2**, or the distances (positive or negative) to push **X1** and/or **X2**. (Naming of positions is for an MLCX machine according to the Jaw labeling standard IEC 61217.)
3. Click **Apply**.

7.2.7 Specify optimization settings

Dose computation options for optimization

In the proton PBS/Line Scanning optimization settings, the user can select several options for dose computation in the drop-down list:

- **Fast Pencil Beam** - an approximate dose computed with the Pencil Beam dose engine.
- **Pencil Beam** - a clinical dose computed with the Pencil Beam dose engine.

  A dose for a proton PBS plan computed with the Pencil Beam dose engine will be approximate when one or more beams have an aperture (block/MLC) or energy selector system (Mevion Hyperscan).
- **Monte Carlo** - a dose computed with the Monte Carlo dose engine. When selecting Monte Carlo, it is also possible to set the number of ions per spot (**Ions/spot**). Optimization using the Monte Carlo dose engine will always result in an approximate dose.

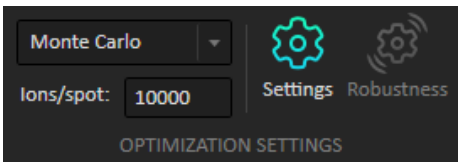


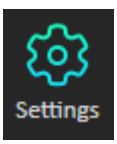
Figure 319. The proton PBS/Line Scanning optimization settings.

Final dose

A final dose can be computed after the optimization. For more information, see *section 7.2.15 Dose computation options on page 604*. It is possible to specify a default dose engine in Clinic Settings.

Edit optimization settings

To edit the optimization settings, click the **Settings** button.



This opens the **Settings** dialog.

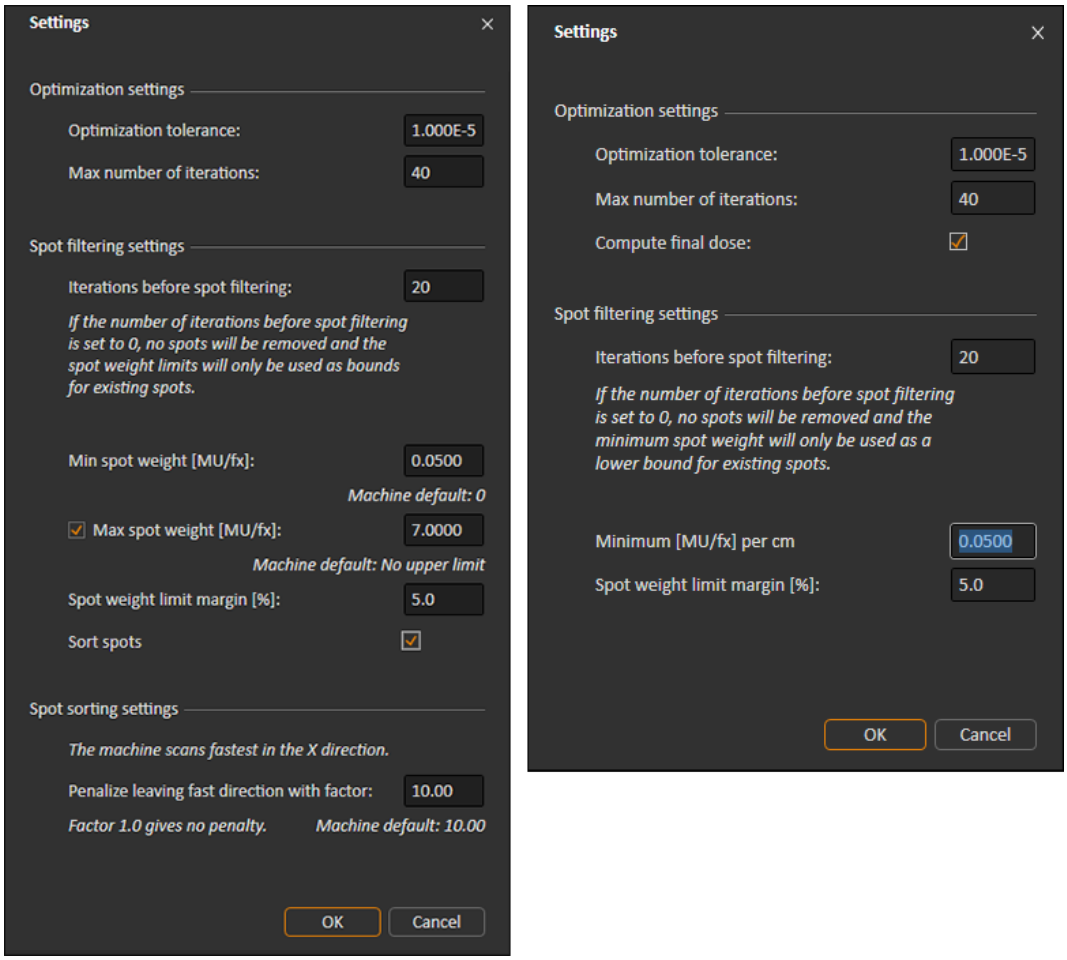


Figure 320. The **Settings** dialog for proton PBS optimization (left) and the **Settings** dialog for proton Line Scanning (right). Note that the **Settings** dialog for Mitsubishi Electric Co SELECT BEAM NOZZLE in PBS mode machines does not include the **Sort spots** checkbox.

The user can edit the following PBS/Line Scanning optimization settings for protons:

Parameter	Description
Optimization tolerance	The software stops the optimization when the change in the Composite Objective value indicates that an optimal solution has been found. This occurs when the change in objective value is less than the tolerance level. The optimization tolerance should be around 1e-5 or 1e-6.

Parameter	Description
Max number of iterations	The optimization algorithm can usually find an optimal solution in 25–100 iterations, but by setting maximal number of iterations the optimization can be stopped prior to this if it is believed that the objectives will not be met or whenever the result already is satisfying.
Compute final dose (Line Scanning only)	For Line Scanning it is possible to select to automatically compute a final dose when the optimization has completed.
Iterations before spot filtering	After the specified number of iterations, all spots with a weight below the minimum spot weight limit are filtered out. For subsequent iterations the limit is used as a lower bound for remaining spots. If set to 0, no spots will be removed and the minimum spot weight will only be used as a lower bound for existing spots.
Min spot weight [MU/fx] (PBS only)	The limit used (with the margin described below added) when filtering out low weight spots. The **Machine default** value is read from the machine. MU or NP depending on primary dosimeter unit in machine.
Max spot weight [MU/fx] (PBS only)	The maximum spot weight limit used in the PBS optimization. The **Machine default** value is read from the machine. MU or NP depending on primary dosimeter unit in machine.
Minimum [MU/fx] per cm (Line Scanning only)	For Line Scanning, line segments are filtered out only in the beginning and the end of the lines based on the Minimum [MU/fx] per cm and the machine limits. In subsequent iterations, lower and upper bounds are applied based on the machine limits. This means that line segments in the middle of the line could have values that are below the specified Minimum [MU/fx] per cm limit. If layer repainting is used, the limits used in line segment filtering and bounding are multiplied by the planned number of paintings. More details on the line segment filtering and bounding can be found in the *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual*.
Spot weight limit margin (%)	The user can add a margin to the minimum spot weight to allow some smaller modifications of the spot weights after optimization without making the plan undeliverable (e.g., allow scale dose to prescription).
Sort spots (PBS only)	When **Sort Spots** is selected, the order of the spots will be sorted to minimize the scan path. The sorting is performed during the spot filtering iteration, if spots are filtered, or if the optimization has been stopped before this iteration. When no spots are to filtered, the spot sorting is performed at the first iteration. For Mitsubishi PBS, the spot sorting is always performed in conjunction to filtering. More details on the spot sorting and filtering for Mitsubishi machines can be found in the *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual*.

Parameter	Description
Spot sorting settings (PBS only)	The spot sorting can be steered to prefer taking steps in the direction for which the machine scans fastest. This is done by setting the **Penalize leaving fast direction with factor** to a value greater than 1. When the spots are sorted to yield the shortest path, distances that leave the fast direction are multiplied by this factor. The **Machine default** values are read from the machine.
Beam interruption settings (PBS only)	For treatment machines that support quasi-discrete PBS (where the beam is on between spots), there are two additional parameters in the **Settings** dialog; **Fixed distance** and **Spot spacing multiplied by**. These are described further in the following section *Quasi-discrete spot islands*.

Optimization settings for quasi-discrete spot islands

For treatment machines that support quasi-discrete PBS (where the beam is on between spots), there is an additional section in the **Settings** dialog called **Beam interruption settings** that contains two parameters: **Fixed distance** and **Spot spacing multiplied by**.

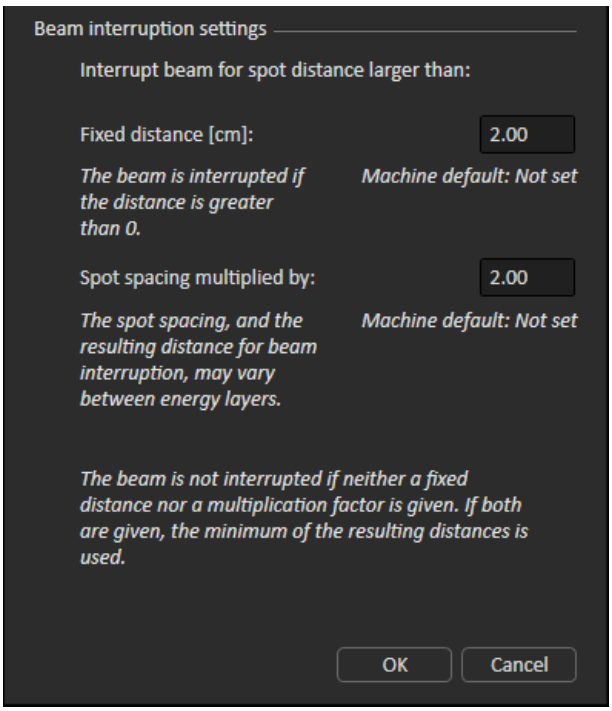

Beam interruption settings
Interrupt beam for spot distance larger than:
Fixed distance [cm]:
2.00
The beam is interrupted if the distance is greater than 0.
Machine default: Not set
Spot spacing multiplied by:
2.00
The spot spacing, and the resulting distance for beam interruption, may vary between energy layers.
Machine default: Not set
The beam is not interrupted if neither a fixed distance nor a multiplication factor is given. If both are given, the minimum of the resulting distances is used.
OK
Cancel

Figure 321. Beam interruption settings for treatment machines that support quasi-discrete PBS.

Following spot sorting, the spots map in each energy layer is separated into "islands", i.e., sequences of positions that the scanned beam should traverse with the beam on. The beam is interrupted between islands. The scan spots direction in BEV can be used to inspect the result of the beam interruption settings after optimization. A dotted line connecting the spots in BEV indicates that the beam is **on** and a solid line connecting the spots indicates that the beam is interrupted (**off**). At DICOM export, the spot islands are indicated with a zero weighted spot at the start of each island.

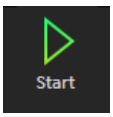
The positions between which to interrupt the beam are determined by two parameters: a **Fixed distance** and the **Spot spacing multiplied by** a factor. For all distances larger than the smaller of these two values, the beam will be turned off. To minimize the number of interruptions of the beam, these parameters are also used in the spot sorting. Steps that are longer than the interruption distance are given a constant penalty of 1000 in addition to the step length. Thus, the resulting scan path will avoid going between positions farther apart than this distance when possible, but will take these steps when no other possibility exists.

Note: *DICOM import of a quasi discrete plan without zero weighted spots will be interpreted as a step-and-shoot PBS plan, and will have the beam off between all spots.*

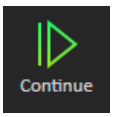
7.2.8 Running the proton PBS and Line Scanning optimization

The optimization process is controlled by the optimization control buttons in the toolbar.

The optimization control buttons



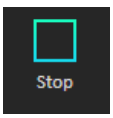
The **Start** button starts a new optimization. Only active if the beams are empty (no energy layers).



The **Continue** button starts an optimization from the current state using the existing energy layers and spots. The optimization will continue using the user-defined optimization functions. Only active if there is at least one energy layer in every beam.

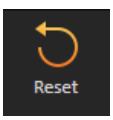
Note: *If the irradiated volume after an optimization is too small or too large, the target volume (as defined through the optimization functions) may need to be modified. After such a modification, it is strongly advised to reset and start a new optimization instead of continuing.*

Note: *It is not possible to use the Continue button for Line Scanning.*

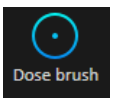


The **Stop** button stops the optimization after the current iteration is finished.

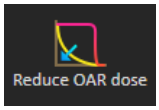
Note: *The Stop button should be used with some care in proton and carbon ion optimization for plans that are intended to be delivered to a patient. Beside the primary point that an optimal plan cannot be ensured, if the optimization is stopped, there is one more reason. The filtering of low and high weight spots is performed after a user-defined number of iterations. This means that the resulting plan will generally not be deliverable, and is therefore not clinically relevant.*



The **Reset** button resets the beams, i.e. removes all energy layers and sets all beam MUs to zero.



Use the **Dose brush** tool in a 2D view to modify the dose distribution within the dose brush sphere. Hold down left mouse button and drag up or down to increase or decrease dose. The magnitude depends on the distance that the mouse is moved.
The optimization starts when the mouse button is released. Click Stop to exit the tool. The size of the sphere is adjusted using Alt + mouse wheel.



The **Reduce OAR dose** button starts an optimization from the current state. Auto-generated reference dose functions are used to reduce the dose in the risk organs (OARs), while maintaining dose homogeneity in the target organs. If the current beam set already has minimal OAR dose, this function will not have any significant effect.

Optimization Progress

The lower right window of the workspace shows the result of the optimization progress. A graph plots the values of the objective functions as a function of the number of iterations. All values are plotted separately but also the sum of the objectives (bold white line) which the optimization tries to minimize. The objective function curves are colored in the same color as the corresponding ROIs.

When using the Reduce OAR dose function, the displayed objective functions are those specified by the user, not the auto-generated ones.

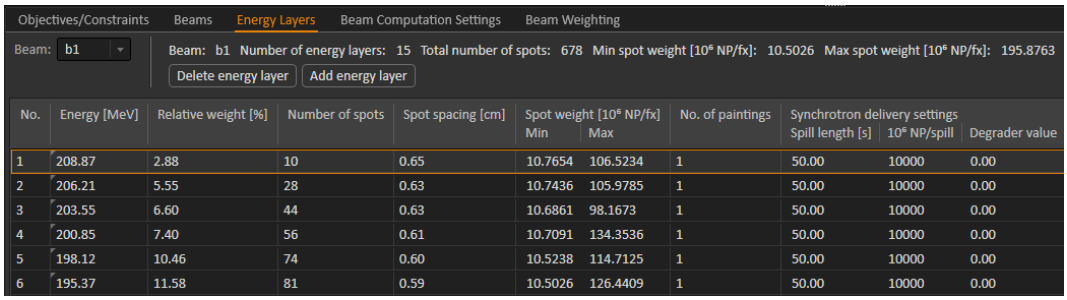
Figure 322. The Optimization progress graph.

Optimization result

When the optimization is completed, the energy layers and the corresponding spots will be visible in the **Energy Layers** tab and in the BEV.

7.2.9 Energy layers

The **Energy Layers** tab for protons contains the energy layers and the corresponding weights used for creating the SOBP for the active beam.


Objectives/Constraints
Beams
Energy Layers
Beam Computation Settings
Beam Weighting
Beam: b1
Beam: b1 Number of energy layers: 15 Total number of spots: 678 Min spot weight [10⁶ NP/fx]: 10.5026 Max spot weight [10⁶ NP/fx]: 195.8763
Delete energy layer
Add energy layer

No.	Energy [MeV]	Relative weight [%]	Number of spots	Spot spacing [cm]	Spot weight [10⁶ NP/fx] Min	Spot weight [10⁶ NP/fx] Max	No. of paintings	Synchrotron delivery settings Spill length [s]	Synchrotron delivery settings 10⁶ NP/spill	Synchrotron delivery settings Degrader value
1	208.87	2.88	10	0.65	10.7654	106.5234	1	50.00	10000	0.00
2	206.21	5.55	28	0.63	10.7436	105.9785	1	50.00	10000	0.00
3	203.55	6.60	44	0.63	10.6861	98.1673	1	50.00	10000	0.00
4	200.85	7.40	56	0.61	10.7091	134.3536	1	50.00	10000	0.00
5	198.12	10.46	74	0.60	10.5238	114.7125	1	50.00	10000	0.00
6	195.37	11.58	81	0.59	10.5026	126.4409	1	50.00	10000	0.00

Figure 323. The **Energy Layers** tab for protons.

The tab header displays information about the active beam, the number of energy layers, the total number of spots and the minimum/maximum spot weight of the beam (PBS only). It is possible to edit the energy for an energy layer directly in the **Energy layers** tab or to delete the selected energy layer by clicking the **Delete energy layer** button. It is also possible to add an energy layer by clicking the **Add energy layer** button, see *Add energy layer on page 592*.

The **Energy Layers** tab is synchronized with the BEV. Click on a row in the list to display the corresponding energy layer in the BEV.

The list contains the following information:

- **Number**: Energy layer number.
- **Energy**: Energy in MeV.
- **Relative weight**: Relative weight in percent.
- **Number of spots**: Number of spots.
- **Number of line segments** (Line Scanning only): The number of line segment end points, i.e., the number of line segments plus one.
- **Spot spacing** (PBS only): The initial distance between spots, before spot editing, as calculated by the optimization.
- **Line spacing** (Line Scanning only): The spacing between the line segments in the line scanning pattern.
- **Spot weight, Min** (PBS only): Minimum spot weight in MU or NP/fraction.
- **Spot weight, Max** (PBS only): Maximum spot weight in MU or NP/fraction.
- **No. of paintings**: The number of repaintings of the energy layer that is exported to DICOM. For Mevion Hyperscan, it is possible to set the Number of paintings for all energy layers simultaneously.

- **Plate configuration** (Mevion Hyperscan only): The energy selector plates that are enabled or disabled on the energy layer as a sequence of 1's (enabled) and 0's (disabled). The sequence is ordered from the source (left) to the patient (right).

Note: *For Mevion Hyperscan only: Due to the spot map conversion, any change in Number of paintings will set the dose to approximate (non-clinical). A clinical dose needs to be computed before the plan can be approved or exported.*

For more information about spot map conversion, refer to RSL-D-RS-7.0-REF, RayStation 7 Reference Manual.

Specific information for synchrotron delivery

- **Synchrotron delivery settings, spill length**: The duration of a beam extraction in seconds.
- **Synchrotron delivery settings, 10^6 NP/spill**: The number of particles that are extracted during a spill.
- **Synchrotron delivery settings, Degrader value**: A degrader can be added to reduce the beam current. The degrader value is in the range 0 to 1, where 0 corresponds to no degradation and 1 to full degradation.

The relative weight is normalized within each beam and the total relative weight sums up to 100%.

Note: *The presented weights are the effective weights used by the dose calculation, these weights may not be the same as those used by the beam delivery system.*

Add energy layer

To add a new energy layer:

1. Click the **Add energy layer** button to open the **Add Energy Layer** dialog.

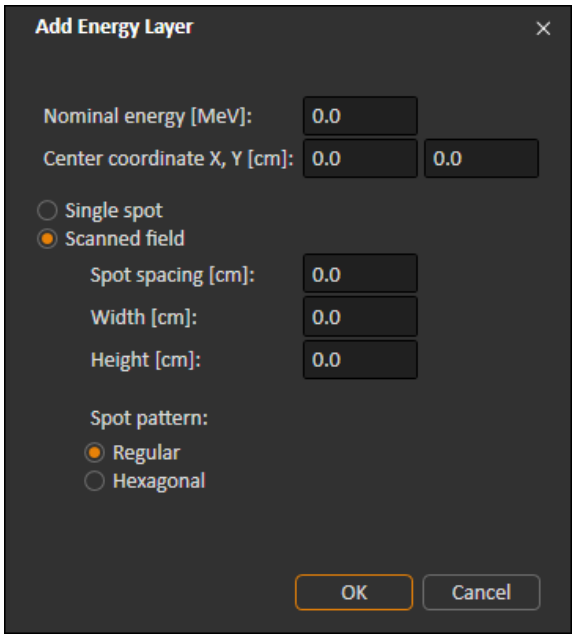


Figure 324. The **Add Energy Layer** dialog.

2. Enter the **Nominal energy [MeV]**.
3. Enter the **Center coordinate X, Y [cm]**.
4. Select a **Single spot** or a **Scanned field**.
5. If a **Scanned field** is selected, also:
   - Enter the **Spot spacing [cm]** in the scanned field.
   - Enter the **Width [cm]** and **Height [cm]** of the scanned field.
   - Select either **Regular** or **Hexagonal** spot pattern.

7.2.10 Spot editing

For proton PBS it is possible to edit the initial spots that have been computed by the optimization. The Spot editing tools are located in the **Spot Editing** tab in the toolbar and operate on the spots in the Beam's Eye View (BEV).

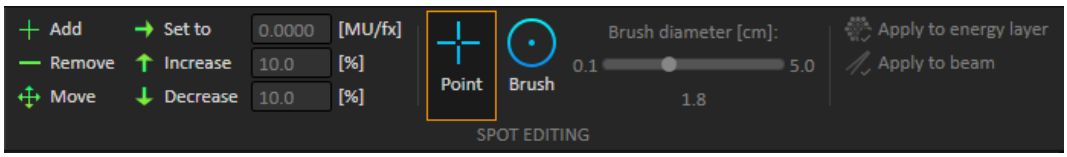


Figure 325. The spot editing tools.

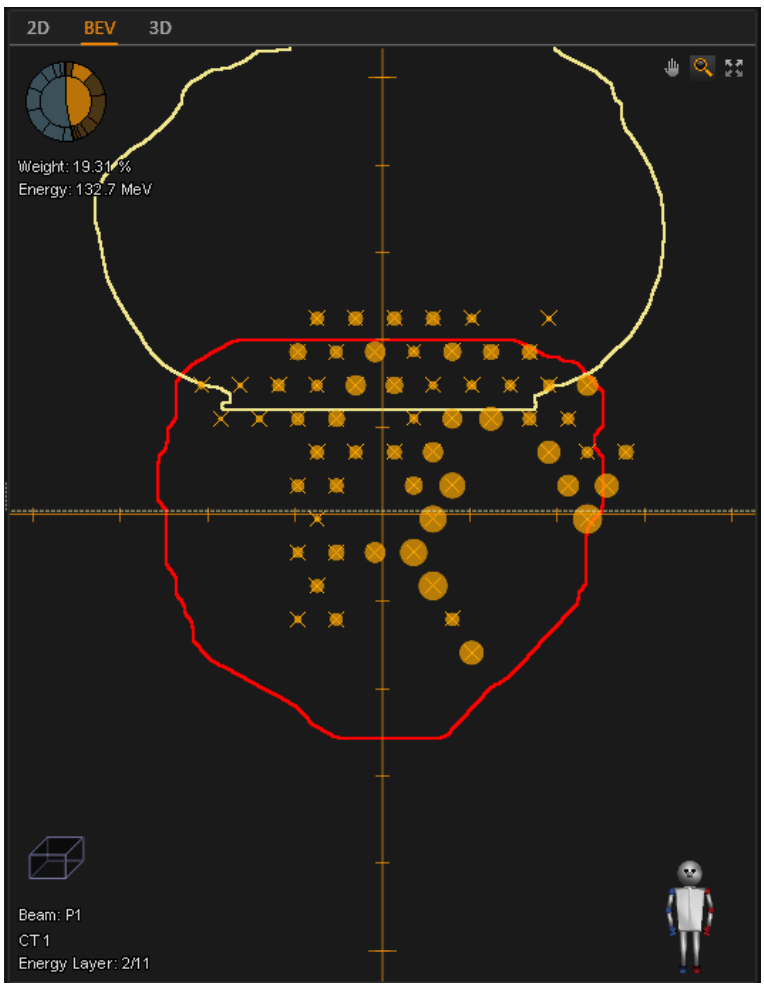
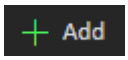


Figure 326. Spot editing in the Beam's Eye View (BEV).

Add a spot in the BEV

A spot with zero initial weight can be added using the point tool.

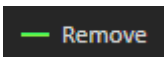
1. Click the **Add** button.



2. Click at a position in the BEV to add the spot.

Remove a spot from the BEV

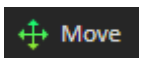
Use the point tool to remove a specific spot or use the brush tool to remove several spots.



Move a spot in the BEV

Move a specific spot using the point tool.

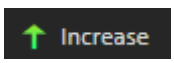
1. Click the **Move** button.



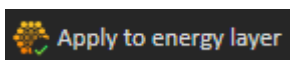
2. Click on a spot and drag and drop it to a desired position.

Increase the weight of a spot by a factor

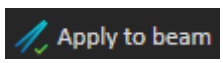
1. Click the **Increase** button.



2. Enter a value in percent in the corresponding field.
3. Select to apply the modification to:
   a. all spots in the selected energy layer by clicking the **Apply to energy layer** button.



   b. all spots in the selected beam by clicking the **Apply to beam** button.

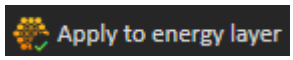


   c. those spots in an energy layer chosen by the brush or point tool.

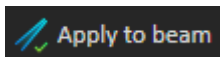
Decrease the weight of a spot by a factor

1. Click the **Decrease** button.

2. Enter a value in percent in the corresponding field.
3. Select to apply the modification to:
   a. all spots in the selected energy layer by clicking the **Apply to energy layer** button.

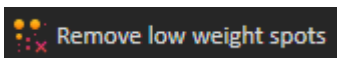
   b. all spots in the selected beam by clicking the **Apply to beam** button.

   c. those spots in an energy layer chosen by the brush or point tool.

Remove low weight spots

1. Click the **Remove low weight spots** button.

   This opens the Remove low weight spots dialog.

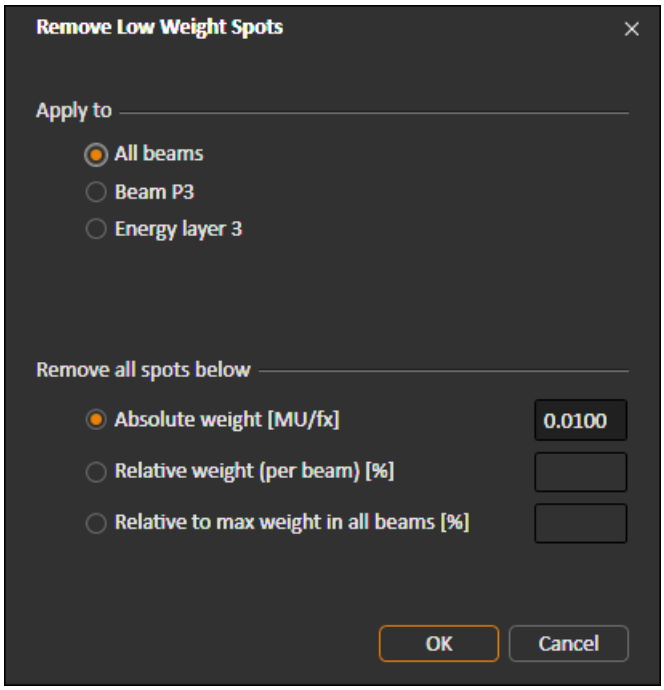
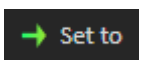


Figure 327. The Remove low weight spots dialog.

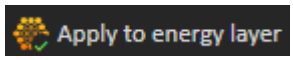
2. Select to remove low weight spots in:
   a. all beams.
   b. a specific beam.
   c. a specific energy layer.
3. Select to remove all spots below:
   a. an absolute weight [MU/Fraction].
   b. a relative weight (per beam) [%].
   c. a fraction of the maximum weight in the energy layer [%].
4. Click **OK**.

Set the number of MU/fraction of spots

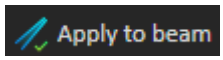
1. Click the **Set to** button.



2. Enter a value in the corresponding field [MU/fraction].
3. Select to apply the modification to:
    a. all spots in the selected energy layer by clicking the **Apply to energy layer** button.

    b. all spots in the selected beam by clicking the **Apply to beam** button.

    c. those spots in an energy layer chosen by the brush or point tool.

Remove energy layer

In order to remove the selected energy layer, click the **Remove energy layer** button.

7.2.11 Bragg peak visualization

During optimization and final dose computation, the positions of the Bragg peaks in the patient will be computed and displayed in the 2D and 3D views, if selected in the Visualization settings.

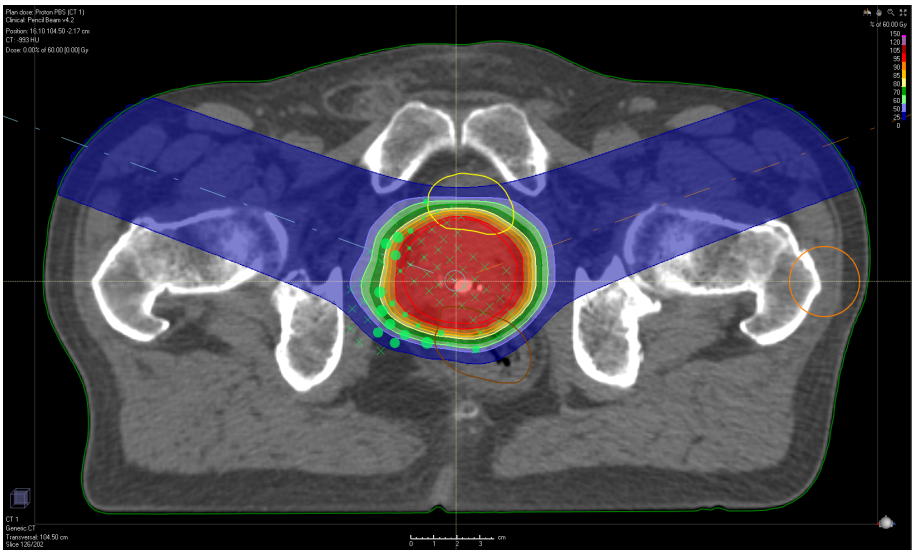


Figure 328. Bragg peak visualization in the 2D view.

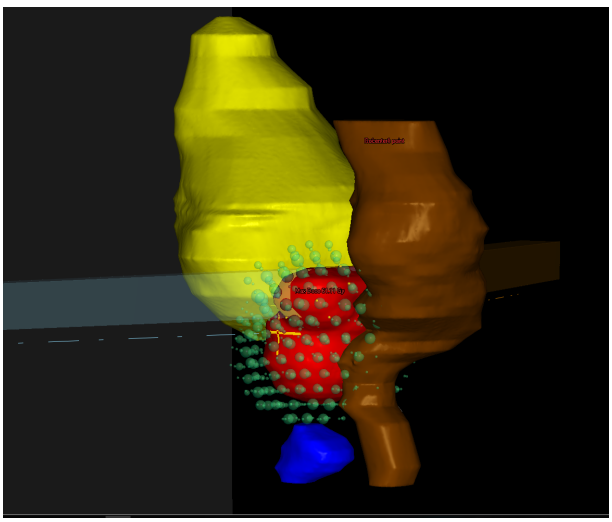


Figure 329. Bragg peak visualization in the 3D view.

The Bragg peak position is defined as the position of the maximum dose value of the reference integrated depth dose curve, scaled along the central axis of the spot according to the relative stopping power along that line. This position does not necessarily coincide with the position of the

maximum dose. For cases with significant lateral inhomogeneities, the deviation between the position of maximum dose (close to end of range) and the visualized Bragg peak position in RayStation may be significantly large. The same algorithm is used for both the Pencil Beam and the Monte Carlo dose engines.

In the 2D views, Bragg peaks are displayed in slices that are within a radius of 2.5 mm from the actual Bragg peak position. This means that one Bragg peak could be displayed in more than one of the CT slices, if the slice resolution is high. Also for low slice resolutions (larger than 5 mm) some Bragg peaks might not be shown.

The position of the Bragg peak in the 2D view is marked with a cross and the spot weight is visualized with a filled circle, the size is proportional to the spot weight. When hovering over the Bragg peaks in the 2D views, the nominal energy and weight of the corresponding spot will be displayed.

For the treatment technique Line scanning, the Bragg peaks will be displayed at the beginning and at the end of each line segment. This results in displaying one more Bragg peak than the number of line segments. The weight shown when hovering over a Bragg peak corresponds to the weight of the following line segment. The Bragg peak position corresponding to the end point of the last segment in a line will get a weight of zero.

Synchronization between spots and Bragg peaks

The Bragg peaks corresponding to the selected energy layer (in the Energy layer list and the BEV) is highlighted with a different color. When hovering over individual spots in the BEV or Bragg peaks in the 2D view, the corresponding Bragg peak or spot will also be emphasized with a different color. By clicking on a Bragg peak, the energy layer comprising the spot corresponding to this Bragg peak will be selected. By clicking on a spot in the BEV, the 2D view will display the slice where the corresponding Bragg peak is located.

With these tools, it is possible to identify a specific Bragg peak in the 2D views and locate the corresponding spot. The spot could subsequently be edited by the spot editing tools described in *section 7.2.10 Spot editing on page 594*.

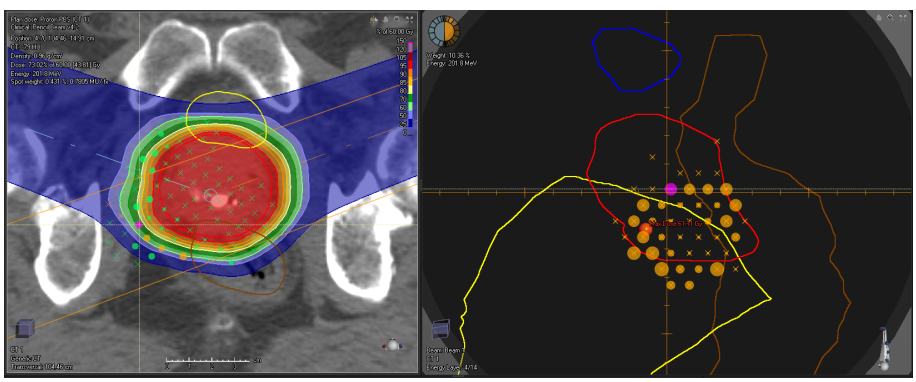


Figure 330. Syncronization between Bragg peaks in the 2D view and spots in the BEV.

7.2.12 Blocks

Blocks for PBS and Line Scanning-beams are edited in the Proton Beam Design module. Refer to the *section 6.5.11 Edit block aperture on page 506* for more information.

7.2.13 Beam weighting

Beam weighting is described in detail in *section 6.3.12 Beam weighting on page 445*.

Note: *For Line Scanning only: Due to MU rounding, the dose will be approximate (non-clinical) after beam weighting. Therefore, a clinical dose (final dose) needs to be computed after beam weighting.*

For Mevion Hyperscan only: Due to spot map conversion, the dose will be approximate (non-clinical) after beam weighting. Therefore, a clinical dose (final dose) needs to be computed after beam weighting.

For more information about MU rounding or spot map conversion, refer to RSL-D-RS-7.0-REF, RayStation 7 Reference Manual.

7.2.14 Define or modify prescription

For instructions on how to to define or modify a dose prescription, see *section 6.1.12 Define or modify prescription on page 343*.

7.2.15 Dose computation options

Figure 331. The proton PBS/Line Scanning dose computation options.

Compute final dose

For the proton PBS/Line Scanning option, the user can select from two options for final dose computation in the drop-down list:

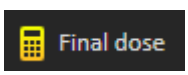
- **Pencil Beam** - a clinical dose computed with the Pencil Beam dose engine.
- **Monte Carlo** - a dose computed with the Monte Carlo dose engine. When selecting Monte Carlo, it is also possible to set the mean number of ions (number of Monte Carlo histories) per spot (**Ions/spot**) or the statistical uncertainty in % (**uncert [%]**). When selecting to compute to a certain statistical uncertainty, the dose computation will continue until the desired statistical uncertainty is reached. The dose will be considered clinical if the statistical uncertainty per beam is below the threshold for clinical dose set in Clinic Settings (see *section D.2 The Clinic Settings application on page 920*).

Note: *For Mevion Hyperscan, the ions/spot option of the Monte Carlo dose engine refers to the number of ions/spot used after spot map conversion. Since this step can modify the number of spots compared to the plan (for example due to repainting), the total number of ions used to compute the dose will not match with the expected number from the number of the spots in the treatment plan.*

A dose for a proton PBS plan with aperture (block/MLC) computed with the Pencil Beam dose engine will always be approximate, since edge scatter is not accurately modeled in the Pencil beam dose algorithm. In the Monte Carlo dose computation, the protons are transported through the block taking the edge scatters effects into account and the dose will be considered clinical. For more details, refer to the *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual*.

For Mevion Hyperscan, a dose computed with the Pencil Beam dose engine will always be approximate, since spot map conversion is not performed. Also, the modelling of multiple range shifters with air gaps is not considered accurate enough for a clinical dose. For more details, refer to the *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual*.

To compute final dose, click the **Final dose** button in the toolbar or type Ctrl + D. It is possible to specify a default dose engine for Final dose in Clinic Settings.



Note: *If there is already a clinical dose computed with the current dose computation parameters, dose will not be recomputed.*

When the computation is completed, the dose will show up in the patient views. The total number of ions used will be displayed in the patient views both for beam set and beam doses. The statistical uncertainty per beam will be displayed for beam doses.

Click the **Cancel** button in the Progress toolbar to abort a started dose computation. For more information, see *section 3.11 Cancel procedure on page 106*

The dose engines is described in detail in *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual*.

WARNING!

Dose computation region. Radiation transport and dose is computed only inside a region consisting of ROIs of type External, Bolus for beam, Support and Fixation. Image data not included in this region will be omitted from dose computation and is regarded as a vacuum (no interactions).

If the beam Field Of View covers part of the patient not inside the External ROI or any equipment not defined by Bolus, Support or Fixation ROIs, the dose computation will be incorrect.

Note also that the computation is limited to the dose grid. There is no warning if the dose grid does not cover the appropriate region. (7285)

WARNING!

Approximate dose is only intended for intermediate treatment planning steps. Approximate dose has lower accuracy compared to the dose displayed as "Clinical" and it must not be used for clinical decisions. A plan with approximate dose cannot be approved or exported. (126034)

Scale dose

The dose can be scaled to fulfill the prescription or to fulfill an arbitrary dose-volume relation for a selected ROI or POI. For instructions on how to scale dose, see *section 6.1.15 Scale dose on page 356*.

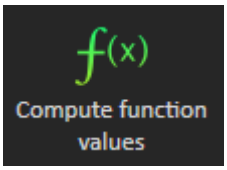
Note: *For Line Scanning only: Due to MU rounding, the scaled dose will be approximate (non-clinical). Therefore, a clinical dose (final dose) needs to be computed after dose scaling.*

For Mevion Hyperscan only: Due to the spot map conversion, scaled dose will be approximate (non-clinical). A clinical dose needs to be computed before the plan cen be approved or exported.

For more information about MU rounding or spot map conversion, refer to RSL-D-RS-7.0-REF, RayStation 7 Reference Manual.

7.2.16 Compute function values

If an optimization function is altered after an optimization is run the value for the changed function can be updated by clicking the **Compute function values** button in the toolbar.



7.2.17 The evaluation views

Dose Volume Histogram (DVH)

The DVH view presents the cumulative dose volume histograms of the ROIs selected in the ROI List. The dose can be displayed as **absolute** or **relative [%]**. It is also possible to manually set the reference value for the relative scale. For a further description of the DVH view, see *section 3.7.1 Dose Volume Histogram (DVH) on page 78*.

Dose statistics

The dose statistics view lists ROI dose information. For more information, see *section 3.7.2 Dose statistics table on page 79*.

Dose difference

The dose difference view displays the dose difference between two treatment plans. See *The Dose difference view on page 75* for more information.

Clinical goals

The clinical goals functionality makes it possible to define evaluation criteria for specific ROIs and POIs. The result (pass/fail) is easy-to-read in a single column. For more information about the clinical goals functionality, see *section 3.7.3 Clinical goals on page 81*.

Note: *The clinical goals will not affect the optimization.*

7.2.18 Evaluation of proton PBS and Line Scanning plans

An optimized PBS and Line Scanning plan may be very sensitive to setup and density uncertainties, as well as to organ motion. These aspects should be taken into account when reviewing an optimized PBS and Line Scanning plan. In the Plan Optimization module, not only the plan and beam set doses should be reviewed, but also individual beam doses. Inhomogeneous beam doses might result in that the plan will not be robust. To fully assess the robustness of a plan, compute perturbed doses in the Plan Evaluation module and compare this with the original plan.

7.3 THE PLAN OPTIMIZATION MODULE - CARBON IONS

This section describes how to generate optimized carbon ion plans for Pencil Beam Scanning in the Plan Optimization module through optimization with respect to user-defined treatment objectives and constraints. The result is a hexagonal spot scan pattern with optimized spot weights.

For carbon ions, the delivered dose (physical ion dose) results in greater damage to the irradiated cell type as compared to the effect caused by the same dose delivered with photons. The Relative Biological Effectiveness, RBE, is a measure of the efficiency of a radiation type in producing a specific response (e.g., damage to the cell type). For carbon ions, the RBE typically varies across a treatment plan. It is defined as the ratio of the photon dose and the physical ion dose giving the same biological effect under otherwise equal conditions. The RBE is used to weight the physical ion dose to obtain a clinically relevant dose called the RBE weighted dose (RBE dose) with the unit Gy (RBE). That is, the RBE can be used to convert a physical ion dose into a photon equivalent dose.

In RayStation, both physical ion dose and RBE dose are presented. Physical ion dose and RBE dose are shown with the units Gy and Gy (RBE), respectively throughout the workspace. The RBE dose is always used for structure definition, clinical goals, prescription and plan approval. The physical ion dose is always used for QA preparation and beam dose specification points, but may also be used for the optimization process. In the planning activities Plan Design and Plan Optimization, it is possible to switch between showing the RBE dose and the physical ion dose. In the Plan Evaluation module both RBE doses and the physical ion doses can be evaluated.

In this section

This section contains the following sub-sections:

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Precautions

WARNING!

The effect of the infinite slab approximation on carbon ion PBS. This approximation, inherent to the pencil beam algorithm, disregards lateral inhomogeneities for individual ray traces, for which the patient is seen as a stack of semi-infinite layers. The user shall therefore be aware that the dose computations may not be fully accurate for patients with large lateral inhomogeneities relative to the beam direction. (261597)

WARNING!

Absolute dose accuracy for carbon ion PBS with range shifters. The dose validation of RayStation 7 covers range shifter air gaps between 3 and 63 cm, with 11.5 cm as the most common air gap. Be extra careful when using air gaps larger than 11.5 cm. (254459)

WARNING!

Field size limitations for carbon ion PBS. The dose engine validation of RayStation 7 covers field sizes between 3 x 3 cm^2 and 20 x 20 cm^2. Be extra careful when creating fields with field sizes that are smaller or larger than these field size limits. (254461)

WARNING!

Quasi-discrete spill dose is not computed in RayStation. A quasi-discrete PBS plan is computed as a step-and-shoot PBS plan and the spill dose between spots will not be considered. The dose difference between the computed plan and the delivered plan needs to be assessed by the user in the commissioning of RayStation as well as during patient specific QA. (123711)

WARNING!

Ensure that spot selection rules will result in an appropriate dose distribution. The choices in the Beam Computation Settings tab (spot pattern, target margin, OAR range margin, minimum radiological depth, and distal edge margin) will influence the number of spots (or line segments for Line Scanning) in the plan and where they are positioned. The user needs to ensure that the resulting spot pattern gives a dose that corresponds to the goals of the treatment. (370108)

WARNING!

Limitations in RBE weighted dose computation. The primary and secondary particle energy spectra used in RBE weighted dose computation were simulated in water. The user should be aware of this limitation and its potential effect on RBE weighted dose in heterogeneous regions, and primarily in materials that differ significantly from water. (235687)

WARNING!

Dose grid effects for ion PBS plans. The proton and carbon Pencil Beam dose engines in RayStation calculates the average dose to a voxel along the Integrated depth dose (IDD) and the dose to the center point of each voxel laterally and lets this dose value represent the dose in the entire voxel, while the RayStation Monte Carlo dose engine calculates the average dose deposited to a voxel. This means that any variation in dose that occurs on a resolution that is finer than that of the current dose grid may be lost in the dose calculation. The user has the responsibility to choose a dose grid resolution that is suitable for each plan, however, for low energy proton fields, and carbon ion fields without a ripple filter, the Bragg peak may be so sharp that even the highest dose grid resolution in RayStation (1 mm) is insufficient to resolve the Bragg peak, leading to a systematic underestimation of the maximum delivered dose.

Be aware of this limitation in the dose calculation. To determine if the potential loss of dose is on a significant level, be extra careful in the patient specific QA process. (261660)

Note: *The proton and carbon ion PBS module in RayStation includes the possibility to set the minimum spot weight limits in the Optimization settings and the maximum spot weight limits in the beam model. It is the responsibility of the user to ensure that the PBS plan produced in RayStation is deliverable with respect to these parameters. The filtering of low and high weight spots is performed after a user defined number of iterations. Spot sorting and creation of islands with beam off (for quasi-discrete scanning) is performed in conjunction with spot filtering, or if the optimization is stopped before the spot filtering iteration number. Note that no filtering is performed if the optimization is stopped before the spot filtering iteration number.*

7.3.1 The Plan Optimization user interface

Workspace

The top left corner shows the result of the optimization process for each visualized ROI in a dose volume histogram (DVH). Behind the DVH are tabs for dose statistics as well as for review of clinical goals.

The bottom view defaults to the **Objectives/constraints** tab – listing the user specified objectives and constraints, with buttons for adding, editing and deleting of such functions. There are also tabs for the beam list, the energy layers and beam computation settings.

The lower right corner, visualizes the **Optimization Progress** in terms of function values per iteration.

The window at the top right corner shows image set data for the current plan in **2D**, **3D** or Beam's Eye View (**BEV**).

The upper right corner contains two buttons that makes it possible to switch between physical ion dose (**PHY**) and RBE dose (**RBE**). When physical ion dose is selected, it is possible to show either Beam Dose or Beam Set dose. When RBE dose is selected, all the doses listed in *The plan and dose selection toolbar on page 51* except beam dose can be displayed.

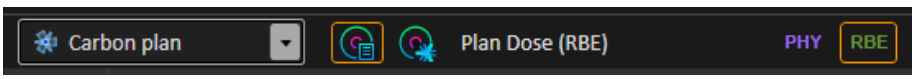


Figure 332. Top toolbar with physical ion dose (**PHY**) and Beam Dose selected.

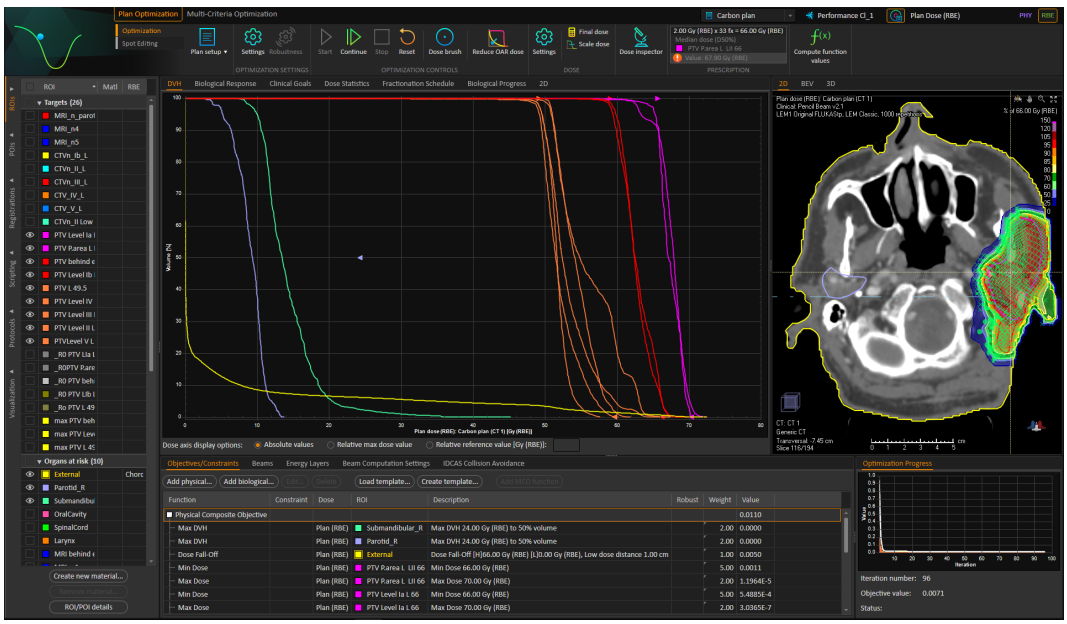
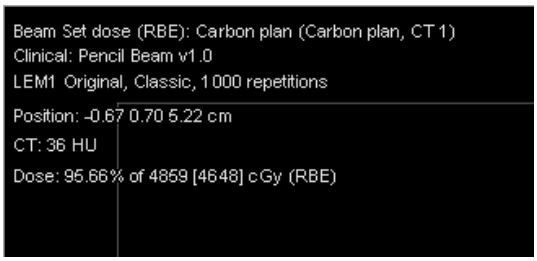


Figure 333. The Plan Optimization workspace for carbon ion PBS.

RBE model name in 2D dose views

For RBE doses, the RBE model name is displayed in the upper left corner of the 2D dose views. Algorithm usage (low dose approximation or classic) is also displayed. For the classic algorithm, the number of repetitions that has been used to compute the dose is also displayed.


Beam Set dose (RBE): Carbon plan (Carbon plan, CT 1)
Clinical: Pencil Beam v1.0
LEM1 Original, Classic, 1 000 repetitions
Position: -0.67 0.70 5.22 cm
CT: 36 HU
Dose: 95.66 % of 4859 [4648] cGy (RBE)

7.3.2 Optimization functions – objectives and constraints

An optimization problem consists of an objective function that is to be minimized and optionally a number of constraints. Constraints are used for requirements that must be fulfilled. The optimal solution to the problem is the one that gives the best value of the objective function without violating any of the constraints.

The user specifies a number of optimization functions. These can either be part of the objective function or used as individual constraints. The optimization functions included in the objective function are assigned weights reflecting their relative importance, i.e. an objective with the weight 10 is 10 times more important than one with weight 1. (Weights are almost only relative. Having all weights at 1 gives almost the same effect as having all weights at 100. The only difference will be in the application of the optimization tolerance and some internal numerical tolerances.)

Note: *In case of multiple beam sets that have a dependency, the optimization functions for the dependent beam set relate to either the combined beam set + background dose or the separate beam set dose. This is selected per optimization function in the Add Optimization Function dialog, see section 7.3.16 Multiple beam set optimization on page 644.*

An objective function or constraint does normally relate to the total RBE dose of the beam set. However, for physical ion dose it is also possible to let an objective relate to the dose of a selected beam. If a beam has been assigned in one beam specific target objective/constraint, the target projection in the spot selection, prior to the optimization, will only cover the ROI of that beam specific objective. If an additional target volume should be covered by that beam, a beam specific target objective/constraint must be defined also for that volume. This is useful for example when working with patch or match plans.

Add objectives and constraints

In order to add an optimization function that relates to the RBE dose, an RBE model needs to be selected, see *section 6.1.3 Create a new plan on page 306*.

Optimization functions can be added in two ways; by defining them one by one or by adding a set of pre-defined functions from a function list template (see *section 7.1.4 Optimization function list templates on page 529*).

To add an optimization function:

1. Click the **Add physical...** button in the **Objectives/Constraints** tab.

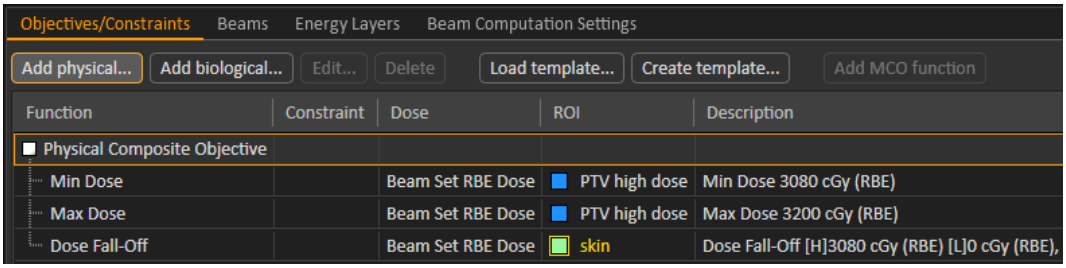


Figure 334. The **Objectives/Constraints** tab.

This opens the **Add Optimization Function** dialog.

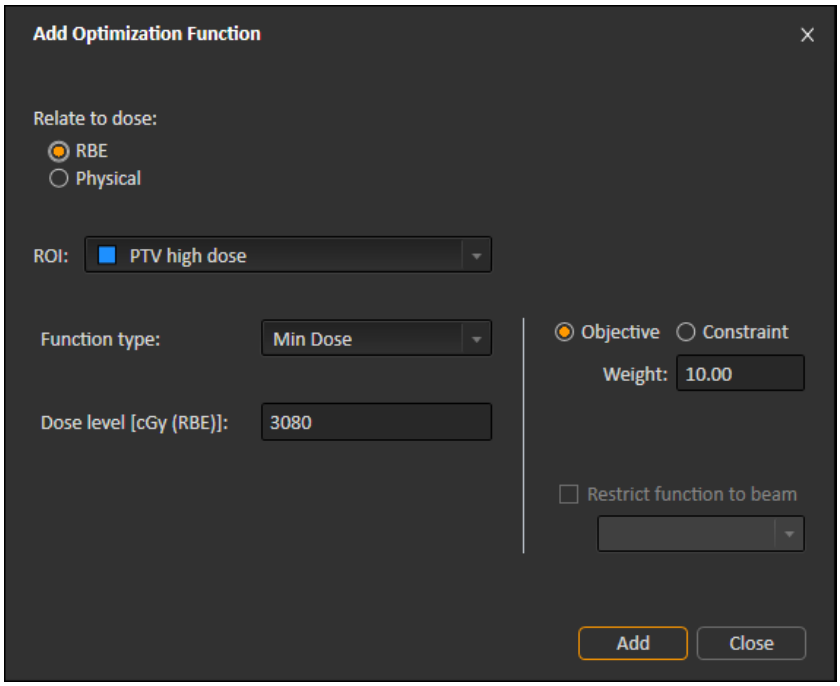


Figure 335. The **Add Optimization Function** dialog for carbon ions.

2. Select which dose the optimization function should relate to: **RBE** dose or **Physical** ion dose.
3. Select the **ROI** for which a function should be added. The function types available depend on the organ type of the ROI.
4. Select **Function type** and specify the function parameters (see the following section *Available objectives and constraints on page 618*).
5. Select if the function is going to be used as an **Objective** or a **Constraint**.
6. Assign a **Weight** to define the relative importance of the objective.

7. For **Physical** ion dose it is also possible to restrict the optimization function to a selected beam by checking the **Restrict function to beam** checkbox.

   In addition to selecting individual beams in the **Restrict function to beam** drop-down list, it is also possible to select **All beams individually**. With this option, one beam specific objective per beam is created automatically, with the dose values set to the given dose values divided by the number of beams.

8. Click **Add**.

Available objectives and constraints

The table below lists available function types dependent on the ROI organ type.

Function type	Organ type	Parameter(s)	Description
Min Dose	Target	Dose level	The objective/constraint is met when all parts of the ROI has a dose that is greater than or equal to the specified Min Dose.
Max Dose	OAR and target	Dose level	The objective/constraint is met when the ROI has a maximum dose that is less than or equal to the specified Max Dose.
Min DVH	Target	Dose level, Volume (%)	The objective/constraint is met when at least the specified % volume of the ROI receives at least the specified Min Dose.
Max DVH	OAR and target	Dose level, Volume (%)	The objective/constraint is met when only the specified % volume of the ROI receives more than the specified Max Dose.
Uniform Dose	Target	Dose level	The objective is met when the entire ROI volume receives a dose equal to the specified dose level.
Min EUD (Equivalent Uniform Dose)	Target	Dose level, Parameter A	A<1: Lower doses are given higher weight so that cold spots influence the EUD to a large extent. A=1: This corresponds to the mean dose. Cold and hot spots are given equal weight. The objective/constraint is met if the EUD value is greater than or equal to the dose level.
Max EUD	OAR and target	Dose level, Parameter A	A>1: Higher doses are given higher weight so that hot spots influence the EUD to a large extent. A=1: This corresponds to the mean dose. Cold and hot spots are given equal weight. The objective/constraint is met if the EUD value is less than or equal to the dose level.

Function type	Organ type	Parameter(s)	Description
Target EUD	Target	Dose level, Parameter A	The objective/constraint is met if the EUD value is exactly equal to the dose level.
Dose Fall-Off	OAR and target	High dose level, Low dose level, Low dose distance, Adapt to target dose levels	This function is a max dose function where the max dose level is a function of the distance to the target. The allowed max dose level falls off linearly from the high dose level at the border of the target to the low dose level at the dose distance from the target. At greater distances, the low dose level is still applied. The objective/constraints is met when all voxel doses within the specified ROI are less than or equal to their respective max dose levels. Note that the function is applied to voxels within the specified ROI. If the dose fall-off function is defined for an ROI of organ type which overlaps a target ROI, then the voxels within the target ROI are disregarded. Likwise, if the dose fall-off function is defined for a target ROI which overlaps other target ROIs, then the voxels within the other target ROIs are disregarded. It is advisable to select **Adapt to target dose levels** for cases with multiple target levels. If **Adapt to target dose levels** is selected, the high dose level is adjusted relative to the highest dose level of each target. ***Note:*** *The high dose level will not be adapted if the target functions are defined on both planned dose and beam set dose.*
Uniformity constraint	OAR and target	Relative standard deviation (Rel. std. dev. (%))	The constraint is met when the variation of dose within the ROI is less than the specified % variation. (The uniformity constraint does not specify the desired dose level – dose level must be specified by applying an additional Min or Max dose objective or constraint for the ROI.)

The optimization functions are described in detail in *RSL-D-RS-7.0-OPT, A guide to optimization in RayStation 7*.

Edit objectives or constraints

It is possible to edit an existing objective/constraint by double-clicking on it in the objectives/constraints tab, or by clicking the **Edit...** button. Another way to modify the objectives/constraints is by dragging the corresponding arrow symbol in the DVH window.

Note: *At least one target function, i.e. Min Dose, Min DVH, Uniform Dose or Min EUD must be included in the optimization problem.*

Delete objectives or constraints

Use the **Delete** button to delete objectives or constraints from the list.

7.3.3 Optimization function list templates

A set of objectives and/or constraints can be stored as a function list template. The function list templates can simplify the planning process, since standard optimization functions can be re-used as a starting point when optimizing new plans.

Add optimization functions from template

To add optimization functions from the function list, click the **Load template...** button. Select a function list template in the drop-down list. The objectives and constraints for the selected template are listed in the dialog's lists. To add the template's functions to the plan, click the **Add** button in the **Select Function List Template** dialog.

To rename the selected template, click **Rename** and enter a new name for the template. To delete the selected template, click **Delete**.

To approve a template, click **Approve**. Only admin users can approve a template. Approved templates have a padlock next to the template name. If a non-approved template is loaded, a warning will be displayed. These warnings can be disabled in Clinic Settings (*section D.2.2 The Preferences tab on page 922*).

A template with functions that relate to RBE dose can be applied to a plan that has a different modality than carbon ions. However, a template that contains a function that relates to physical dose cannot be applied to a plan with a different modality than carbon ions.

Optimization functions from a template that has been created from a plan with another modality than carbon ions, can be added to a carbon ion plan. The optimization functions will in this case relate to RBE dose.

Create function list template

A function list template can be created from a plan's existing set of optimization functions. To store the current plan's functions as a template, click the **Create template...** button and enter a name for the new template. (The template can later be renamed or deleted from the **Select Function List Template** dialog.)

Note: *In case of multiple beam sets that have a dependency, function list templates cannot be created for the second beam set if it contains objectives that relate to the beam set dose.*

7.3.4 Beam list

The **Beams** tab contains the beam list and includes columns for **Isocenter**, **Treatment machine**, **Snout Name**, **Snout Position**, **Gap**, **Gantry angle**, **Couch angle**, **Spot Tune ID**, **Range shifter**, **Range modulator**, **Number of energy layers**, **10^6 NP/fx** and **Spot weight**. For more information, see *section 6.1.6 Add, edit, copy or delete beams on page 316*.

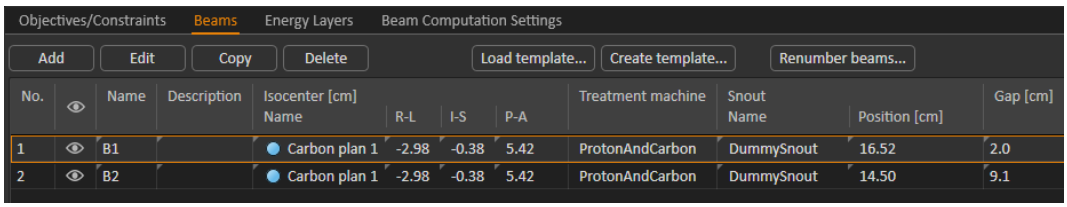
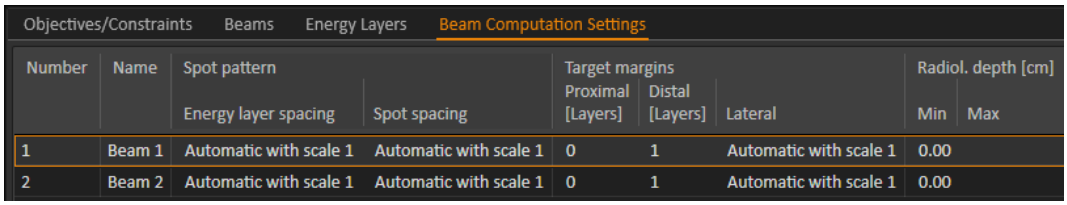


Figure 336. The **Beams** tab for carbon ions.

The Spot tune id name will be DICOM exported. The Spot tune id is selected in the Add beam dialog, but the Spot tune id column will not be populated until after the optimization. In RayStation 7 only one spot tune id is supported. The Range modulator applied on the beam is visible in the beam list. This object is set during beam commissioning and cannot be modified by the user. In RayStation 7, only one range modulator is supported for a given beam model. The Range modulator name will be DICOM exported.

7.3.5 Beam Computation Settings

The **Beam Computation Settings** tab contains the following columns: **Number**, **Name**, **Spot pattern**, **Target margins** (**Proximal**, **Distal** and **Lateral**), **Min** and **Max Radiol. Depth**, **OAR range margin**, **Distal edge Margin**, **Spot Tune ID** and **Layer repainting**. These are described further in the *Define spot selection and layer repainting settings* below.



Number	Name	Spot pattern		Target margins			Radiol. depth [cm]	
		Energy layer spacing	Spot spacing	Proximal [Layers]	Distal [Layers]	Lateral	Min	Max
1	Beam 1	Automatic with scale 1	Automatic with scale 1	0	1	Automatic with scale 1	0.00	
2	Beam 2	Automatic with scale 1	Automatic with scale 1	0	1	Automatic with scale 1	0.00	

Figure 337. The **Beam Computation Settings** tab for carbon ions.

Define spot selection and layer repainting settings

The table below lists the parameters that are used during the initial spot selection when starting a new optimization and the parameters that are used when setting layer repaintings at the end of an optimization.

Parameter	Description
Spot pattern, **Energy layer spacing**	The **Energy layer spacing** can be either a constant water equivalent distance or an automatic distance with a scaling factor: • **Automatic with scale**: This option is a variable distance that depends on the Bragg peak width. The energy separation between two adjacent energy layers equals the energy loss over the width (80% dose level) of the most distal Bragg peak in the pair. This means that each Bragg peak will intersect the following Bragg peak at approximately 80% of the dose maximum for a scaling factor of 1. The distance will decrease with a smaller scaling factor value. The default value for this variable can be defined in Clinic Settings. • **Constant [cm water]**: This option is a constant distance. The energies will be set so that the distance between the Bragg peaks will correspond to the user-defined value (in water).

Parameter	Description
Spot pattern, **Spot spacing**	The **Spot spacing** can be either a constant distance or an automatic distance with a scaling factor: • **Automatic with scale**: This option is a variable distance that depends on the radial spread in the Bragg peak for a specific energy. The spot distance is determined as 1.06 times the projected sigma multiplied by a scaling factor chosen by the user. The spot distance is constant within an energy layer but can deviate between different energy layers. The distance will increase with a larger scaling factor value. The default value for this variable can be defined in Clinic Settings. • **Constant [cm]**: This option is a constant distance.
Target margins: **Proximal**, **Distal** and **Lateral**	It is possible to set target margins during spot selection in the proximal, distal and lateral directions: • **Proximal [Layers]** - The selected number of energy layers will be added as a proximal target margin. The default value for this variable can be defined in Clinic Settings. • **Distal [Layers]** - The selected number of energy layers will be added as a distal target margin. The default value for this variable can be defined in Clinic Settings. • **Lateral** - If the **Automatic with scale** option is selected, the lateral target margin is determined as a function of the average spot size at the Bragg peak maximum for the highest energy. It is possible to increase or decrease the automatic margin by entering a scaling factor. The default value for this variable can be defined in Clinic Settings. If the **Constant [cm]** option is selected, it is possible to set the lateral margin as specified in cm.
Radiol. Depth [cm]	Bragg peaks are positioned at radiological depths larger (or smaller) than the specified minimum (or maximum) radiological depth in cm. If no value is specified for the maximum radiological depth, no upper limit will be applied to the radiological depth.
OAR range margin	The OAR range margin (cm water) is applied proximal to the specified organ-at-risk. Bragg peaks are not positioned within or distal to the specified organ-at-risk including this margin.
Distal edge Margin [cm]	A distal edge margin of 0.0 cm aims at setting the spots at the distal target edge. It is possible to increase and or decrease the margin in order to obtain the desired dose distribution.

Parameter	Description
Spot Tune ID	The spot tune id selected in the Add/Edit Beam dialog.
Layer repainting	The number of paintings for each energy layer of a beam is set at stop and at the end of an optimization. The options for layer repainting are: **No. of paintings**: The number of paintings of each energy layer is set to the entered number. **Max 10^6 NP/layer paint**: The number of paintings of each energy layer is set so that the 10^6 NP of each layer paint is lower than the specified value. ***Note:*** *If the beam 10^6 NP or energy layer weight is modified after optimization, the number of paintings of the energy layers are not automatically updated.*

The spot positions are set at the start of the optimization in such a way that all spot centers fit inside the inner dimensions of the selected snout at the specified location.

If a range shifter is used, the region in which spots can be placed is also constrained by the location and shape of the range shifter, with an additional inner margin of 10 mm. The range shifter lateral dimensions are by default determined by the snout outer dimensions, but could optionally be assigned in the machine model to individual shapes and dimensions.

If the snout or range shifter restricts the spot positions to a too large extent compared to the target projection, the optimizer may try to increase the weights of the spots close to the target border. This will generate a non-uniform dose distribution with cold and hot spots. It is the responsibility of the user to ensure that spots cover the treated volume with adequate margin.

7.3.6 Specify optimization settings

Click the **Settings** button to open the **Settings** dialog.

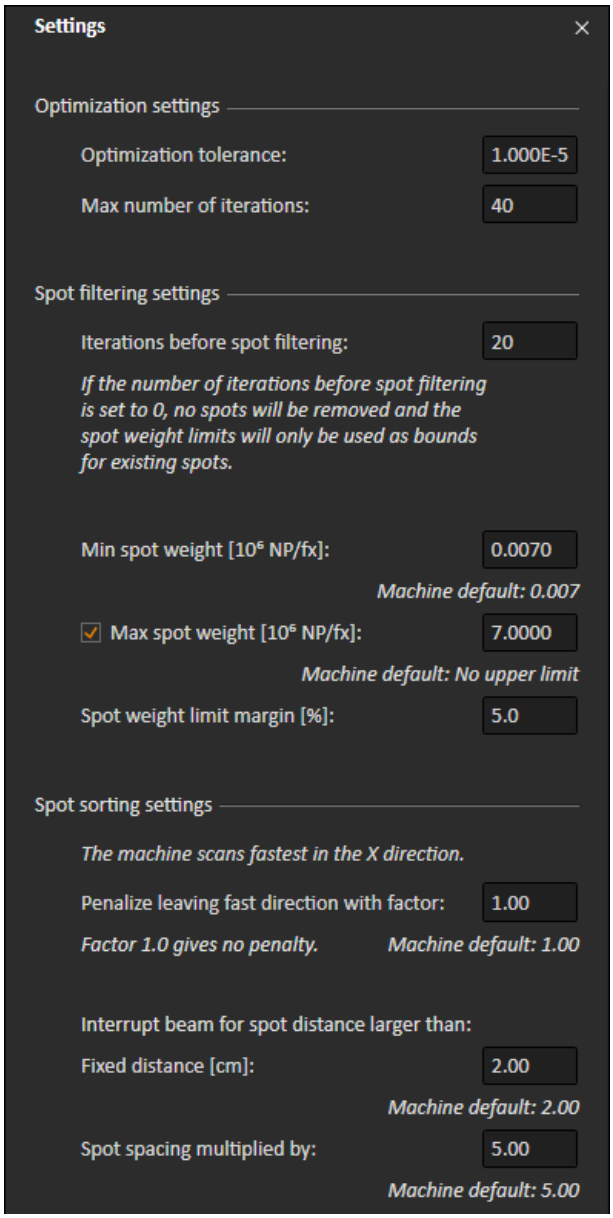

Settings
Optimization settings
Optimization tolerance:
1.000E-5
Max number of iterations:
40
Spot filtering settings
Iterations before spot filtering:
20
If the number of iterations before spot filtering is set to 0, no spots will be removed and the spot weight limits will only be used as bounds for existing spots.
Min spot weight [10⁶ NP/fx]:
0.0070
Machine default: 0.007
Max spot weight [10⁶ NP/fx]:
7.0000
Machine default: No upper limit
Spot weight limit margin [%]:
5.0
Spot sorting settings
The machine scans fastest in the X direction.
Penalize leaving fast direction with factor:
1.00
Factor 1.0 gives no penalty.
Machine default: 1.00
Interrupt beam for spot distance larger than:
Fixed distance [cm]:
2.00
Machine default: 2.00
Spot spacing multiplied by:
5.00
Machine default: 5.00

Figure 338. The **Settings** dialog for carbon ion PBS optimization.

The user can edit the following PBS optimization settings for carbon ions:

Parameter	Description
Optimization tolerance	The software stops the optimization when the change in the Composite Objective value indicates that an optimal solution has been found. This occurs when the change in objective value is less than the tolerance level. The optimization tolerance should be around 1e-5 or 1e-6.
Max number of iterations	The optimization algorithm can usually find an optimal solution in 25–100 iterations, but by setting maximal number of iterations the optimization can be stopped prior to this if it is believed that the objectives will not be met or whenever the result already is satisfying.
Iterations before spot filtering	After the specified number of iterations, all spots with a weight below the minimum spot weight limit are filtered out. For subsequent iterations the limit is used as a lower bound for remaining spots. If set to 0, no spots will be removed and the minimum spot weight will only be used as a lower bound for existing spots.
Min spot weight (10^6 NP/fx)	The limit used (with the margin described below added) when filtering out low weight spots. The **Machine default** value is read from the machine.
Max spot weight (10^6 NP/fx)	The maximum spot weight limit used in the PBS optimization. The **Machine default** value is read from the machine.
Spot weight limit margin (%)	The user can add a margin to the minimum spot weight to allow some smaller modifications of the spot weights after optimization without making the plan undeliverable (e.g., allow scale dose to prescription).
Spot sorting settings	The spot sorting can be steered to prefer taking steps in the direction for which the machine scans fastest. This is done by setting the **Penalize leaving fast direction with factor** to a value greater than 1. When the spots are sorted to yield the shortest path, distances that leave the fast direction are multiplied by this factor. The **Machine default** values are read from the machine. For treatment machines that support quasi-discrete PBS (where the beam is on between spots), there are two additional parameters in the **Settings** dialog; **Fixed distance** and **Spot spacing multiplied by**. These are described further in the following section *Quasi-discrete spot islands*.

Quasi-discrete spot islands

For treatment machines that support quasi-discrete PBS (where the beam is on between spots), there are two additional parameters in the **Settings** dialog; **Fixed distance** and **Spot spacing multiplied by**.

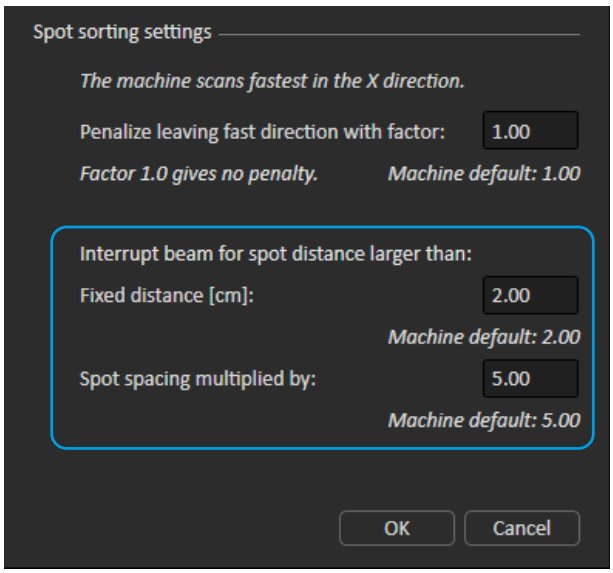


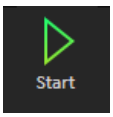
Figure 339. Spot sorting settings for treatment machines that support quasi-discrete PBS.

Following spot sorting, the spots map in each energy layer is separated into "islands", i.e., sequences of positions that the scanned beam should traverse with the beam on. The beam is interrupted between islands. The positions between which to interrupt the beam are determined by two parameters: a **Fixed distance** and the **Spot spacing multiplied by** a factor. For all distances larger than the smaller of these two values, the beam will be turned off. To minimize the number of interruptions of the beam, these parameters are also used in the spot sorting. Steps that are longer than the interruption distance are given a constant penalty of 1000 in addition to the step length. Thus, the resulting scan path will avoid going between positions farther apart than this distance when possible, but will take these steps when no other possibility exists.

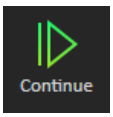
7.3.7 Running the carbon ion PBS optimization

The optimization process is controlled by the optimization control buttons in the toolbar.

The optimization control buttons



The **Start** button starts a new optimization. Only active if the beams are empty (no energy layers).

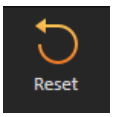


The **Continue** button starts an optimization from the current state using the existing energy layers and spots. The optimization will continue using the user-defined optimization functions. Only active if there is at least one energy layer in every beam.

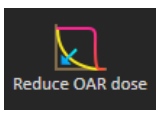
Note: *If the irradiated volume after an optimization is too small or too large, the target volume (as defined through the optimization functions) may need to be modified. After such a modification, it is strongly advised to reset and start a new optimization instead of continuing.*

The **Stop** button stops the optimization after the current iteration is finished.

Note: *The Stop button should be used with some care in proton and carbon ion optimization for plans that are intended to be delivered to a patient. Beside the primary point that an optimal plan cannot be ensured, if the optimization is stopped, there is one more reason. The filtering of low and high weight spots is performed after a user-defined number of iterations. If the optimization is stopped before this iteration number, no filtering or sorting is performed. This means that the resulting plan will generally not be deliverable, and is therefore not clinically relevant.*



The **Reset** button resets the beams, i.e. removes all energy layers and sets all beam MUs to zero.



The **Reduce OAR dose** button starts an optimization from the current state. Auto-generated reference dose functions are used to reduce the dose in the risk organs (OARs), while maintaining dose homogeneity in the target organs. If the current beam set already has minimal OAR dose, this function will not have any significant effect.

Optimization Progress

The lower right window of the workspace shows the result of the optimization progress. A graph plots the values of the objective functions as a function of the number of iterations. All values are plotted

separately but also the sum of the objectives (bold white line) which the optimization tries to minimize. The objective function curves are colored in the same color as the corresponding ROIs.

When using the Reduce OAR dose function, the displayed objective functions are those specified by the user, not the auto-generated ones.

Figure 340. The Optimization progress graph.

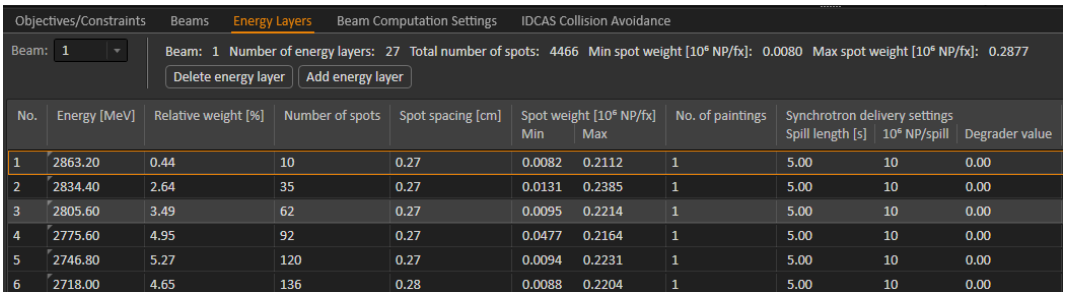
Optimization result

When the optimization is completed, the energy layers and the corresponding spots will be visible in the **Energy Layers** tab and in the BEV.

The RBE dose after optimization will be approximate due to that the Low dose approximation is used during optimization. Therefore, a final clinical dose needs to be computed after RBE dose optimization.

7.3.8 Energy layers

The **Energy Layers** tab for carbon ions contains the energy layers and the corresponding weights used for creating the SOBP for the active beam.


Objectives/Constraints
Beams
Energy Layers
Beam Computation Settings
IDCAS Collision Avoidance
Beam: 1
Beam: 1 Number of energy layers: 27 Total number of spots: 4466 Min spot weight [10⁶ NP/fx]: 0.0080 Max spot weight [10⁶ NP/fx]: 0.2877
Delete energy layer
Add energy layer

No.	Energy [MeV]	Relative weight [%]	Number of spots	Spot spacing [cm]	Spot weight [10⁶ NP/fx] Min	Spot weight [10⁶ NP/fx] Max	No. of paintings	Synchrotron delivery settings Spill length [s]	Synchrotron delivery settings 10⁶ NP/spill	Synchrotron delivery settings Degrader value
1	2863.20	0.44	10	0.27	0.0082	0.2112	1	5.00	10	0.00
2	2834.40	2.64	35	0.27	0.0131	0.2385	1	5.00	10	0.00
3	2805.60	3.49	62	0.27	0.0095	0.2214	1	5.00	10	0.00
4	2775.60	4.95	92	0.27	0.0477	0.2164	1	5.00	10	0.00
5	2746.80	5.27	120	0.27	0.0094	0.2231	1	5.00	10	0.00
6	2718.00	4.65	136	0.28	0.0088	0.2204	1	5.00	10	0.00

Figure 341. The **Energy Layers** tab for carbon ions.

The tab header displays information about the active beam, the number of energy layers, the total number of spots and the minimum/maximum spot weight of the beam. It is possible to edit the energy for an energy layer directly in the **Energy layers** tab or to delete the selected energy layer by clicking the **Delete energy layer** button. It is also possible to add an energy layer by clicking the **Add energy layer** button, see *Add energy layer on page 632*.

The list contains the following information:

- **Number**: Energy layer number.
- **Energy**: Energy in MeV.
- **Relative weight**: Relative weight in percent.
- **Number of spots**: Number of spots.
- **Spot spacing**: Spot spacing in centimeters.
- **Spot weight, Min**: Minimum spot weight in 10^6 NP/fraction.
- **Spot weight, Max**: Maximum spot weight in 10^6 NP/fraction.
- **No. of paintings**: The number of repaintings of the energy layer that is exported to DICOM.
- **Synchrotron delivery settings, spill length**: The duration of a beam extraction in seconds.
- **Synchrotron delivery settings, 10^6 NP/spill**: The number of particles that are extracted during a spill.
- **Synchrotron delivery settings, Degrader value**: A degrader can be added to reduce the beam current. The degrader value is in the range 0 to 1, where 0 corresponds to no degradation and 1 to full degradation.

The relative weight is normalized within each beam and the total relative weight sums up to 100%.

Note: *The presented weights are the effective weights used by the dose calculation, these weights may not be the same as those used by the beam delivery system.*

The **Energy Layers** tab is synchronized with the BEV. Click on a row in the list to display the corresponding energy layer in the BEV.

Add energy layer

To add a new energy layer:

1. Click the **Add energy layer** button to open the **Add Energy Layer** dialog.

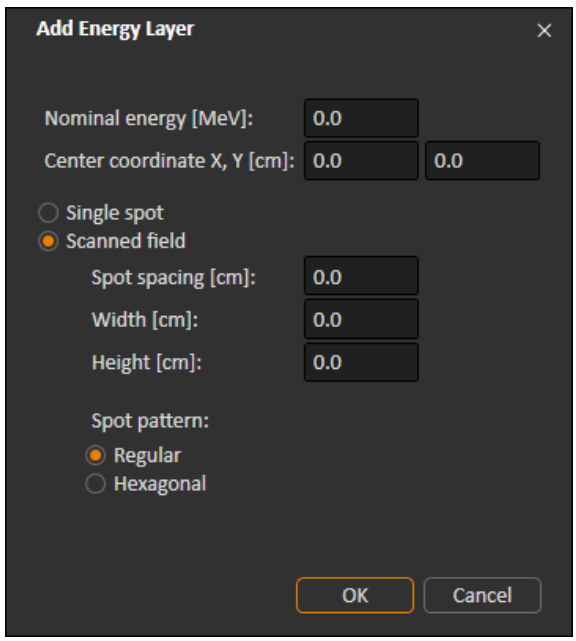


Figure 342. The **Add Energy Layer** dialog.

2. Enter the **Nominal energy [MeV]**.
3. Enter the **Center coordinate X, Y [cm]**.
4. Select a **Single spot** or a **Scanned field**.
5. If a **Scanned field** is selected, also:
   - Enter the **Spot spacing [cm]** in the scanned field.
   - Enter the **Width [cm]** and **Height [cm]** of the scanned field.
   - Select either **Regular** or **Hexagonal** spot pattern.

7.3.9 Spot editing

The Spot editing tools are located in the **Spot Editing** tab in the toolbar and operate on the spots in the BEV.

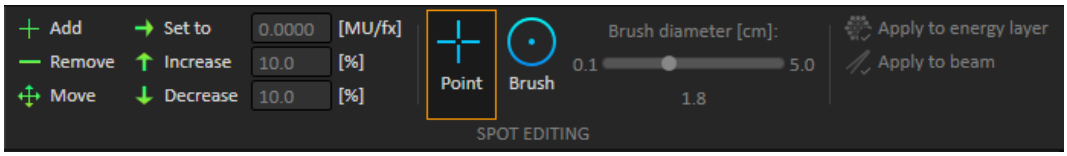


Figure 343. The spot editing tools for carbon ions.

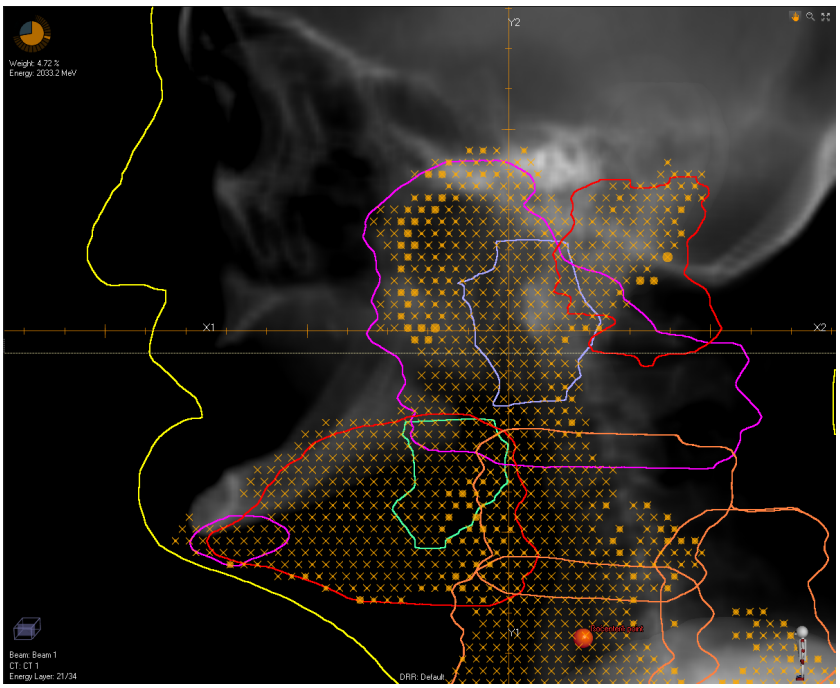
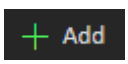


Figure 344. Spot editing in the Beam's Eye View (BEV).

Add a spot in the BEV

A spot with zero initial weight can be added using the point tool.

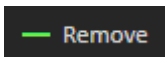
1. Click the **Add** button.



2. Click at a position in the BEV to add the spot.

Remove a spot from the BEV

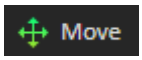
Use the point tool to remove a specific spot or use the brush tool to remove several spots.



Move a spot in the BEV

Move a specific spot using the point tool.

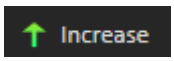
1. Click the **Move** button.

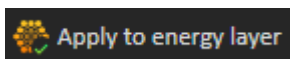
2. Click on a spot and drag and drop it to a desired position.

Increase the weight of a spot by a factor

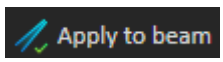
1. Click the **Increase** button.

2. Enter a value in percent in the corresponding field.
3. Select to apply the modification to:
   a. all spots in the selected energy layer by clicking the **Apply to energy layer** button.

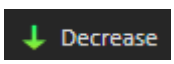
   b. all spots in the selected beam by clicking the **Apply to beam** button.

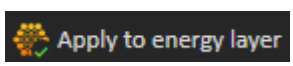
   c. those spots in an energy layer chosen by the brush or point tool.

Decrease the weight of a spot by a factor

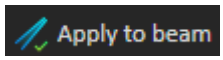
1. Click the **Decrease** button.

2. Enter a value in percent in the corresponding field.
3. Select to apply the modification to:
   a. all spots in the selected energy layer by clicking the **Apply to energy layer** button.

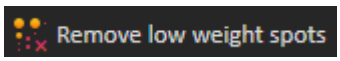
b. all spots in the selected beam by clicking the **Apply to beam** button.



c. those spots in an energy layer chosen by the brush or point tool.

Remove low weight spots

1. Click the **Remove low weight spots** button.



This opens the Remove low weight spots dialog.

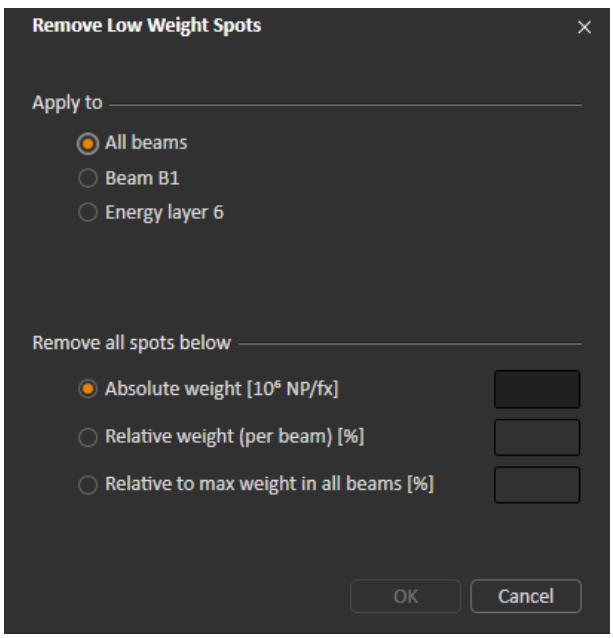


Figure 345. The Remove low weight spots dialog.

2. Select to remove low weight spots in:
   a. all beams.
   b. a specific beam.
   c. a specific energy layer.
3. Select to remove all spots below:
   a. an absolute weight [10^6 NP/Fraction].

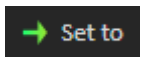
b. a relative weight (per beam) [%].

c. a fraction of the maximum weight in the energy layer [%].

4. Click **OK**.

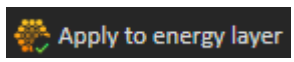
Set the number of 10^6 NP/fraction of spots

1. Click the **Set to** button.

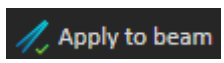


2. Enter a value in the corresponding field [10^6 NP/fraction].
3. Select to apply the modification to:

a. all spots in the selected energy layer by clicking the **Apply to energy layer** button.



b. all spots in the selected beam by clicking the **Apply to beam** button.



c. those spots in an energy layer chosen by the brush or point tool.

Remove energy layer

In order to remove the selected energy layer, click the **Remove energy layer** button.

7.3.10 Bragg peak visualization

During optimization and final dose computation, the positions of the Bragg peaks will be computed. For more information, see *section 7.2.11 Bragg peak visualization on page 599*.

7.3.11 Define or modify prescription

For carbon ions the prescription always relates to the RBE dose. For instructions on how to to define or modify a dose prescription, see *section 6.1.12 Define or modify prescription on page 343*.

7.3.12 Compute dose

Dose computation can be performed using the buttons in the **DOSE** toolbar.

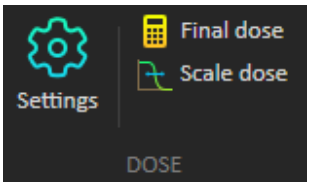
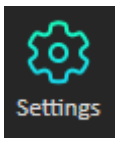


Figure 346. The **DOSE** toolbar.

Dose computation settings

To edit the dose computation settings:

1. Click the **Settings** button.



2. This opens the **Dose Computation Settings** dialog.

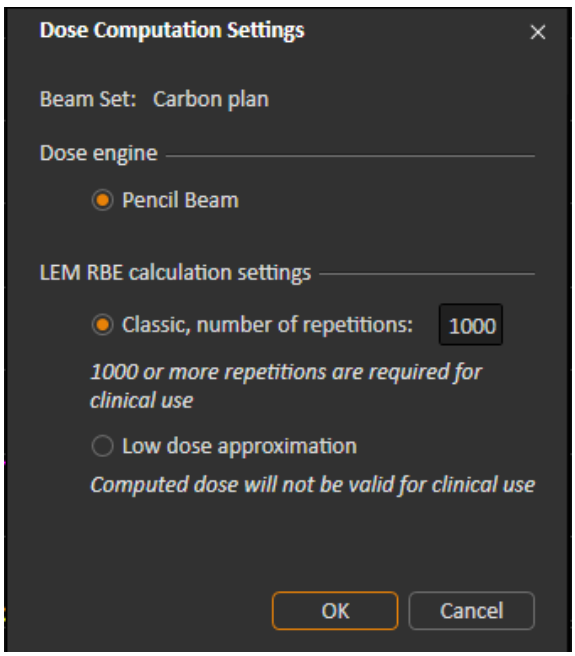


Figure 347. The **Dose Computation Settings** dialog.

3. Select setting for LEM RBE calculation:

- **Classic, number of repetitions** - with this option, the number of repetitions can be entered. For clinical use 1000 or more repetitions are required.
- **Low dose approximation** - with this option, the dose calculation is approximate and will not be valid for clinical use.

4. Click **OK**.

Plan approval prerequisites

For carbon ions, the following is also required in order to compute a final clinical dose:

- An RBE model must be selected in the **New plan**/**Edit plan** dialog.

  For more information, see *section 6.1.3 Create a new plan on page 306*.

- The RBE model must be allowed for clinical use. This is set in the RayBiology application by checking the **Allow for clinical use** checkbox.

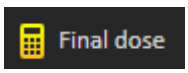
  For more information about the RayBiology application, see *Appendix E RayBiology*.

- The **Classic** LEM RBE calculation needs to be selected for dose computation and at least 1000 repetitions has to be entered.

  For more information about the dose computation settings, see *section 7.3.12 Compute dose on page 639*.

Compute final dose

A final dose can be computed using the selected settings for dose computation. Click the **Final dose** button or type Ctrl + D to calculate the final dose.



The dose engine is described in detail in *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual*.

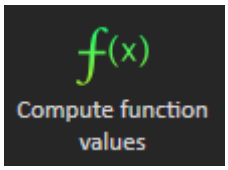
7.3.13 Scale dose

It is allowed to scale dose for carbon ions, but note the following:

- If dose scaling is performed on a dose using a nonlinear RBE model, a dose computation will automatically be triggered after clicking **OK**. Dose scaling may be automatically iterated to get closer to the desired value. Note that since the scaling factor is computed linearly, the resulting RBE dose will not, especially for large scaling factors, correspond with the desired value.
- If dose scaling is performed on an imported RBE dose, only the physical dose will be scaled and the imported RBE dose will be invalidated, since there is no information about the linear nature of the underlying RBE model.

7.3.14 Compute function values

If an optimization function is altered after an optimization is run the value for the changed function can be updated by clicking the **Compute function values** button in the toolbar.



7.3.15 The evaluation views

Dose Volume Histogram (DVH)

The DVH view presents the cumulative dose volume histograms of the ROIs selected in the ROI List. The dose can be displayed as **absolute** or **relative [%]**. It is also possible to manually set the reference value for the relative scale. For a further description of the DVH view, see *section 3.7.1 Dose Volume Histogram (DVH) on page 78*.

Note: *The optimization function markers in the DVH will always be displayed regardless of which dose they relate to. The tooltip will tell if it relates to RBE dose, physical beam set dose or physical beam dose.*

Dose statistics

The dose statistics view lists ROI dose information. For more information, see *section 3.7.2 Dose statistics table on page 79*.

Dose difference

The dose **Difference** view in the Plan Evaluation module displays the dose difference between two treatment plans. It is not possible to compare an RBE dose with a physical ion dose. For more information about comparing plans, see *section 8.1.4 Plan comparison on page 728*.

For carbon ions it is also possible to visualize the RBE factor in the **Difference** view. For instructions on how to visualize the RBE factor, see *section 7.3.17 RBE factor visualization on page 647*.

Clinical goals

The clinical goals functionality makes it possible to define evaluation criteria for specific ROIs and POIs. The result (pass/fail) is easy to read in a single column.

Clinical goals for carbon ions are always defined based on the RBE dose. For more information about the clinical goals functionality, see *section 3.7.3 Clinical goals on page 81*.

Note: *The clinical goals will not affect the optimization.*

7.3.16 Multiple beam set optimization

Multiple beam set planning and beam set dependencies are described in detail in *section 6.1.20 Multiple beam set planning on page 372*. This section describes optimization of multiple beam sets.

Independent beam sets

For independent beam sets the objectives/constraints always apply to the beam set dose. This means that, if the additional beam set is set as independent, the optimization will be carried out looking only at the dose of the separate beam set.

Dependent beam sets

If the additional beam set is set as dependent of the first beam set, the objectives/constraints can be defined to either relate to the separate beam set dose or, for RBE dose only, to relate to the combined beam set + background dose.

Any biological equivalent dose can be used as background dose. For carbon ion plans, this means that the RBE dose will be used.

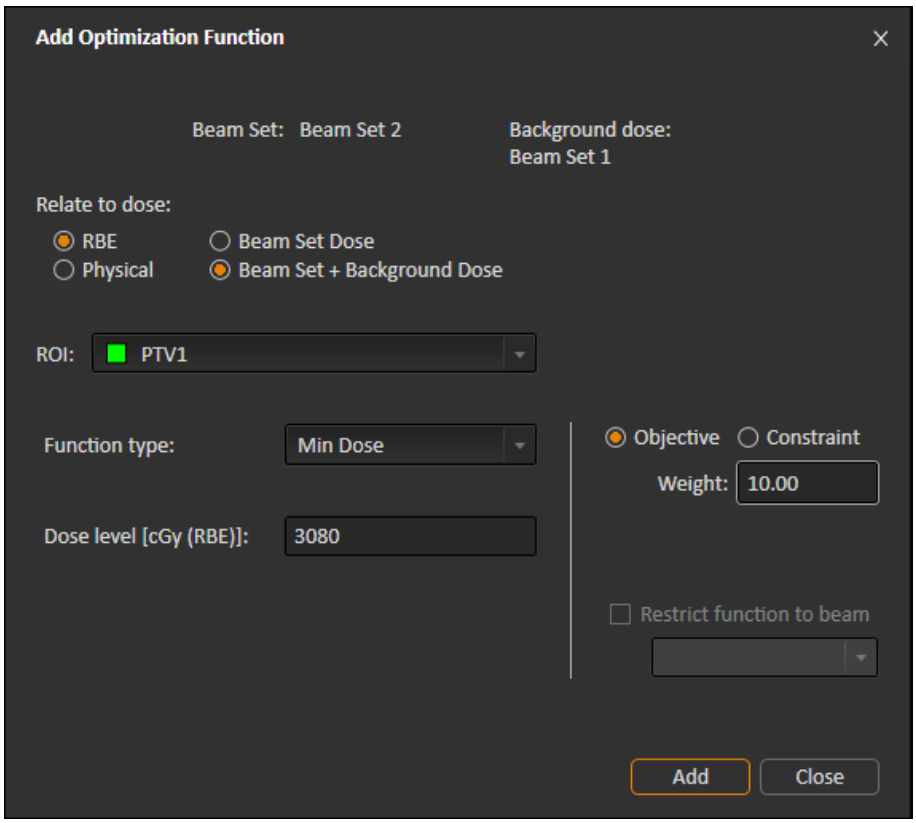


Figure 348. The Edit Optimization Function dialog where the objective function is defined to relate to the beam set + background dose.

If the objective is set to relate to the beam set + background dose, the selected beam set will try to create whatever dose is needed to reach the specified objectives/constraint for the combined dose from this beam set and the background dose that this beam set is dependent on. The background dose for a dependent beam set is the dose from the beam set it is dependent on plus, if applicable, the background dose for that beam set. For instance, if the background beam set has an underdosage of a corner of the target, the other beam set will try to create a higher dose in that area in order to compensate and achieve a homogenous beam set + background dose. There has to be a computed dose for the background beam set before the other dependent beam set can be optimized.

It is possible to define a composite objective function consisting of some objectives that relate to the beam set + background dose and other objectives that relate to the beam set dose.

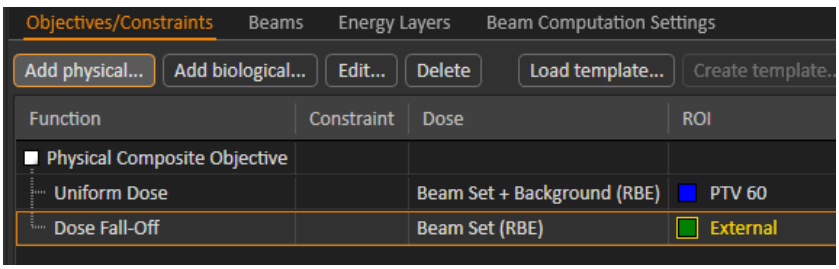


Figure 349. In the Dose column in the Objectives/Constraints tab it is possible to see if an objective/constraint relates to the beam set + background dose or only the beam set dose.

Note: *If the objectives/constraints for the dependent beam set applies to the beam set + background dose, the requested dose level must be reasonably higher than the background dose.*

Note: *Making the additional beam set dependent or independent will clear all existing prescriptions and objectives/constraints, since the dose levels will no longer be relevant.*

When planning with dependent beam sets, the DVHs will include checkboxes for dose presentation to allow simultaneous studying of the different planning doses. The dose presentation buttons are described further in *Dose presentation for multiple beam sets on page 374*.

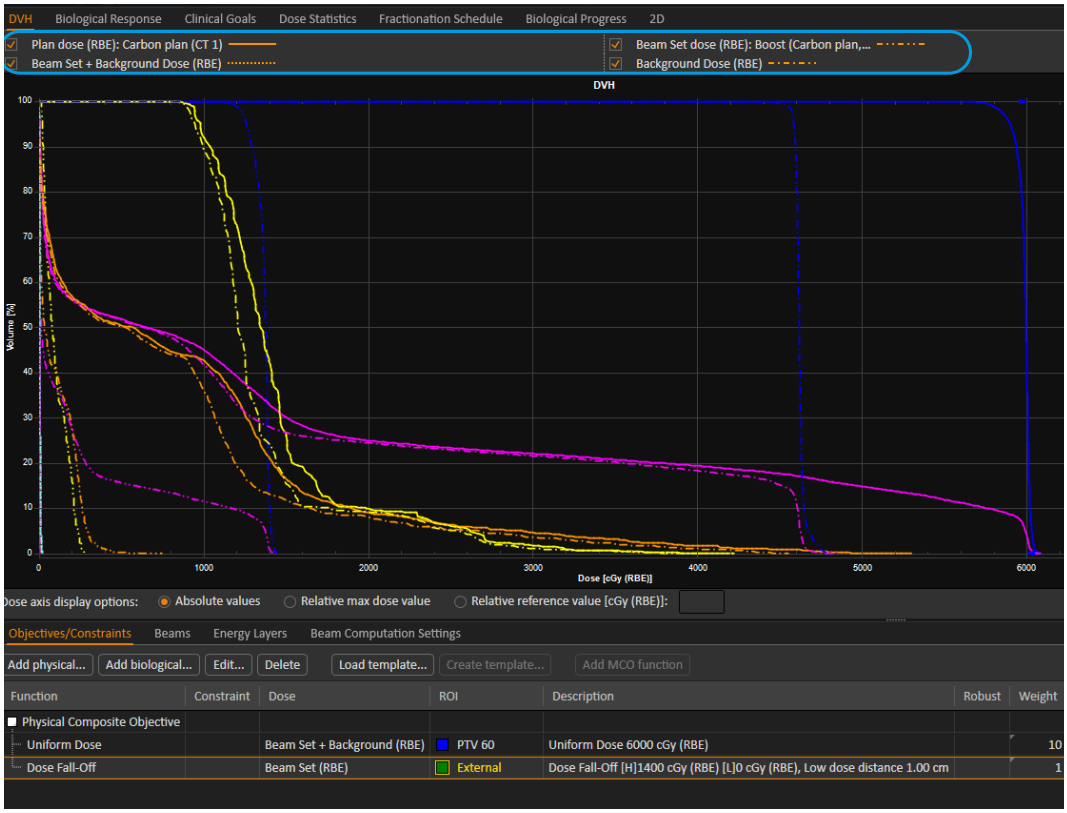


Figure 350. In the DVH view it is possible to study plan dose, beam set dose, beam set + background dose and background dose by checking the corresponding checkbox.

Note: *If a non-linear RBE model is used (e.g., the Local Effect Model), the RBE weighted dose must be computed collectively for all included beams and energies when they are delivered within the same fraction. Summation of individual RBE weighted beam doses is only relevant if they are delivered in different fractions. The user shall be aware that multiple beam sets, as well as separate treatment plans, are assumed to be delivered in separate fraction groups.*

7.3.17 RBE factor visualization

When comparing dose in the dose difference view, it is possible to display the RBE factor (i.e., the quotient when dividing the RBE dose with the physical ion dose).

To visualize the RBE factor:

1. In the Plan Evaluation module, click the **Select layout** button and select the following workspace layout:

2. Select the RBE dose in the **Current** view (the upper view or DOSE 1). This can either be done by clicking the **Select dose for plan** button, or by drag and drop from the **Doses** tab.

Figure 351. The **Current** view with the RBE dose selected.

3. Select the corresponding physical ion dose in the **Compare 1** view (the lower view or DOSE 2). This can either be done by clicking the **Select dose** button, or by drag and drop from the **Doses** tab.

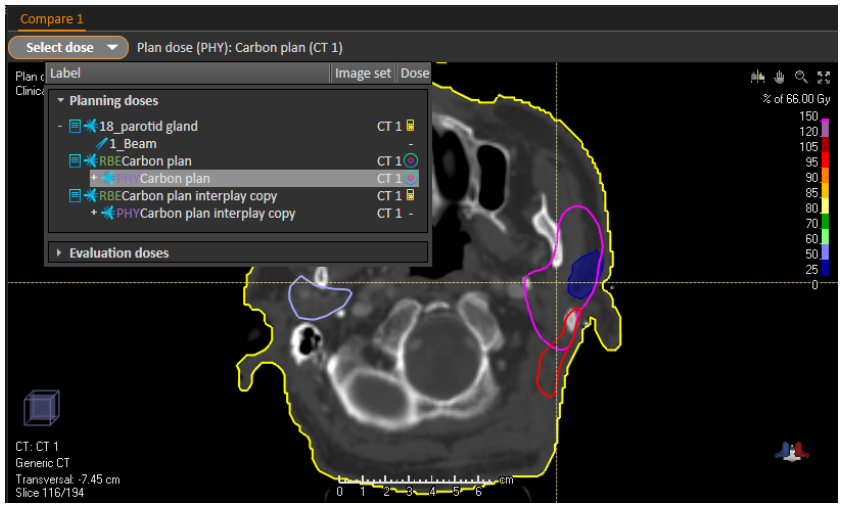


Figure 352. The **Compare 1** view with the physical ion dose selected.

4. The RBE factor can now be visualized in the **Difference** view (lower right view or DIFF). Only voxels displaying RBE dose are displaying RBE. The settings for the color table showing dose can be reviewed and changed in Edit color table.

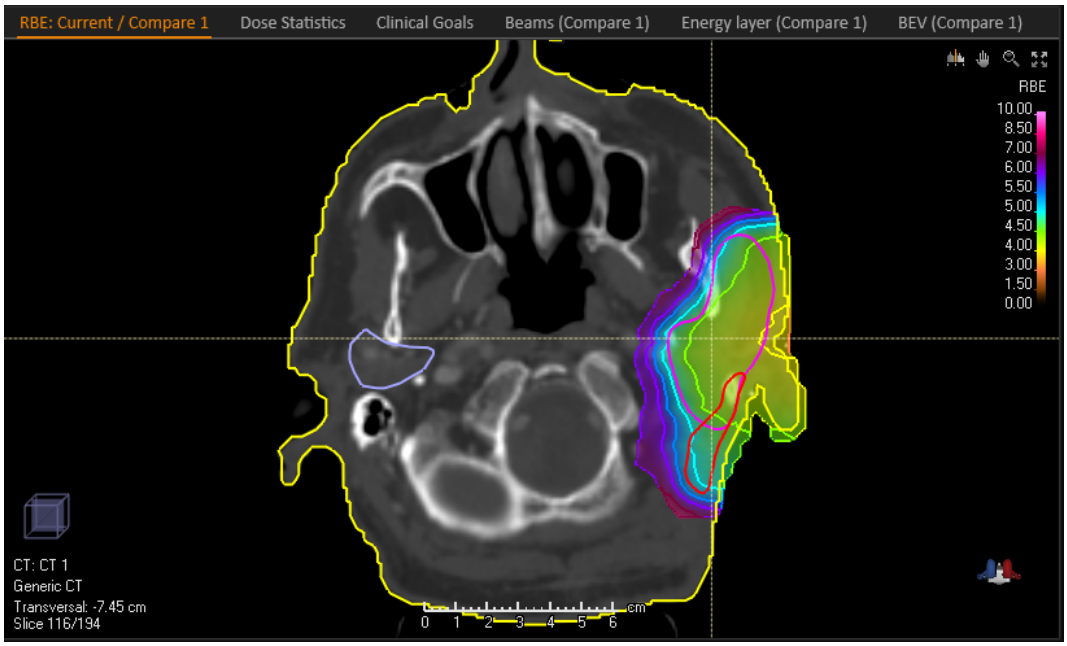


Figure 353. The RBE factor visualized in the **Difference** view.

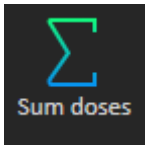
7.3.18 Evaluation of carbon ion PBS plans

An optimized PBS plan may be very sensitive to setup and density uncertainties, as well as to organ motion. These aspects should be taken into account when reviewing an optimized PBS plan. In the Plan Optimization module, not only the plan and beam set doses should be reviewed, but also individual beam doses. Inhomogeneous beam doses might result in that the plan will not be robust. To fully assess the robustness of a plan, compute perturbed doses in the Plan Evaluation module and compare this with the original plan.

7.3.19 Sum carbon ion doses

To sum doses:

1. In the Plan Evaluation module, click the **Sum doses** button.



This opens the **Sum Doses** dialog.

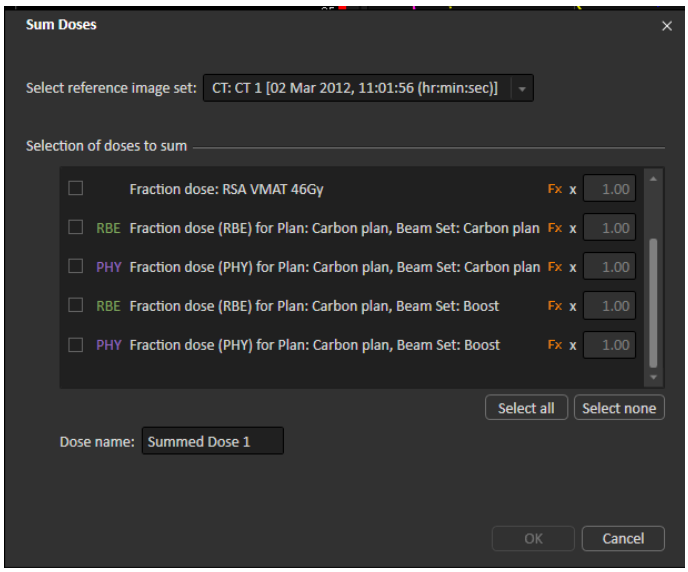

Sum Doses
Select reference image set:
CT: CT 1 [02 Mar 2012, 11:01:56 (hr:min:sec)]
Selection of doses to sum
Fraction dose: RSA VMAT 46Gy
Fx x 1.00
RBE Fraction dose (RBE) for Plan: Carbon plan, Beam Set: Carbon plan
Fx x 1.00
PHY Fraction dose (PHY) for Plan: Carbon plan, Beam Set: Carbon plan
Fx x 1.00
RBE Fraction dose (RBE) for Plan: Carbon plan, Beam Set: Boost
Fx x 1.00
PHY Fraction dose (PHY) for Plan: Carbon plan, Beam Set: Boost
Fx x 1.00
Select all
Select none
Dose name:
Summed Dose 1
OK
Cancel

Figure 354. The **Sum Doses** dialog.

2. Select **Reference image set**. Note that only doses calculated on the same image sets can be summed.
3. Select the doses to be summed by checking the corresponding checkboxes in the **Selection of doses to sum** list. It is possible to scale each dose by specifying the number of fractions to use in the summation - just enter a value in the x field to the right of each fraction dose in the list.

   Note: *It is not possible to sum RBE dose and physical ion dose.*

   It is possible to sum doses with either an RBE dose or a physical ion dose. The result is:

   - If one of the doses in the summation is an RBE dose, the summed dose will be an RBE dose.

- If one of the doses in the summation is a physical ion dose, the summed dose will be a physical ion dose.

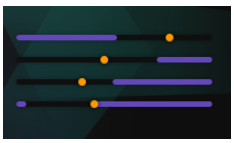
4. Enter a **Dose name** for the summation.
5. Click **OK**. Now the summed dose appears in the dose list, and from there it can be dragged into a view in the workspace.

7.4 THE MULTI CRITERIA OPTIMIZATION MODULE

The Multi Criteria Optimization (MCO) module provides unique tools for finding a sound tradeoff between conflicting treatment goals in treatment plan optimization. In contrast to traditional plan optimization, where optimal plans are created in an iterative fashion based on the execution of a series of optimizations, the module supports real-time exploration of the optimal solution space produced in a single optimization step.

As in the Plan Optimization module, input is provided in terms of objective functions and constraints, but no weight is assigned to the objectives. Instead, an interactive navigation tool is used to explore the tradeoffs of the treatment plan.

Supported treatment techniques are SMLC, DMLC, VMAT, TomoHelical and proton PBS.



In this section

This section contains the following sub-sections:

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7.4.2	The Multi Criteria Optimization user interface	p. 655
7.4.3	The Multi Criteria Optimization workflow	p. 657
7.4.4	Adding tradeoff objectives and constraints	p. 661
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7.4.6	Pareto plans	p. 664
7.4.7	Navigation	p. 667
7.4.8	Create a deliverable plan	p. 671
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7.4.1 Introduction to Multi Criteria Optimization (MCO)

An MCO approach to treatment planning allows exploration of, and makes it possible to understand, the tradeoff between getting the required dose to the tumorous regions and not overdosing the surrounding healthy organs, and thus providing means to select the best plan for each patient.

The RayStation approach – computation of Pareto plans

The RayStation approach to MCO treatment planning is based on the computation of a set of so-called Pareto optimal plans. A treatment plan is Pareto optimal if it cannot be improved in any one objective without worsening another. The set of all Pareto optimal plans constitutes the so-called Pareto surface. In RayStation the user explores an approximation of the Pareto surface to find a satisfactory treatment plan.

The Pareto surface is approximated by a discrete set of Pareto plans, which are optimal with respect to machine parameters or fluence. For treatment technique VMAT the Pareto plans are optimal with respect to fluence. For treatment techniques PBS and TomoHelical the Pareto plans are optimal with respect to machine parameters. For treatment techniques SMLC and DMLC it may be specified if Pareto plans shall be optimal with respect to fluence or machine parameters.

The number of Pareto plans that constitute the approximation is specified by the user, with the minimum requirement being N+1, where N denotes the number of user-specified objectives. The first N plans are generated by optimizing each objective individually. The (N+1)th plan is generated by equally balancing all N objectives. The preference weights of any Pareto plan generated beyond this stage are chosen towards minimizing the approximation error of the current Pareto surface representation. For $N < 10$, the selection is based on an inner and outer polyhedral approximation of the Pareto surface. For $N \geq 10$, the preference weights are instead chosen by pairing together the most anti-correlated objectives. Constraints are required throughout Pareto plan generation to ensure satisfactory target coverage and hot spot control.

Dose distributions form a basis for the user-controlled Pareto surface navigation

The dose distributions of the Pareto plans form a basis for the user-controlled Pareto surface navigation. The pre-computed Pareto plans are combined into a navigated dose distribution based on the user-input from a set of slider controls, thereby allowing the Pareto surface representation to be examined in a continuous fashion. In general, any convex combination of plans is allowed during navigation. There is hence no guarantee that the navigation stays on the Pareto surface. However, the navigation algorithm is designed to push the navigated states towards the piecewise linear approximation of the Pareto surface.

When a satisfactory navigated dose distribution has been found it is converted to a deliverable treatment plan by solving a reference dose optimization problem.

The reference dose optimization problem minimizes quadratic penalties on:

- discrepancies between the DVH curves of the current dose distribution and the DVH curves of the reference dose distribution and/or
- discrepancies in dose per voxel between the current and the reference dose distribution.

7.4.2 The Multi Criteria Optimization user interface

Workspace

The workspace is divided into five sub-windows. The lower left window holds a set of tabs used for setting up the multi criteria environment. The lower left view defaults to the **Tradeoffs/constraints** tab – listing the user specified tradeoffs (objectives) and constraints, with buttons for adding, editing and deleting of such functions. The **Navigation** tab holds the sliders used to explore the solution space to find a satisfactory treatment plan. Also, a tree-list of different dose distributions associated with an MCO plan is available in the **Navigation** tab. The lower left view also contains tabs for the beam list, the control point list, beam optimization settings and beam weighting.

The upper row of windows displays visual information of the plan. The view in the top left corner contains the dose volume histogram (DVH). Behind the DVH is a tab showing the Beam's Eye View (BEV). The view in the middle holds a 2D patient view for the selected dose. The right view either shows the selected dose or a comparative (reference) dose in a 2D patient view.

The window in the lower right corner contains tabs for displaying different information evaluating the plan; a 2D patient view of the selected dose, a dose difference view (the selected dose minus the reference dose), dose statistics, and a tab for specification and review of clinical goals.

For TomoHelical plans there is a **Leaf Open Times** view that displays a histogram for the leaf open time of all leaves and of all projections.

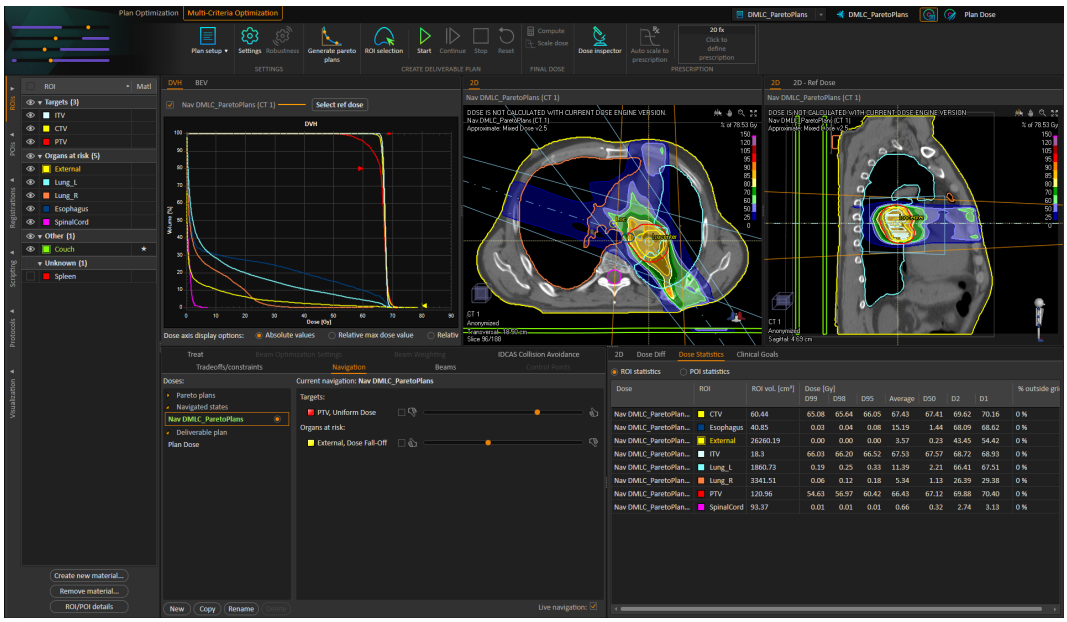


Figure 355. The Multi Criteria Optimization module workspace.

Graphical User Interface

For more information about the tools, operations and various view types in the Graphical User Interface, see *chapter 3 The Graphical User Interface*.

Tradeoff

A tradeoff is a formulation of one of the treatment goals where there is no immediate level that must be fulfilled, and hence the goal may be evaluated against other goals and be given a lower weight when finding a compromise using the sliders in the **Navigation** tab. The formulation is preferably the goal in its extremest form.

Example: Assume that a treatment goal is to have a maximum dose of 40 Gy in the surrounding tissue volume. However, the formulation can still be of 0 Gy and then the optimizer will find the lowest dose possible for corresponding Pareto plan in terms of the defined constraints (see constraints). This goal can then be traded against other goals when using the sliders by allowing it to get closer to the 40 Gy dose.

Constraint

A constraint is a formulation of one of the treatment goals that must be fulfilled and may not be evaluated against other goals. The formulation is similar to the one in the Plan Optimization module (see *Available objectives and constraints on page 525*). These functions must be met in all Pareto plans with some tolerance. The main purpose of these constraints are to create a selection of solutions that are clinically relevant.

7.4.3 The Multi Criteria Optimization workflow

This section describes a suggested workflow for creating an optimized plan in the Multi Criteria Optimization module:

1. **Create a new plan and add treatment beams.** For standardized treatment plans, it is preferable to set up a new plan via a plan generation protocol in the **Protocols** tab. See *section 6.1.2 Plan generation protocols on page 300* for more details.

   If no plan generation protocol exists, perform the following steps:

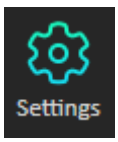
   a. **Create a new plan** in either the Plan Setup module or directly in the Multi Criteria Optimization module. Add a prescription if desired. For more information on how to create a plan, see *section 6.1.3 Create a new plan on page 306*.

   b. **Add the treatment beams** by loading a template, or add them manually. For more information on how to add beams, see *section 6.1.6 Add, edit, copy or delete beams on page 316*.

2. **Set up optimization functions (tradeoff objectives and constraints).** Define them one by one or by adding a set of pre-defined functions from a function list template (see *section 7.4.5 Create and add function list templates on page 663*).

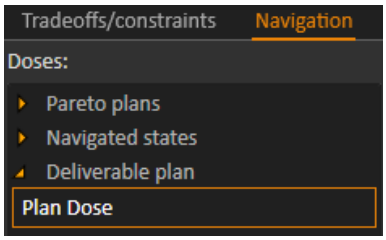
   The tradeoffs are typically defined according to what the user really wants to achieve, e.g., EUD 0 cGy, Parameter A = 1 to an OAR, while the constraints are defined according to minimum requirements, e.g., a clinically relevant Min Dose for the Target. Add the tradeoff objectives and constraints according to the instructions in *section 7.4.4 Adding tradeoff objectives and constraints on page 661*.

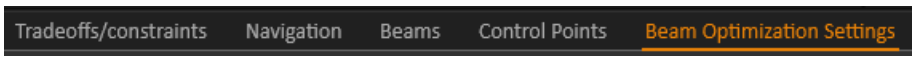
3. **Specify the optimization settings.** For photons, follow the instructions in *section 7.4.9 Optimization settings - photons on page 674*. For protons, follow the instructions in *section 7.4.10 Optimization settings – protons on page 680*.



4. **Verify the Beam Optimization Settings** for the applicable parameters.

   To make the **Beam Optimization Settings** tab editable, select Plan Dose in the dose list in the **Navigation** tab. The available settings will depend on the selected treatment technique.

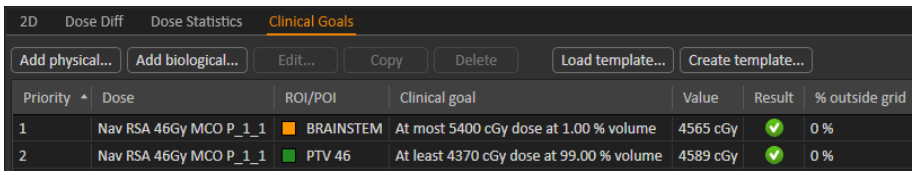




   For more information about beam optimization settings, see *section 7.1.9 Beam optimization settings on page 542*.

5. **Generate Pareto plans** according to the instructions in *Generate Pareto plans on page 665*.

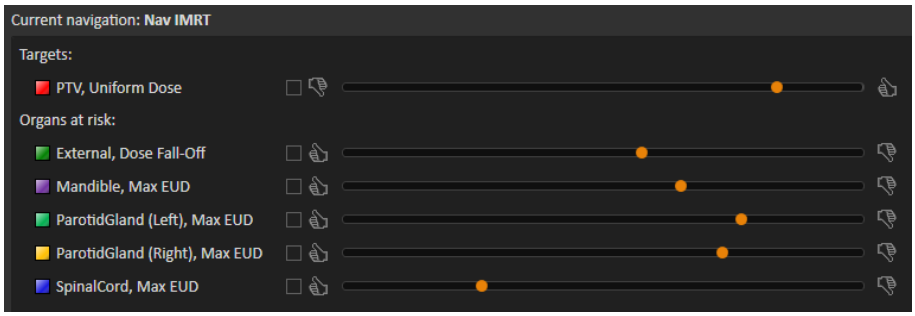
6. **Add the clinical goals.** Define them one by one or by adding a set of pre-defined goals from a clinical goals template.



   For information about clinical goals and instructions on how to add them, see *section 3.7.3 Clinical goals on page 81*.

7. **Navigate to a satisfactory dose distribution.**

   In the **Navigation** tab, use the sliders to explore the solution space until a satisfactory dose distribution is found. Use the **Clamping** checkboxes to narrow the reachable solution space.

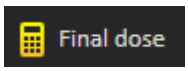


   For more information, see *section 7.4.7 Navigation on page 667*.

8. **Create a deliverable plan based on the navigated dose distribution** according to the instructions in *section 7.4.8 Create a deliverable plan on page 671*.

   When a deliverable plan is created, a dose matching is performed where machine parameters are optimized to match the reference dose.

9. **Compute final dose.** If a final dose has not yet been computed, compute a final dose according to the instructions in *section 7.1.15 Compute dose on page 553*.



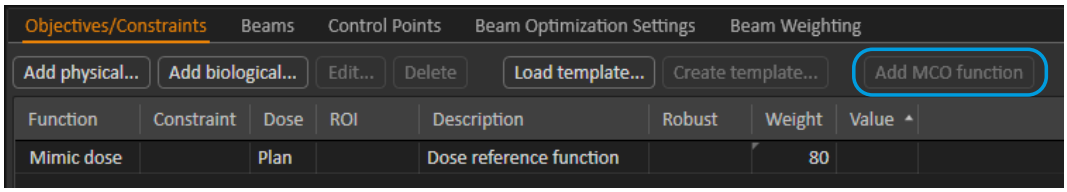
   For SMLC, DMLC, VMAT and TomoHelical, the dose for the current MLC settings is computed using the Collapsed Cone dose engine. For PBS the dose for the current spots is computed using the dose engine selected in the drop-down list. It is possible to define a default dose engine for the final dose in clinic settings.

10. **Scale dose (if desired).** The dose can be scaled to fulfill the prescription or to fulfill an arbitrary dose-volume relation for a selected ROI or POI. For instructions on how to scale dose, see *section 6.1.15 Scale dose on page 356*.

11. **Define or modify prescription (if desired).** Add or modify a prescription if desired. For more information, see *section 6.1.12 Define or modify prescription on page 343*.

12. **Repeat steps 7 to 9 (if desired).** If the dose distribution is not satisfactory, repeat steps 7 to 9.

13. **Add MCO function (if desired).** The MCO plan can, if desired, be further optimized in the Plan Optimization module. To continue to optimize the plan, create an MCO function by clicking the **Add MCO function** button in the **Objectives/Constraints** tab.



For more information, see *section 7.4.11 Add MCO function on page 684*.

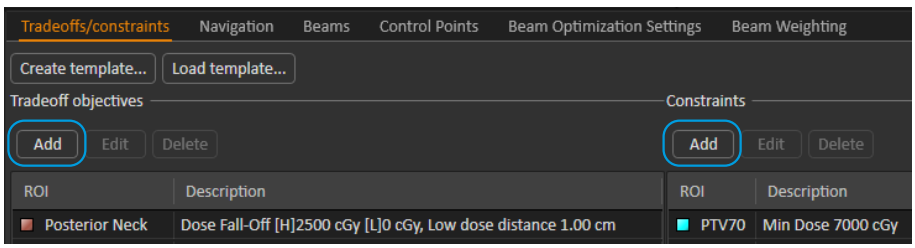
7.4.4 Adding tradeoff objectives and constraints

The Multi Criteria Optimization module contains the same optimization functions as the Plan Optimization module (see *Available objectives and constraints on page 525*). A Multi-Criteria Optimization problem must however always contain at least one dose promoting constraint and at least one dose limiting constraint.

Tradeoff objectives and constraints can be added in two ways; by defining them one by one or by adding a set of pre-defined functions from a function list template (see *section 7.4.5 Create and add function list templates on page 663*).

Add a tradeoff objective or a constraint

1. In the **Tradeoff/constraints** tab, click the **Add** button in the Tradeoff objectives list to add tradeoff objectives and the **Add** button in the Constraints list to add constraints.



This opens either the **Add tradeoff objective** dialog or the **Add tradeoff constraint** dialog.

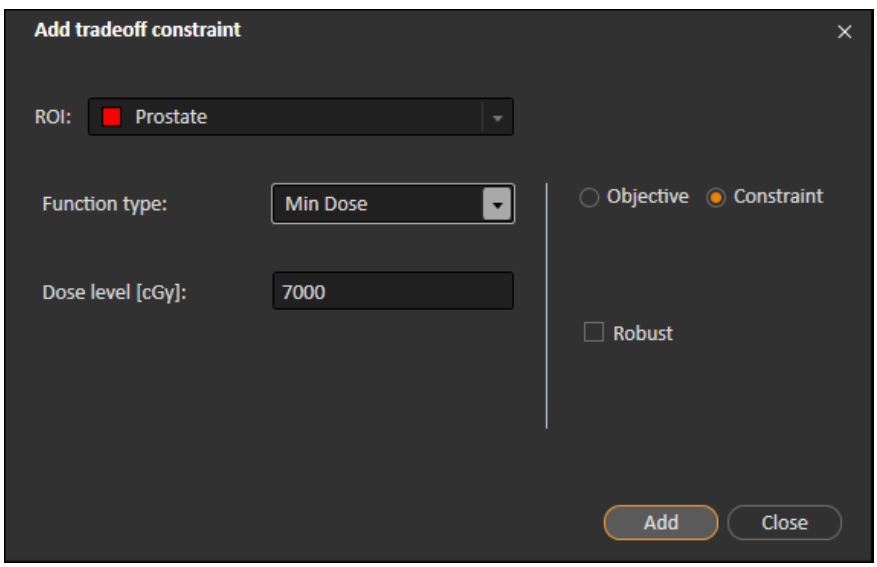


Figure 356. The **Add tradeoff constraint** dialog.

2. Select the **ROI** that the tradeoff objective or constraint should be added to.

3. Select **Function type** and specify the function parameters (see the table in *Available objectives and constraints on page 525*). The function types available depend on organ type of the ROI.

   For treatment technique PBS, tradeoff and constraint functions may be beam specific. Beam specific optimization functions are described in detail in *Beam specific objectives on page 574*. However, note that the Add Optimization Function dialog is called Add tradeoff objective.

4. If the function is a constraint, select if the function should be robust by checking the **Robust** checkbox. Note that the tradeoff objectives in MCO cannot be selected as robust.

5. Click **Add**.

   Note: *A minimum of two tradeoff objectives have to be defined to enable Pareto plan generation.*

   Note: *At least one target constraint, i.e., Min Dose, Min DVH, Min EUD, or Target EUD, and one maximum dose constraint, i.e., Max Dose, Max DVH, or Max EUD, must be included to enable Pareto plan generation.*

Edit or delete tradeoff objective/constraint

To edit an existing tradeoff objective or a constraint function, double-click on it in the corresponding list, or click the **Edit** button above the list. To delete the selected tradeoff objective/constraint, click the **Delete** button.

7.4.5 Create and add function list templates

A set of tradeoff objectives and/or constraints can be stored as a function list template. The function list templates can simplify the planning process, since standard optimization functions can be re-used as a starting point when optimizing new plans.

Create function list template

A function list template is created from a plan's existing set of optimization functions. To store the current plan's functions as a template, click the **Create template...** button and enter a name for the new template. (The template can later be renamed or deleted from the Load template dialog)

Add functions from template

To add optimization functions from the function list, click the **Load template...** button. Select a function list template in the drop-down list. The objectives and constraints for selected template are listed in the dialog's lists. To add the template's functions to the plan, click the **Add** button.

To rename the selected template, click **Rename** and enter a new name for the template. To delete the selected template, click **Delete**.

To approve a template, click **Approve**. Only admin users can approve a template. Approved templates have a padlock next to the template name. If a non-approved template is loaded, a warning will be displayed. These warnings can be disabled in Clinic Settings. For more information on template approval, see *Approval of templates on page 43*.

Note: *Function list templates containing biological functions is not available for MCO.*

7.4.6 Pareto plans

The first step of the MCO planning process is to specify the clinical criteria for the plan. Based on these criteria – tradeoff objectives and constraints – a set of Pareto plans is generated. The addition of tradeoffs and constraints is presented in *section 7.4.4 Adding tradeoff objectives and constraints on page 661*.

Anchor plans, Balance plans and Auxiliary plans

The Pareto plans constituting the approximation of the Pareto surface are defined by their weighting of the user-specified objectives. There are three types of Pareto plans; Anchor plans, Balance plans and Auxiliary plans:

- Plans generated by optimizing a single objective are called Anchor plans. One Anchor plan is created for every tradeoff objective (N).
- One Balance plan is created from an equal weight value for all objectives.
- Any additional plan that is (optionally) created beyond these initial N+1 plans is called an Auxiliary plan. Such plans are named according to its two constituent objectives that are given highest priority, e.g., Aux: objective A, objective B. An auxiliary plan can have more than two constituent objectives if the total number of tradeoffs is less than ten. The full list of constituent objectives, and their relative weightings, are displayed in a tooltip when holding the mouse pointer over the corresponding entry in the dose list in the **Navigation** tab.

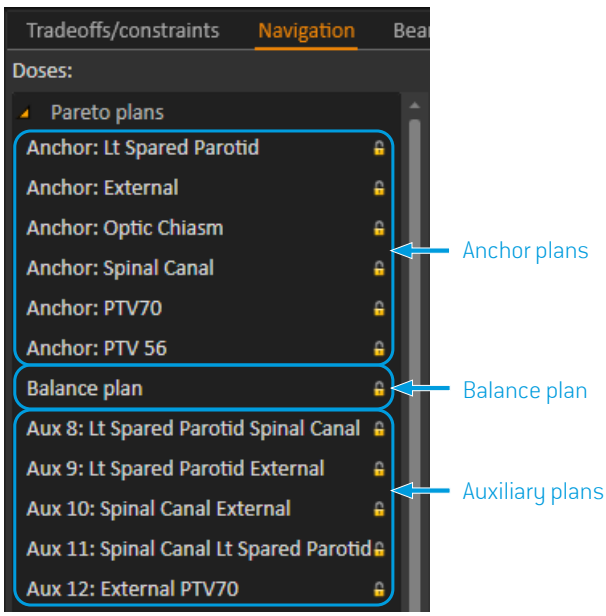


Figure 357. There are three types of Pareto plans; Anchor plans, Balance plans and Auxiliary plans (if created). These are found in the dose list in the **Navigation** tab.

All Pareto plans are read-only and cannot be altered. This is indicated by a padlock symbol in the dose list in the **Navigation** tab. However, each Pareto plan may be copied and become a starting point for a navigation state that can be explored, see *section 7.4.7 Navigation on page 667*.

ROIs must be classified as targets or organs at risk

Only ROIs that are classified as targets or organs at risk can be used for planning in MCO; i.e. before defining tradeoff objectives or constraints for an ROI the organ type has to be set. To set organ type, right-click the ROI in the ROI List tool page and select **Properties** from the context menu, or double-click the ROI in the ROI List. In the ROI Properties dialog, select the organ type and click **OK**. Organ type is set at DICOM import for all ROIs.

Note: *Only ROIs that are classified as Targets or Organs at Risk can be used in MCO.*

Generate Pareto plans

1. Click the **Generate pareto plans** button to open the **Generate pareto plans** dialog.

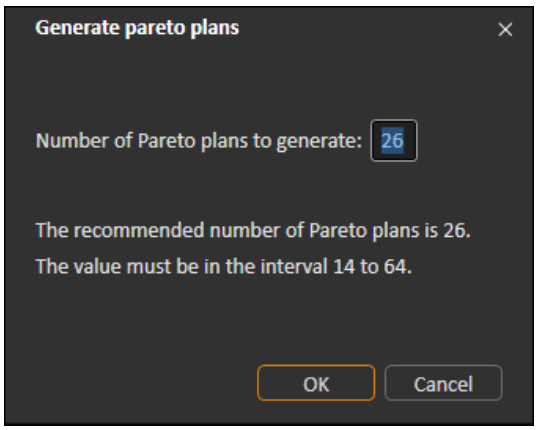

Generate pareto plans
Number of Pareto plans to generate:
26
The recommended number of Pareto plans is 26.
The value must be in the interval 14 to 64.
OK
Cancel

Figure 358. The **Generate pareto plans** dialog.

2. Enter the **Number of Pareto plans** to generate. This number is required to lie within the interval N+1 to N+51. The default number of Pareto plans to generate is set to 2N, where N is the number of tradeoff objectives.
3. Click **OK**. This starts the optimization process to generate a user-specified number of Pareto plans.

In the lower left sub-window of the Multi Criteria Optimization module there are six tabs available. Tradeoffs and constraints are found in the **Tradeoff/constraints** tab. The Pareto plans (anchor plans and balance plans) are found in the **Navigation** tab.

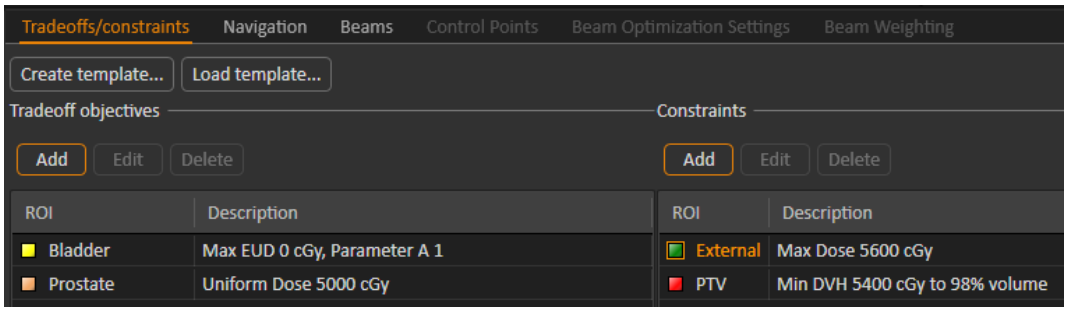


Figure 359. A very simple plan to be optimized is prepared with only two tradeoffs and two constraints. These are listed in the Tradeoffs/constraints tab in the lower left sub-window.

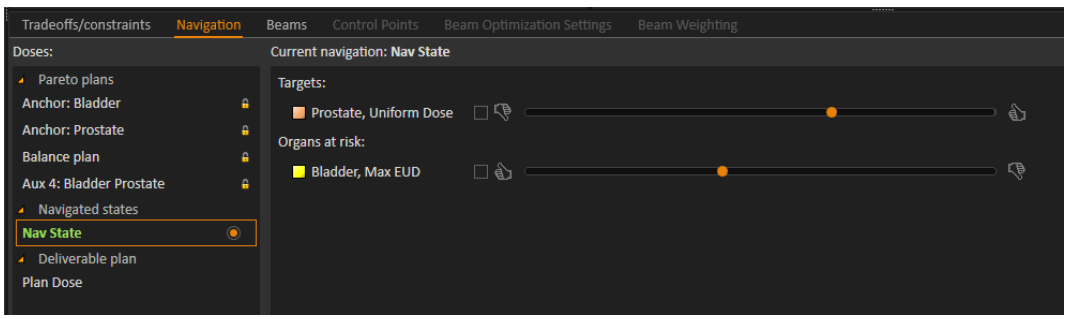


Figure 360. The generation of Pareto plans with only two tradeoffs results in two anchor plans, one for each tradeoff, and one balance plan. A padlock symbol to the right of the Pareto plans indicates that these plans are not editable.

7.4.7 Navigation

When the Pareto plans are generated, the search of a suitable dose in the solution space can start. The solution space navigation is managed from the **Navigation** tab, in the lower left corner of the workspace. By moving the navigation sliders it is straightforward to navigate between different solutions defined by the underlying Pareto plans.

The combination of all sliders' positions, and the corresponding dose distribution, is called a navigation state. It is possible to work with several rival navigation states in parallel, which one is currently active is selected via option buttons in the dose list or by right clicking on item.

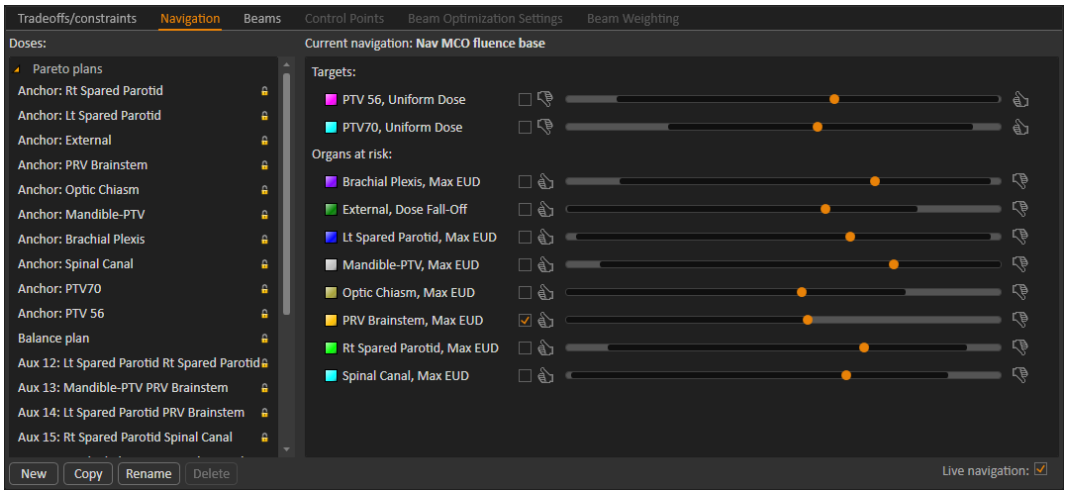


Figure 361. By moving the navigation sliders it is straightforward to navigate between different solutions defined by the underlying Pareto plans. The live navigation checkbox at the bottom right controls how the dose display will be updated during navigation.

The dose list

The doses list, to the left in the **Navigation** tab, lists all available dose distributions for the current plan; the Pareto plans, the navigation states, and the deliverable plan. The dose distribution that is selected in the dose list is also displayed in the DVH view, the dose statistics view, the 2D patient view etc.

The doses in the list are grouped in three categories:

- **Pareto plans**. A Pareto plan can be selected for display. The dose will be displayed and the navigation sliders' positions will reflect the state of the selected Pareto plan – but the plan is read-only, i.e., it is not possible to move the sliders for a Pareto plan. To navigate a Pareto plan, copy the plan and select the option button of the new navigation state.
- **Navigated states**. A dose distribution created by weighting the various Pareto plans using the navigation sliders. Several navigation states can be created and compared. As a post step to the Pareto plan generation the system creates an initial navigation state, **Nav1**, set as the

average dose of all Pareto plans. Use the **New** and **Copy** buttons at the bottom of the dose list to create new navigated states.

All navigation states can be selected for display but only the active navigation state will be used when creating a deliverable plan. The navigation sliders are enabled for the active dose only. Use the display option button to select the active navigation state.

Figure 362. Use the display option button to select the active navigation state.

- **Deliverable plan**. The underlying treatment plan. Initially this plan specifies the beam configuration, i.e., treatment machine and number of beams etc., but after the optimization step (create deliverable plan) it constitutes the realization of the desired dose distribution.

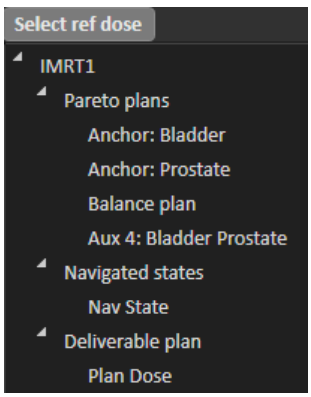


Figure 363. The dose list in the **Navigation** tab lists all dose distributions available for the current plan.

Navigation sliders

The navigation is performed using sliders; there is one slider for each tradeoff objective defined. The dose solution space is explored by pulling the slider handles. Moving a slider means improving or worsening the objective function for the underlying tradeoff objective. When a slider is moved the dose distribution and DVH are automatically updated, since the weights of the underlying Pareto plans (and the resulting dose distribution) are altered.

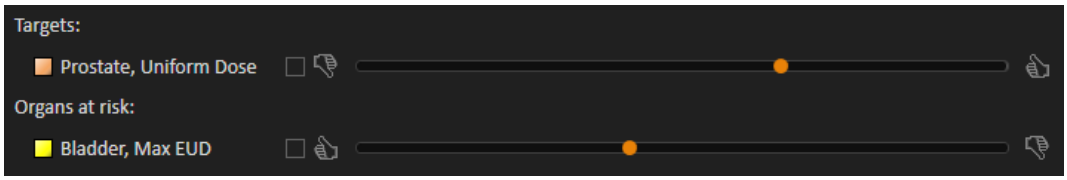


Figure 364. Sliders enable the navigation through dose solution space.

As a guide there is a hand showing thumbs up beside the slider in the direction where the current objective function is improved, and a hand showing thumbs down at the other end.

For minimum and maximum dose objectives (i.e., Max dose, Min dose, Max DVH, Min DVH, Max EUD, Min EUD), moving the slider to the right increases the dose for the corresponding ROI, while moving it to the left reduces the dose for the same ROI. Adjusting one slider will in general affect the position of other sliders due to that optimization variables are coupled — for example, for a prostate case, increasing the radiation to the prostate will typically affect the radiation delivered to the colon.

The optimal solution would be to place the sliders corresponding to minimizing functions to the far right, and the sliders corresponding to maximizing functions to the left. This is however not a feasible solution in general.

By checking the checkbox to the left of the slider, the corresponding objective is constrained to fulfill at least the current value. This limits the achievable values for the other variables, which is seen by the grayed out fields constraining the positions of the other sliders.

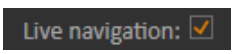
Note: *The clamping should be viewed as a guideline and not as a hard boundary.*

Figure 365. By checking the checkbox the corresponding objective is constrained to fulfill at least the current value.

After each slider change the DVH also displays the previous navigation state (Previous move) with dashed lines. Select Undo from the title bar toolbar, or press CTRL+Z, to return to the previous state.

Live navigation

The live navigation checkbox controls how the dose will be displayed in the patient views when moving the navigation sliders. When the live navigation checkbox is unchecked, the dose will be updated when the navigation slider is released. When the live navigation checkbox is checked, the dose will be updated continuously when moving the navigation sliders.



Live navigation can in some cases be heavy to compute, depending on for example the resolution of the dose grid, the number of ROIs or the current computer performance. In these cases, the live navigation can be switched off.

Create and maintain navigation states

There are two ways to create a new navigation state:

- Click the **New** button to create a state navigated as the average dose of all Pareto plans.
- Click **Copy** to make a duplicate of the currently selected dose in the list. (Pareto plans and navigated states can be copied, but not the deliverable plan.)

Click the **Rename** button to rename the current navigation state. Click the **Delete** button to delete the current navigation state.

7.4.8 Create a deliverable plan

Moving the sliders in the **Navigation** tab will affect the navigated dose but will not create a deliverable plan.

Click **Start** in the Create Deliverable Plan section of the toolbar to translate the selected active dose distribution, obtained from the navigation, into a dose distribution that is deliverable with the selected treatment machine.

Result:

- For treatment techniques SMLC, DMLC and VMAT, this initializes a dose matching where leaf positions and segment weights are optimized simultaneously to match the reference dose.
- For treatment technique PBS, this initializes a dose matching where spots are optimized to match the reference dose.
- For treatment technique TomoHelical, this initializes a dose matching where leaf open fractions are optimized to match the reference dose.

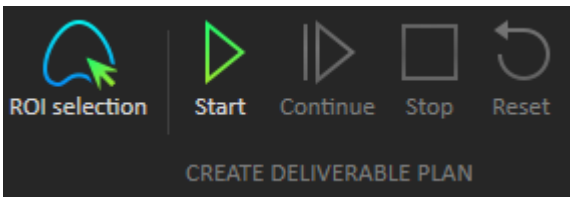
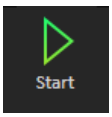


Figure 366. Controls for creating a deliverable plan.

The optimization control buttons

Below is a description of the optimization control buttons.



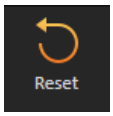
The **Start** button starts a new optimization. Only active for:

- SMLC, DMLC, VMAT, or TomoHelical, if there are no fluence maps or control points in the beams, or
- PBS, if there are no energy layers in the beams.

The **Continue** button starts an optimization from the current state. Only active for:

- SMLC, DMLC, VMAT, or TomoHelical, if there is at least one control point in every beam, or
- PBS, if there are at least one energy layer with spots in every beam.

The **Stop** button stops the optimization after the current iteration is finished.



The **Reset** button resets the beams.

- For SMLC, DMLC, VMAT, or TomoHelical, all control points are removed and the fluence maps are cleared for all beams.
- For PBS, all energy layers are removed and the spots are cleared for all beams.

Beam list

For information about the Beam list, see *section 7.1.6 Beams in the Plan Optimization module on page 537* and for PBS see *section 7.2.3 Beam list on page 576*.

Optimization settings

The optimization settings can be edited if desired. For more information, see *section 7.4.9 Optimization settings - photons on page 674* and/or *section 7.4.10 Optimization settings – protons on page 680*.

Beam optimization settings (SMLC, DMLC, VMAT and TomoHelical)

The **Beam Optimization Settings** tab in the Multi Criteria Optimization module is displayed for treatment techniques SMLC, DMLC, VMAT and TomoHelical and is identical to the corresponding tab in the Plan Optimization module. Changing the settings in one of the modules will affect the settings in the other module. See *section 7.1.9 Beam optimization settings on page 542* for more information. Select **Deliverable plan: Plan dose** in the **Navigation** tab in order to enable the **Beam Optimization Settings** tab.

Beam computation settings (PBS)

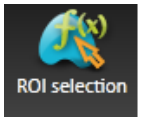
The **Beam Computation Settings** tab in the Multi Criteria Optimization module is displayed for treatment technique PBS and is identical to the corresponding tab in the Plan Optimization module. Changing the settings in one of the modules will affect the settings in the other module. See section *section 7.2.5 Beam Computation Settings on page 578* for more information.

Note that the beam computation settings only affect the spot pattern explicitly in the optimization of the Pareto plans. The spot pattern of the deliverable plan is inherited from the selected navigated state and thus indirectly from the Pareto plans. This means that any changes to the beam computation settings after the generation of the Pareto plans will not affect the deliverable plan. The **Beam Optimization Settings** tab is therefore enabled and editable only if the Pareto plans have not been generated yet.

The above applies to all beam computation settings except the **Layer repainting** option, which is a post-processing step that only affects the deliverable plan generation.

ROI selection

1. Click the **ROI selection** button.



This opens the ROI selection dialog.

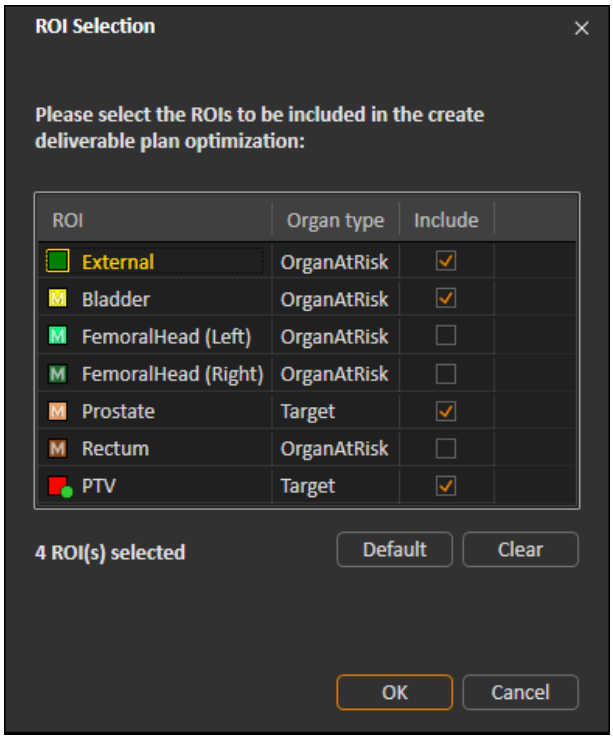


Figure 367. The ROI selection dialog.

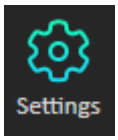
2. Select the ROIs to include in the Create deliverable plan optimization. The result is the underlying ROIs that are used for matching the reference dose. The default selection is the unique set of ROIs that defines the corresponding tradeoffs and constraints. The default set of ROIs is set automatically after Pareto plan generation.

Beam weighting

Beam weighting is described in detail in *section 6.3.12 Beam weighting on page 445*.

7.4.9 Optimization settings - photons

To edit the optimization settings, click the **Settings** button.



This opens the Settings dialog.

The Settings dialog is divided into two main parts, the **Pareto plans** part and the **Deliverable plan** part. The settings in the Settings dialog varies depending on the selected treatment technique as described in the following sections.

Pareto plan settings

Pareto plan mode defines if Pareto plans shall be optimized based on fluence or based on segment shapes and segment MU (segment based). Direct optimization of segment shapes and segment MU is available for treatment techniques SMLC and DMLC.

The description of the other optimization settings and the segmentation settings are for SMLC the same as for regular SMLC optimization, see *Specify optimization and segmentation settings for SMLC on page 530*, and for DMLC the same as those for regular DMLC optimization, see *Specify optimization and segmentation settings for DMLC on page 532*.

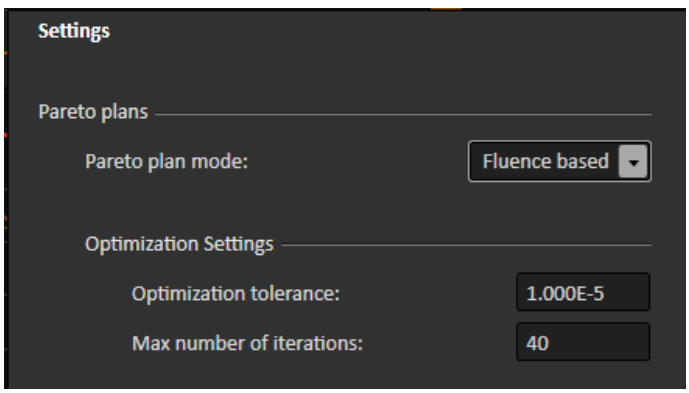


Figure 368. The Pareto plan part of the Settings dialog for fluence based optimization (available for SMLC, VMAT and DMLC).

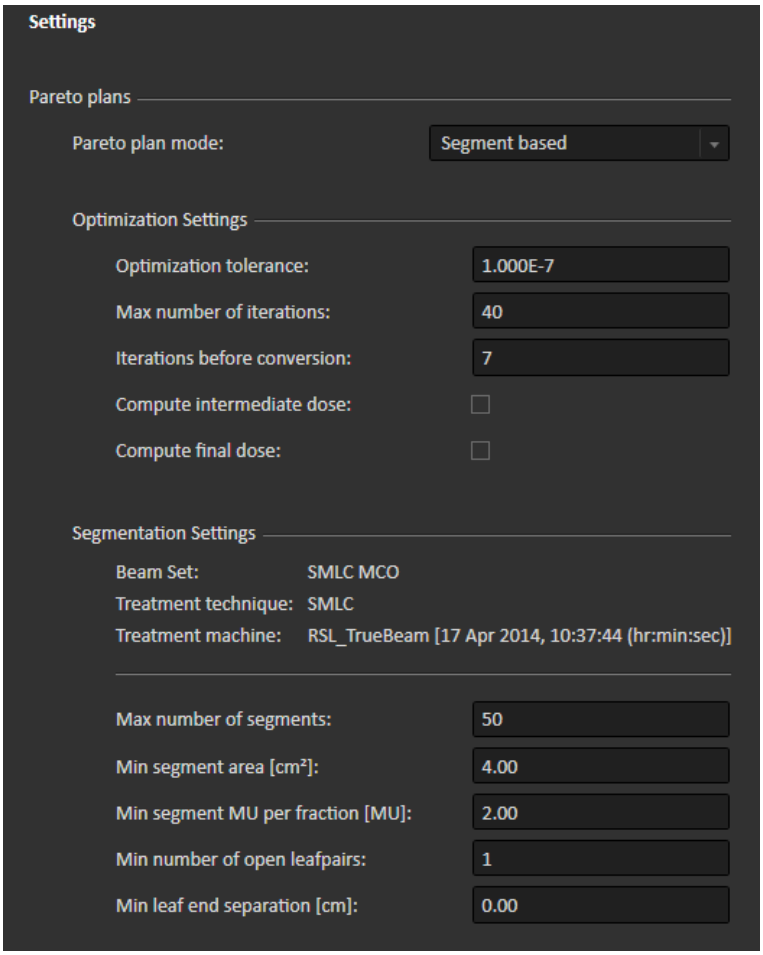


Figure 369. The Pareto plan part of the Settings dialog for SMLC optimization in the segment based mode.

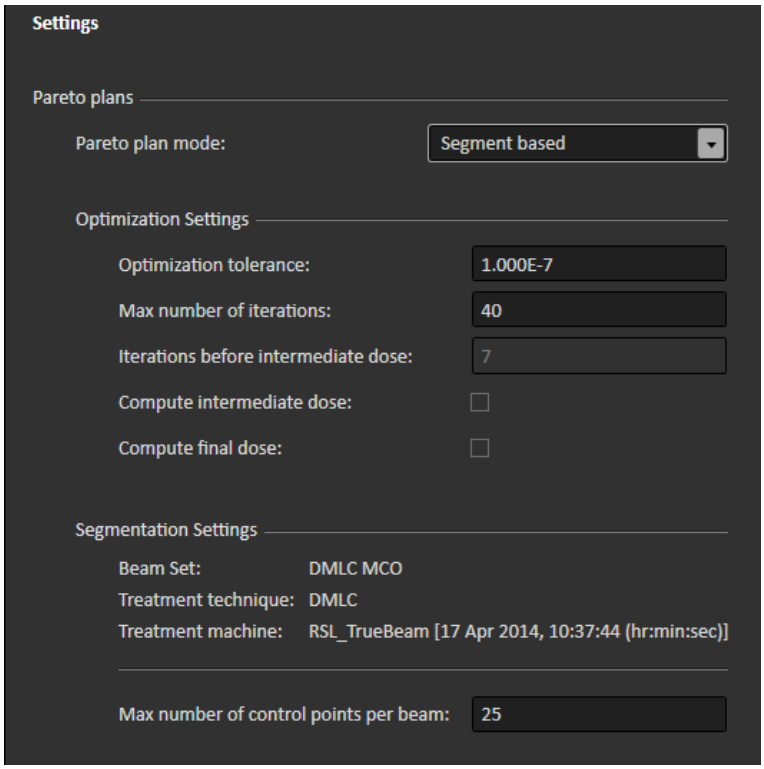


Figure 370. The Pareto plan part of the Settings dialog for DMLC optimization in the segment based mode.

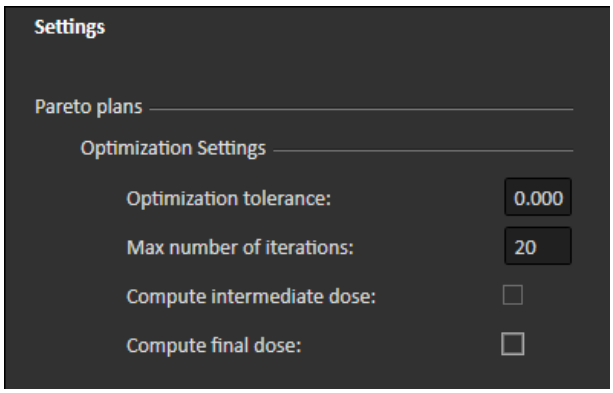


Figure 371. The Pareto plan part of the Settings dialog for TomoHelical optimization.

Note: *If Pareto plans are available and the Compute intermediate dose setting is changed and new Pareto plans are generated, the current Pareto plans are invalidated.*

Deliverable plan settings

Target priority is the priority between the target objectives and the OAR objectives. The higher the number, the higher priority of the target objectives.

The descriptions of the other optimization and segmentation settings are the same as for SMLC, VMAT, DMLC and TomoHelical optimization, see *section 7.1.5 Specify optimization and segmentation settings on page 530*.

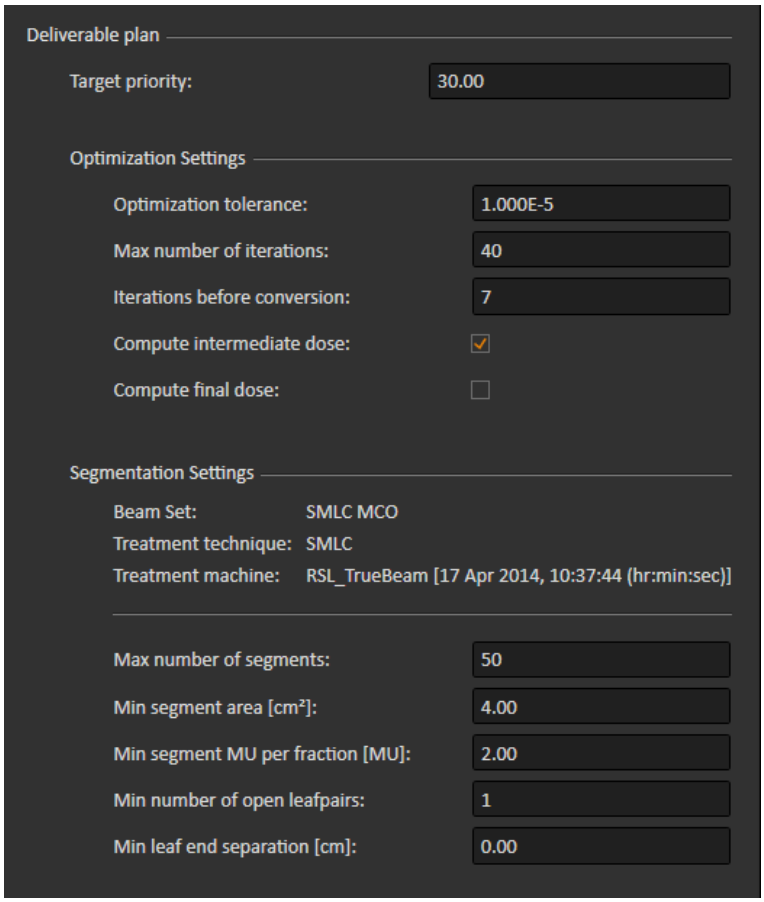


Figure 372. The Deliverable plan part of the Settings dialog for SMLC optimization and segmentation.

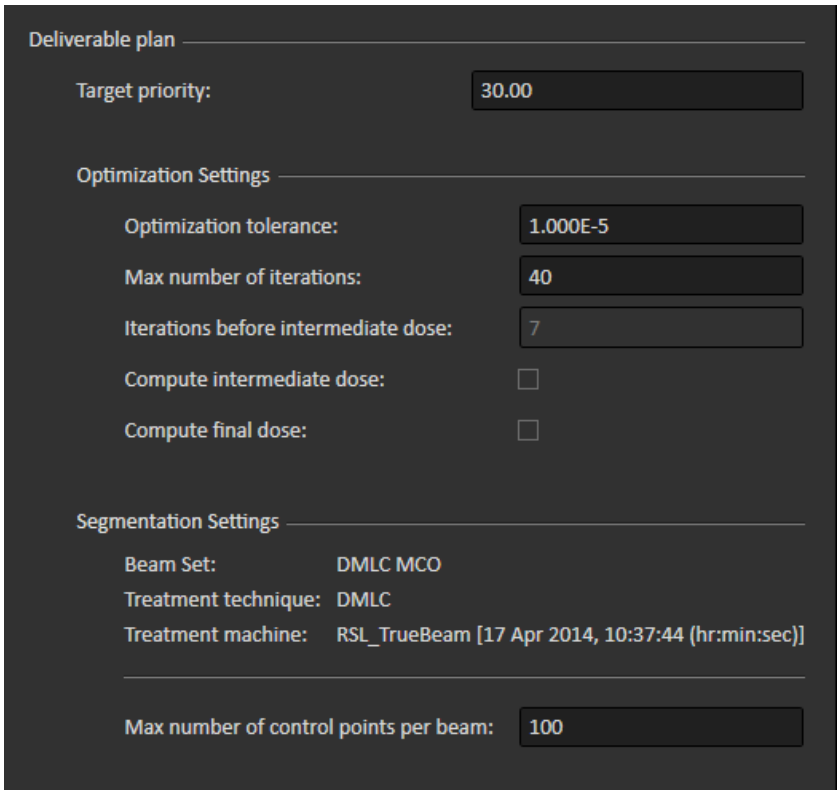


Figure 373. The Deliverable plan part of the Settings dialog for DMLC optimization and segmentation.

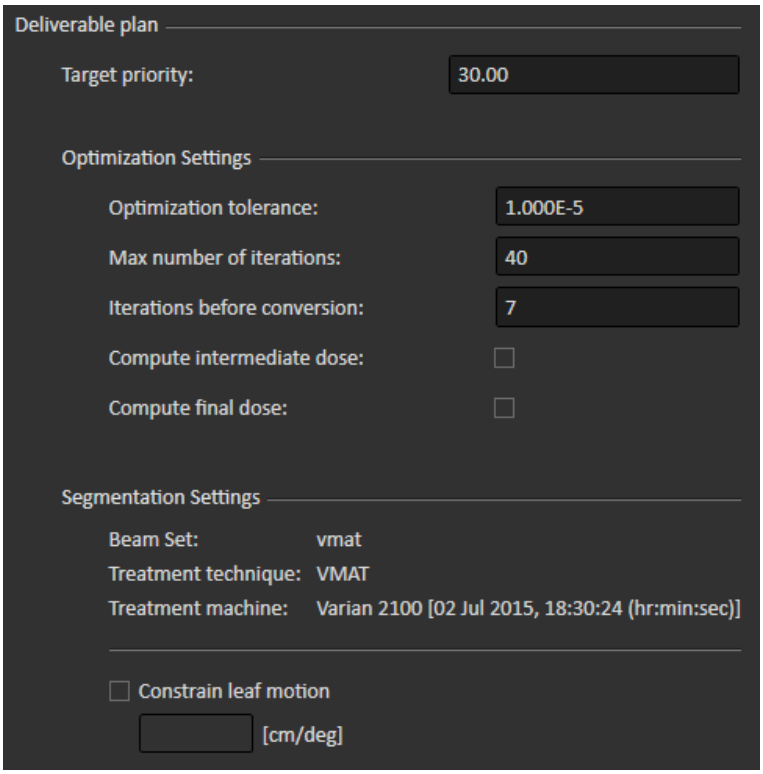


Figure 374. The Deliverable plan part of the Settings dialog for VMAT optimization and segmentation.

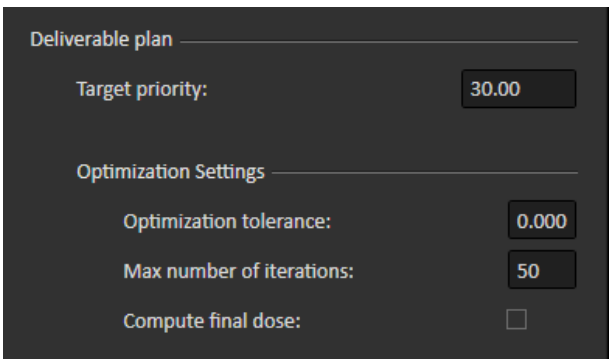
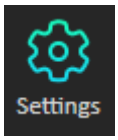


Figure 375. The Deliverable plan part of the Settings dialog for TomoHelical optimization (no segmentation parameters).

7.4.10 Optimization settings – protons

To edit the optimization settings, click the **Settings** button.



This opens the Settings dialog.

The Settings dialog is divided into two main parts, the **Pareto plans** part and the **Deliverable plan** part.

Pareto plan settings

In the **Pareto plans** part of the Settings dialog it is possible to configure **Optimization Settings** and **Spot filtering settings**. The Pareto plan settings in the MCO module are analogous to settings used for standard PBS optimization. Individual settings are described in detail in *section 7.2.7 Specify optimization settings on page 583*. Note that as no spot sorting occurs for Pareto plans, there are no spot sorting settings available in the Pareto plan settings.

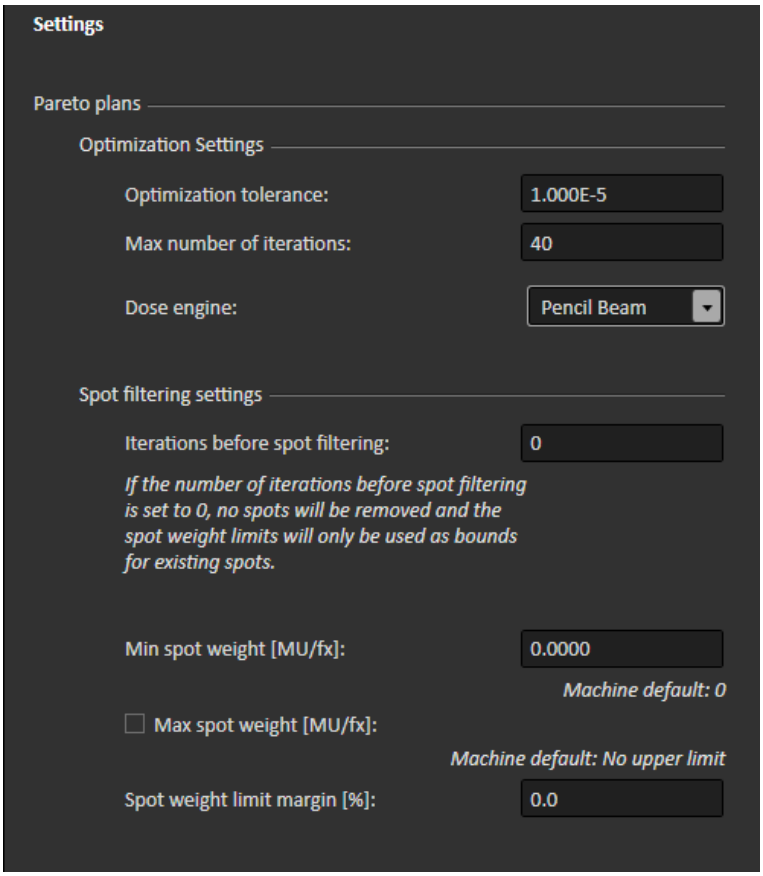

Settings
Pareto plans
Optimization Settings
Optimization tolerance:
1.000E-5
Max number of iterations:
40
Dose engine:
Pencil Beam
Spot filtering settings
Iterations before spot filtering:
0
If the number of iterations before spot filtering is set to 0, no spots will be removed and the spot weight limits will only be used as bounds for existing spots.
Min spot weight [MU/fx]:
0.0000
Machine default: 0
Max spot weight [MU/fx]:
Machine default: No upper limit
Spot weight limit margin [%]:
0.0

Figure 376. The Pareto plans part of the Settings dialog for treatment technique PBS.

Note: *When Pareto plans are computed, all existing Pareto plans computed with a different dose engine than specified in the settings will be recomputed.*

Deliverable plan settings

In the **Deliverable plan** part of the Settings dialog it is possible to configure **Target priority**, **Optimization Settings**, **Spot filtering settings** and **Spot sorting settings**. **Target priority** is the priority between the target objectives and the OAR objectives. The higher the number, the higher priority of the target objectives.

The other Deliverable plan settings in the MCO module are analogous to the settings used for standard PBS optimization and individual settings are described in detail in *section 7.2.7 Specify optimization settings on page 583*. Note that since spot filtering in the optimization of the deliverable plan always occurs in the first iteration of the optimization, it is not possible to configure the iterations before spot filtering. Furthermore, note that additional spot sorting settings only are available for treatment machines that supports quasi-discrete PBS.

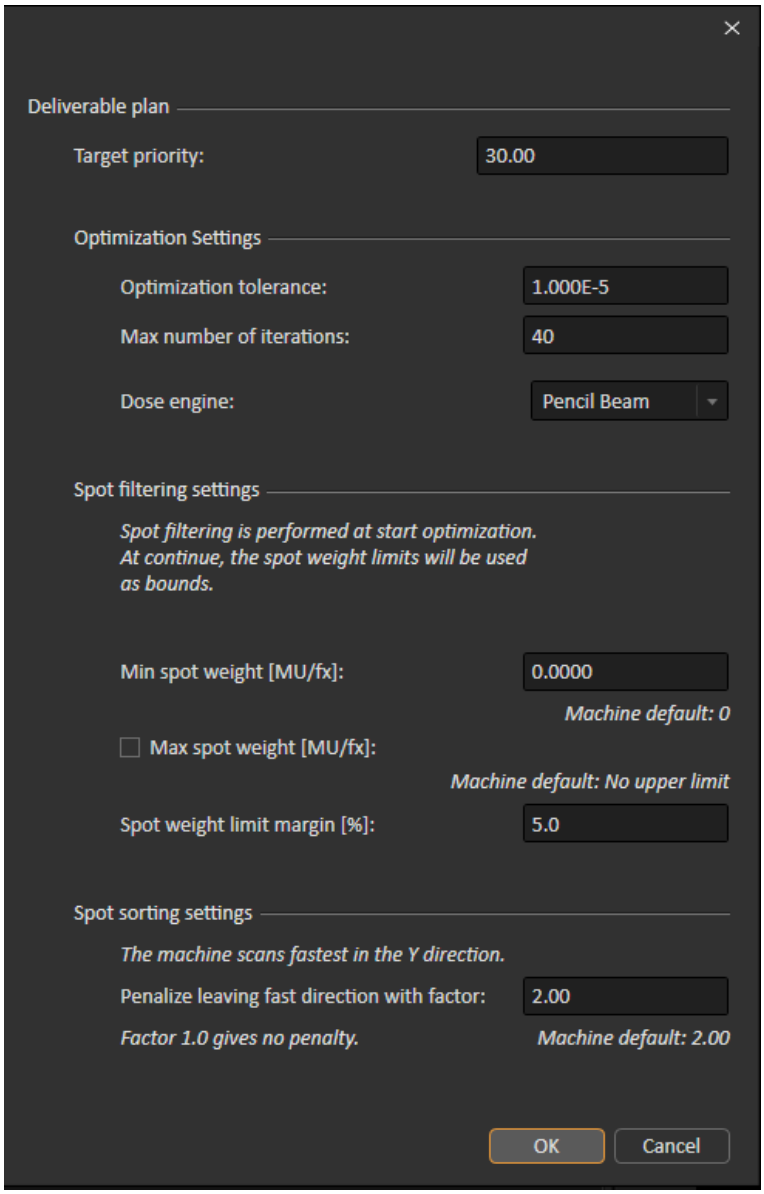


Figure 377. The Deliverable plan part of the Settings dialog for PBS.

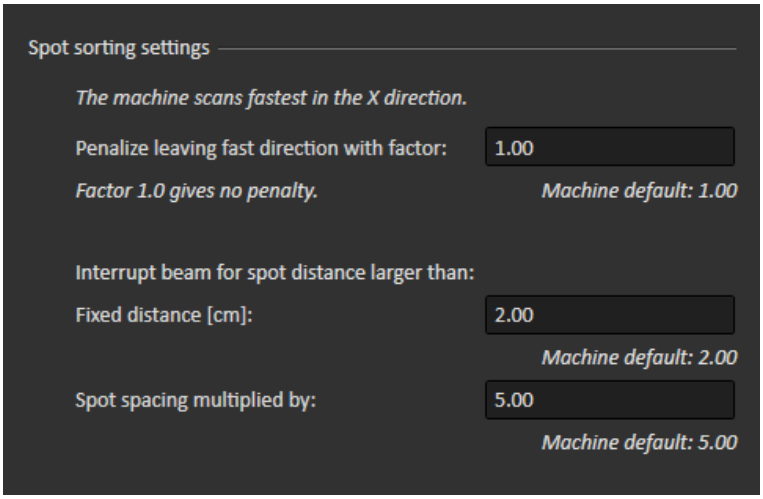


Figure 378. The Spot sorting settings for treatment machines that supports quasi-discrete PBS.

The default dose engine for pareto plan generation and deliverable plan creation will be the same and can be specified in clinic settings.

7.4.11 Add MCO function

The optimization problem used in the MCO module to create a deliverable plan can be set up and optimized in the Plan Optimization module. Thus deliverable plan generation may, if needed, be accomplished in the Plan Optimization module.

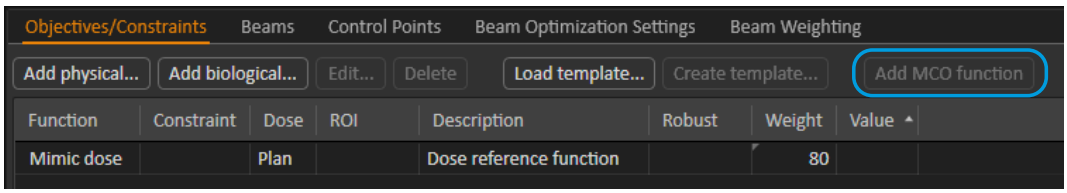


Figure 379. The **Add MCO function** button in the **Objectives/Constraints** tab.

The **Add MCO function** button is:

- Only visible in the Plan Optimization module if the user has an MCO license
- Activated when creating a deliverable plan in MCO (using the **Start** or **Continue** buttons)
- Inactivated if the navigated state used to create the deliverable plan is changed

Reference dose functions

When clicking the **Add MCO function** button, the optimization functions used to create the deliverable plan will be copied to the "general" optimization problem in the Plan Optimization module. When optimizing using the optimization function "Mimic dose", RayStation will try to reproduce the dose/DVH curves for the user specified ROIs related to the referenced dose (i.e., in this case, the navigated dose that was used to create a deliverable plan). The user can then continue the optimization in the Plan Optimization module, which supports adding new functions and configuration of the weight for the dose reference function.

Note: *The weight is the only parameter that can be changed in the dose reference function.*

Note: *The optimization functions created refer to a reference dose. If this reference dose is changed, the optimization function will be invalidated. In this case, the reference dose is the navigated dose that was used to create the deliverable plan. If navigating this dose, the created optimization functions will be invalidated (without warning the user).*

The ROI configuration affects the reference dose generation

It is possible to configure the ROIs to take into consideration when creating a deliverable plan. This is done by clicking the **ROI selection** button and selecting the desired ROIs (see *ROI selection on page 673* for more information).When creating a deliverable plan the underlying optimization problem is configured based on the current ROI Selection. It is therefore possible to control for which ROIs the reference dose optimization functions will be created for by selecting them in the ROI selection dialog.

7.4.12 Compare plans

To support the process of selecting the best dose distribution, the various doses can be compared side-by-side in 2D patient views, in the DVH view, in the dose statistics view and using clinical goals.

To compare two dose distributions, select a dose item in the **Navigation** tab's dose list. Then select a dose distribution to compare with using the **Select ref dose** menu button located under the **DVH** tab and the **2D-ref dose** tab. The Select ref dose menu lists the various doses for the current MCO plan, but also all other plans for the current patient. This makes it possible to compare a specific navigation state not only with another navigation state for the current plan, but also with another plan's dose.

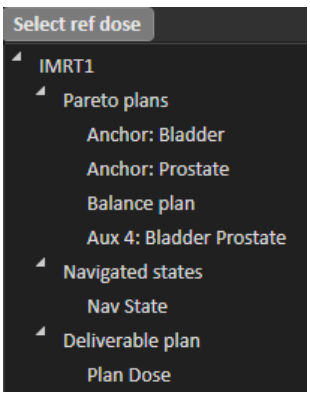


Figure 380. The Pareto plan Anchor in the **Select ref dose** menu list: Bladder is selected to compare other doses with.

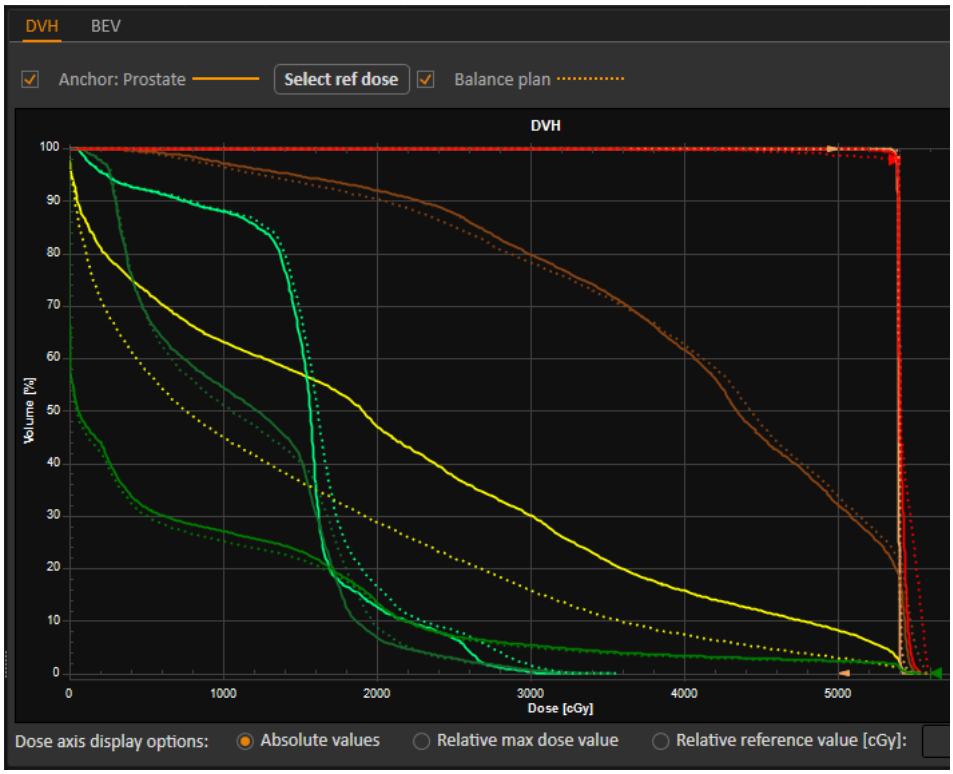


Figure 381. The doses for various ROIs in two Pareto plans are compared; Anchor: Prostate and Balance plan. The Select ref dose button lists available plans to choose for comparison. By checking the box next to the Select ref dose button the plan for comparison is displayed in the DVH histogram.

7.4.13 The evaluation views

Dose Volume Histogram (DVH)

The DVH view presents the cumulative dose volume histograms of the ROIs selected in the ROI List. The dose can be displayed as **absolute** or **relative [%]**. It is also possible to manually set the reference value for the relative scale.

For a detailed description of the DVH view, see *section 3.7.1 Dose Volume Histogram (DVH) on page 78*.

Dose difference

The dose difference view displays the dose difference, i.e., dose 1 (image set 1) minus dose 2 (image set 2). Only the dose within the area of image set 1 will be visualized. If dose in image set 2 is present outside this area it will not be displayed.

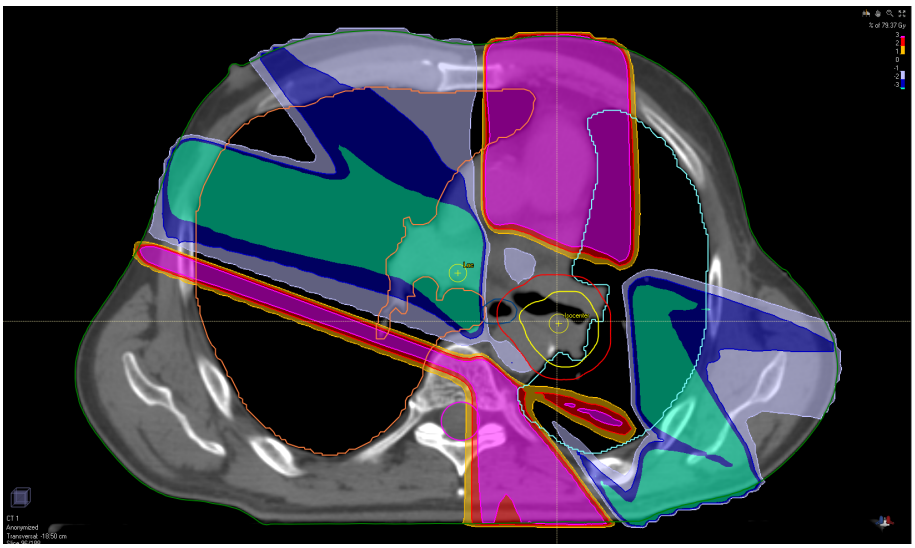
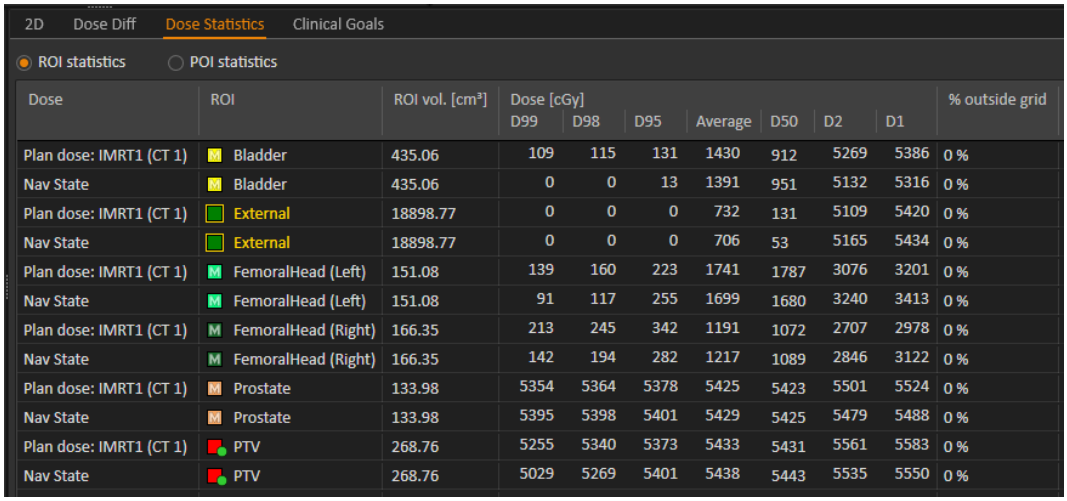


Figure 382. The Dose difference view.

Dose statistics

The dose statistics view lists ROI dose information for each dose distribution selected for evaluation. For more information, see *section 3.7.2 Dose statistics table on page 79*.



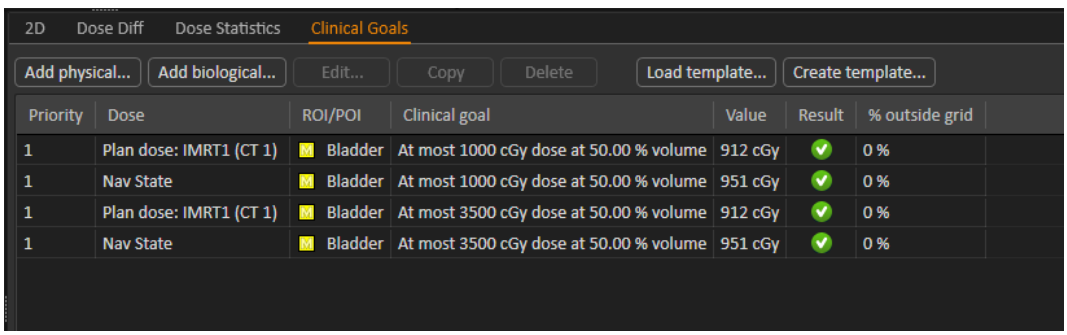
Dose	ROI	ROI vol. [cm³]	Dose [cGy] D99	D98	D95	Average	D50	D2	D1	% outside grid
Plan dose: IMRT1 (CT 1)	Bladder	435.06	109	115	131	1430	912	5269	5386	0 %
Nav State	Bladder	435.06	0	0	13	1391	951	5132	5316	0 %
Plan dose: IMRT1 (CT 1)	External	18898.77	0	0	0	732	131	5109	5420	0 %
Nav State	External	18898.77	0	0	0	706	53	5165	5434	0 %
Plan dose: IMRT1 (CT 1)	FemoralHead (Left)	151.08	139	160	223	1741	1787	3076	3201	0 %
Nav State	FemoralHead (Left)	151.08	91	117	255	1699	1680	3240	3413	0 %
Plan dose: IMRT1 (CT 1)	FemoralHead (Right)	166.35	213	245	342	1191	1072	2707	2978	0 %
Nav State	FemoralHead (Right)	166.35	142	194	282	1217	1089	2846	3122	0 %
Plan dose: IMRT1 (CT 1)	Prostate	133.98	5354	5364	5378	5425	5423	5501	5524	0 %
Nav State	Prostate	133.98	5395	5398	5401	5429	5425	5479	5488	0 %
Plan dose: IMRT1 (CT 1)	PTV	268.76	5255	5340	5373	5433	5431	5561	5583	0 %
Nav State	PTV	268.76	5029	5269	5401	5438	5443	5535	5550	0 %

Figure 383. The Dose statistics tab.

Clinical goals

The clinical goals functionality makes it possible to define evaluation criteria for specific ROIs and POIs. The result (pass/fail) per dose distribution is easy-to-read in a single column. For more information, see *section 3.7.3 Clinical goals on page 81*.

Note: *The clinical goals will not affect the optimization.*



Priority	Dose	ROI/POI	Clinical goal	Value	Result	% outside grid
1	Plan dose: IMRT1 (CT 1)	Bladder	At most 1000 cGy dose at 50.00 % volume	912 cGy	✓	0 %
1	Nav State	Bladder	At most 1000 cGy dose at 50.00 % volume	951 cGy	✓	0 %
1	Plan dose: IMRT1 (CT 1)	Bladder	At most 3500 cGy dose at 50.00 % volume	912 cGy	✓	0 %
1	Nav State	Bladder	At most 3500 cGy dose at 50.00 % volume	951 cGy	✓	0 %

Figure 384. The **Clinical Goals** tab.

7.5 BIOLOGICAL OPTIMIZATION

This section describes how radiobiological models and a combination of biological and physical criteria may be used to optimize a treatment plan in the Plan Optimization module. It describes Biological Optimization and explains the individual components and their possible commands.

This section also describes a typical biological optimization workflow. Each workflow step has a reference to a sub-section in this section where more information about how to perform the individual step is found.

The radiobiological models included in this version of Biological Optimization and Biological Evaluation are described in the *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual*.

Biological optimization uses a library of biological model parameters which comes with default parameters upon installation (factory defaults). These may be edited and amended, using a separate application called RayBiology. How to edit the parameters is described in *Appendix E RayBiology*.

Note: *Biological optimization is not supported for carbon ions.*

In this section

This section contains the following sub-sections:

7.5.1	Using biological optimization	p. 691
7.5.2	The biological optimization user interface	p. 693
7.5.3	The biological optimization functions	p. 694
7.5.4	Specify optimization and segmentation settings	p. 700
7.5.5	Edit beam properties	p. 701
7.5.6	Running the biological optimization	p. 702
7.5.7	Evaluating fluence in Beam's Eye View (BEV)	p. 703
7.5.8	Compute function values	p. 704
7.5.9	The evaluation views	p. 705
7.5.10	Biological optimization workflow	p. 708
7.5.11	Evaluating the plan – assessing plan quality	p. 710

Precautions

WARNING!

Biological model parameters. The biological model parameters are only valid if the correct reference volume is outlined when creating the ROI. (98329)

WARNING!

Always evaluate physical dose. Biological functions can be used as auxiliary tools to evaluate a treatment plan, but the physical dose distribution must always be evaluated. (97716)

WARNING!

Biological models. When using biological models, carefully review the selection of model parameters before clinical use. (96233)

WARNING!

Factory default biological models. The database of factory default biological model parameters comes from published clinical and pre-clinical studies. Still, this is an evolving field of science and more recent studies may provide evidence for other biological model parameters that are more suitable for clinical use.

The user shall always review the literature and base their usage of biological model parameters on the current state of knowledge in the field and clinic-specific treatment techniques. (96234)

WARNING!

Biological evaluation and optimization for protons. The underlying biological model is based on photon survival curves. The proton dose is not scaled when performing biological evaluation and biological optimization for protons. When using biological evaluation and optimization for protons, the machine must include an RBE factor in the absolute dosimetry. (103740)

7.5.1 Using biological optimization

Dose volume requirements

Conventional SMLC optimization is based on dose volume requirements, often in the form of planning protocols. For instance, a protocol can specify that the maximum allowed dose to the spinal cord is 45 Gy. During planning, the user can evaluate the quality of the plan based on the fulfillment of such requirements. Since it is often possible to fulfill all requirements, it has not been very important to distinguish between objectives and constraints in a technical sense. Dose volume requirements are almost exclusively implemented as objectives in treatment planning, but are often referred to as dose volume constraints.

Assessing plan quality

The dose levels prescribed by planning protocols are ultimately based on an intended biological effect. In the example of the spinal cord, keeping the maximum dose below 45 Gy has been correlated with an acceptable risk of complication. When using biological optimization, this is modeled directly, without the intermediate step of specifying dose levels. Therefore, in the same way, the DVHs and dose statistics can be inspected to decide if the dose volume requirements are met, the biological indices (NTCP and TCP values) can be directly related to the biological planning goals. It must, however, be kept in mind that the biological models of today have a limited predictive power, and that the physical dose distributions must also be inspected and found acceptable in conventional terms before approving a plan for delivery.

When to be satisfied

A question which often arises in treatment planning is when to be satisfied with the current solution. This is a non-trivial question in all kinds of treatment planning. When using optimization techniques, the question is twofold (at least). One question is whether or not the optimizer has solved the current optimization problem to a satisfying degree. This question is often answered by technical criteria on the objective function and its derivative. Though global optimality is often difficult to guarantee, experience has shown that most optimizers are capable of finding acceptable solutions to a given optimization problem.

A much more complex question is whether or not the solution to the current optimization problems constitutes the best (or even an acceptable) treatment plan. Considering the fact that a typical physical optimization problem can contain about a hundred user specified parameters (dose levels, volumes, weights) it becomes almost impossible to answer this. In biological optimization, the problem structure is often much simpler, with only one objective or constraint per organ. It is, however, also possible (and often necessary) to use dose volume constraints. This, in combination with the different options in configuring a biological optimization problem, still constitutes a large parameter space. Therefore, the experience of the dose planner is still important to assess the plan quality and when to be satisfied.

Margins and artificial structures

The biological models do not model geometrical uncertainties. As with physical optimization, it is necessary to apply planning margins to the target structures. It is an open question how biological models should best be applied to such expanded volumes, but current practice is to apply models based on the actual tumor type and stage. Other artificial structures, such as ring ROIs and

surrounding tissue have unspecified biological properties, and it is advised to use physical constraints if such structures are needed in the optimization problem. It is possible to use the biological models for artificial structures, but they have obviously no biological meaning.

Biological optimization of multiple beam sets

In contrast to the biological functions used for evaluation (clinical goals, biological evaluation functions) where the TCP and NTCP functions are applied to all fractions of the treatment plan, the biological functions used for optimization depends on the beam set used for optimization. The entire treatment plan (delivered fractions and all beam set doses) are considered only if the other beam set is set as background dose to the optimized beam set. Only in this case, the biological functions have their biological meaning. If the beam sets are optimized independently of each other or if the first beam set is optimized, the functions are applied only to the delivered fractions and the selected beam set. In this way, the biological functions can still be used as a tool to drive the optimization even though there is no biological meaning.

7.5.2 The biological optimization user interface

Workspace

The top left corner shows the result of the optimization process for each ROI in a dose volume histogram (**DVH**). Behind the DVH are the **Biological Response** tab which indicates how the biological response would change if the dose per fraction is scaled, and the number of fractions is held constant, the **Clinical goals** tab, the **Dose statistics** tab, the **Fractionation schedule** tab and the **Biological Progress** tab which indicates how the biological response evolves with time.

The bottom view defaults to the **Objectives/constraints** tab – listing the user specified objectives and constraints, with buttons for adding, editing and deleting of such functions. There are also tabs for the beam list, the control point list, the beam optimization settings and beam weighting.

The lower right corner, visualizes the **Optimization Progress** in terms of function values per iteration.

The window in the top right corner shows image set data for the current plan in 2D, 3D or Beam's Eye View (BEV).

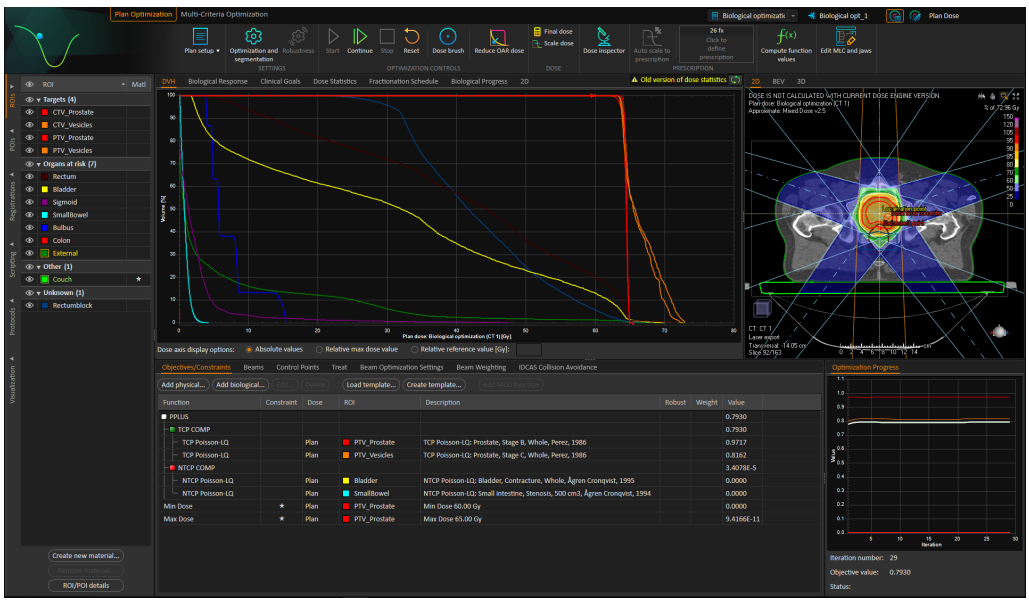


Figure 385. The Plan Optimization module workspace showing biological optimization.

7.5.3 The biological optimization functions

The objectives and constraints table lists the physical or biological objective functions, and biological and physical constraints that are included in an optimization problem and allows you to add new and edit and delete existing optimization functions.

Available biological optimization functions

An optimization problem consists of an objective function which is to be maximized or minimized. Optionally, it is allowed to define a number of constraints which the optimizer will fulfill if possible. The optimal solution to the problem is that which gives the best value of the objective function without violating any of the constraints. The objective function consists either of physical functions or of biological functions. It is not allowed to combine biological and physical functions in the objective function. If more than one objective is defined a composite objective function is automatically generated by Biological Optimization. Such composite functions are described below.

The following biological objective functions are supported:

Objective functions	Description
TCP (maximization)	The TCP function is a composite function which contains one or more constituent TCP function. Each such constituent, models the probability for tumor control in a specific target. To specify a proper TCP maximization problem: • Add one or several biological objective(s) for target ROIs to specify a TCP (maximization) objective function. • Add one or several biological NTCP constraints and/or physical dose constraints to limit the NTCP or dose levels to OARs, or to ensure dose homogeneity to the target.
NTCP (minimization)	Similarly to TCP, the NTCP function contains one or more constituent NTCP function which models the probability of complications in various organs. Add one or several biological objective(s) for OAR ROIs to specify a NTCP (minimization) objective function. Biological TCP constraints or physical dose constraints may be used to model the target dose. To specify a proper NTCP minimization problem: • Add one or several biological NTCP objectives to some of the organs at risk. • Add one or more biological NTCP or physical constraints for remaining OAR. • Add one or more biological TCP or physical constraints for target ROIs to ensure sufficient target effect.

Objective functions	Description
PPLUS (maximization)	This function contains a composite TCP and a composite NTCP function and represents the probability for obtaining tumor control (in all tumors) while avoiding normal tissue complication (in all organs at risk). Whenever both TCP and NTCP constituents are defined in a problem, PPLUS will be the objective function used.

In addition to the objective it is possible to define constraints. Constraints are used to set up requirements on the treatment which cannot (as in the case with objectives) be negotiated.

Constraints	Description
Biological constraints	The biological constraints are defined like the constituent TCP or NTCP function, but they are assigned individual bounds. • For TCP constraints, it makes sense to use a lower bound, representing the minimum probability of tumor control which can be accepted. • For NTCP constrains, upper bounds are used to represent the maximum probability for a complication which can be tolerated.
Dose volume constraints	The dose volume based constraints does not have bounds in the same sense as the biological constraints. Instead the bound is represented by dose and volume levels included in the function description.
Uniformity constraints	The uniformity constraint is a physical constraint, limiting the standard deviation of the dose distribution to a structure. Its upper bound is the allowed standard deviation. The lower the value of this bound, the more uniform doses are obtained.

Adding a biological objective function

To add a biological objective function:

1. Delete all physical objectives. It is not allowed to mix biological and physical functions in the objective function.
2. Click the **Add biological...** button in the **Objectives/Constraints** table.

   This opens the **Add Biological Optimization Function** dialog.

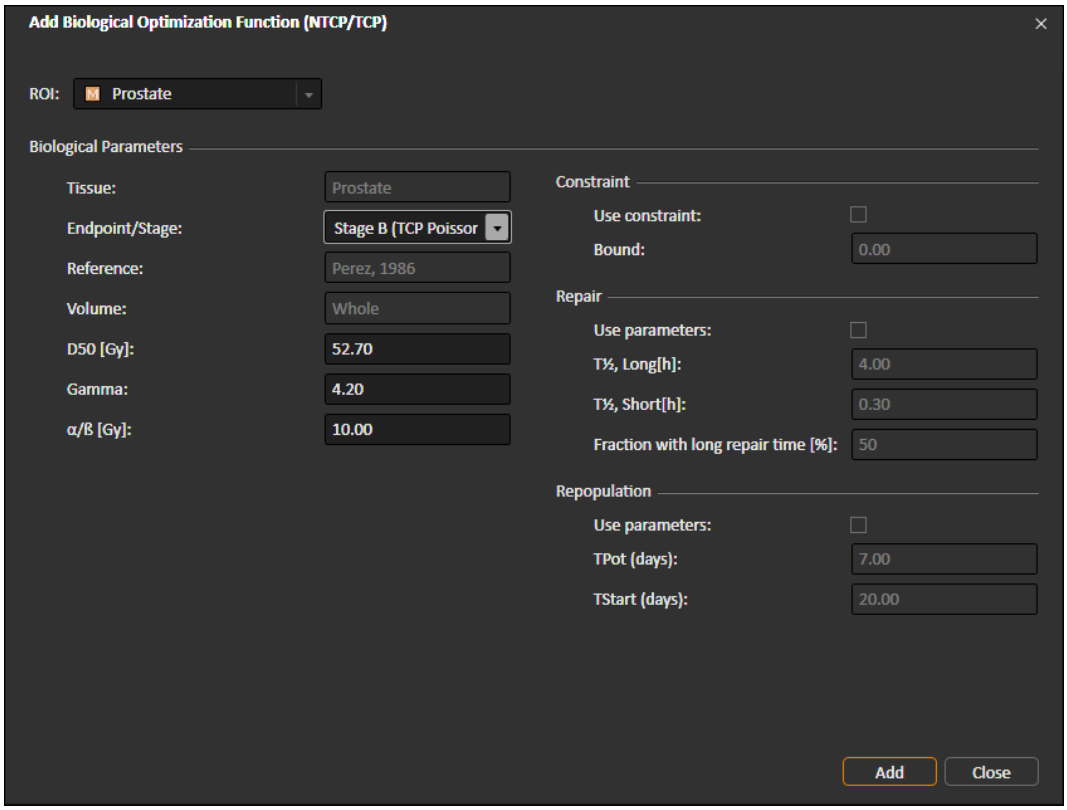


Figure 386. The **Add Biological Optimization Function** dialog.

3. Select the **ROI** for which a biological optimization function should be added.

   Note: *Make sure that the correct organ type and tissue type are defined in the ROI Properties dialog, see section 3.4.1 The ROI list on page 54.*

4. Select **Endpoint/Stage** if more than one endpoint/stage exists.

   Editable parameter values from the model parameter database are automatically added for the selected model. If any of the model parameters (D50, Gamma, etc.) are modified by the user, the reference will be set to **User defined**.

WARNING!

Biological model parameters. The biological model parameters are only valid if the correct reference volume is outlined when creating the ROI. (98329)

5. (Optional) Check the **Use parameters** checkbox in the **Repair** group box to enable the repair parameters **T1/2 Long[h]**, **T1/2 Short[h]** and **Fraction with long**.

   Define repair parameters to apply repair to the biological model.

   Note: *When using a repair model, make sure that the fractionation schedule is correct because the repair model depends on the recovery time between fractions.*

6. (Optional) Check the **Use parameters** checkbox in the **Repopulation** group box to enable the repopulation parameters **Tpot** and **TStart**. Only applicable for TCP functions.

   Define the repopulation parameters to apply repopulation to the biological model.

   Note: *When using a repopulation model, make sure that the total treatment time is correct because the repopulation model depends on the time of delivery of the last fraction.*

7. Click **Add** to close dialog and add function to the Objectives and constraints table.

   Click **Cancel** to close the dialog without modification.

Refer to *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual* for information about the models and their parameters.

Adding a physical objective function

To add a physical objective function:

1. Delete all biological objectives. It is not allowed to mix biological and physical functions in the objective function.
2. Add a physical objective function. See *Add objectives and constraints on page 524* for detailed information.

Adding a biological constraint function

To add a biological constraint function:

1. Follow the same procedure as when adding a biological objective function. See *Adding a biological objective function on page 695*.

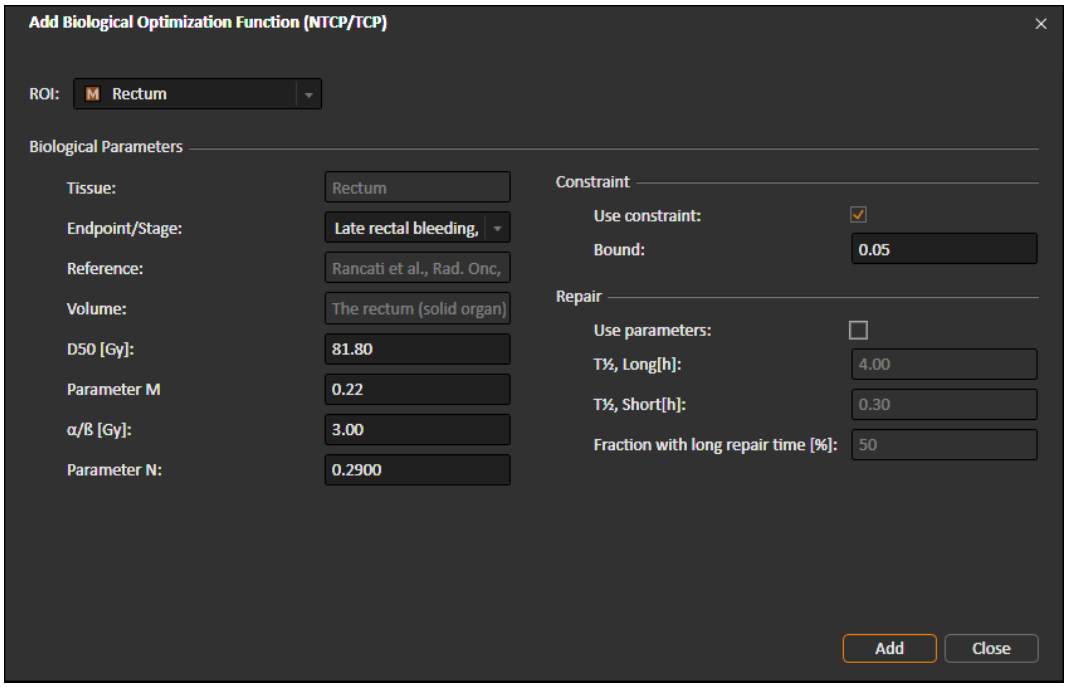


Figure 387. The **Add Biological Optimization Function** dialog. In this example, the Bound is set to 0.05 which means that the maximum allowed NTCP value is 5% at the optimal solution. In case of a TCP function it is the minimum allowed TCP value.

2. Check the **Use constraint** checkbox in the **Constraint** group box and enter a value for the **Bound**.

Example: The probability of causing myelitis/necrosis in the Spinal Cord may not exceed 5%.

ROI: Spinal Cord

Tissue: Spinal Cord

Endpoint/Stage: Myelitis/necrosis

D50: 68,60 Gy
Gamma: 1.90
Alpha/Beta: 3.00 Gy
Seriality: 4.00

Constraint
Use constraint: checked
Bound: 0.05

Note: *The biological parameters can either be edited directly in the Add function dialog or configured in the database using the RayBiology application.*

Adding a physical (dose) constraint

See *Add objectives and constraints on page 524* for detailed information. If the objective function is biological, it is not possible to use the physical function as an objective.

Editing existing objectives and constraints

It is possible to edit an existing objective/constraint by double-clicking on it in the **Objectives/Constraints** list, or by clicking the **Edit...** button, to open the Edit Optimization Function dialog. Another way to modify a physical objective/constraint is by dragging the corresponding arrow symbol in the DVH window. It is also possible to drag the TCP and NTCP bounds for a biological constraint in the **Biological Response** and the **Biological Progress** graphs.

To change the associated ROI (the function must be deleted and a new one added):

1. Select the function that you want to delete in the **Objectives/Constraints** list.
2. Click the **Delete** button.
3. Add a new optimization function. See *Adding a biological objective function on page 695* for more information.

Note: *Rows in the Objectives/Constraints list may be sorted differently after the function has been edited.*

Deleting existing objectives and constraints

To delete an existing objective and constraint:

1. Select the function that you want to delete in the **Objectives/Constraints** list.
2. Click the **Delete** button.

The objective/constraint is deleted and thus removed from the list.

7.5.4 Specify optimization and segmentation settings

The optimization and segmentation settings can be edited in the same way as for physical optimization. For more information, see *section 7.1.5 Specify optimization and segmentation settings on page 530*.

7.5.5 Edit beam properties

The beams can be edited directly in the **Beams** tab. For more information, see *section 7.1.6 Beams in the Plan Optimization module on page 537*.

7.5.6 Running the biological optimization

How to run the optimization is described in detail in *section 7.1.12 Running the optimization on page 549*.

Optimization Progress

The **Optimization Progress** graph shows the rate at which the optimization is converging. The iteration number is visible on the x-axis while the composite objective function value is shown on the y-axis. One curve is shown for each objective, with colors corresponding to the ROI color. Composite objectives are always colored black.

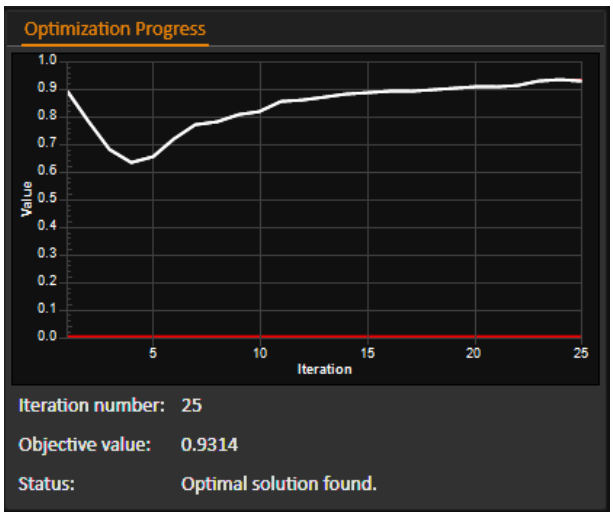


Figure 388. The Optimization progress graph.

Note: *The composite TCP and P+ are maximized and the best objective is 1.0.*

Use mouse over on a optimization progress curve to see legend information about that curve. The optimization progress curve legend show: Optimization function type and model: ROI, Tissue, Endpoint/Stage: [iteration number, probability].

Right click in the progress of optimization view to see right-click options that allows zooming in the optimization progress view.

7.5.7 Evaluating fluence in Beam's Eye View (BEV)

The **BEV** can be used to inspect fluence (only for non-VMAT/Conformal Arc photon plans) and individual beam segments. Use the pie chart in the upper left corner to navigate among the beams and beam segments. For more information, see *Navigation options on page 103*. The current beam and segment can also be selected in the **Beams** list and **Control points** list respectively.

Edit beam angles in BEV

As in the Plan Setup module the user can edit beam angles (gantry, collimator and couch angles) visually in the BEV. These tools are activated from the BEV context menu. For more information, see *section 6.2.6 Edit beam properties on page 402* and *Edit beam angles in patient views on page 327*.

Editing beam angles invalidates the dose and requires re-computation of the dose distribution.

Retract MLC

Right-click in the BEV to open the context menu and select **Retract MLC**.

Evaluating Leaf Open Times in BEV

The leaf open times are visualized using transparency, where complete transparency represents an opening time of 100% per projection, and completely opaque an opening time of 0% respectively. This representation is disabled if the user starts the **Beam animation**, and is instead animated using the actual leaf open times, opening and closing the leaves according to the values presented in the **Control points** list.

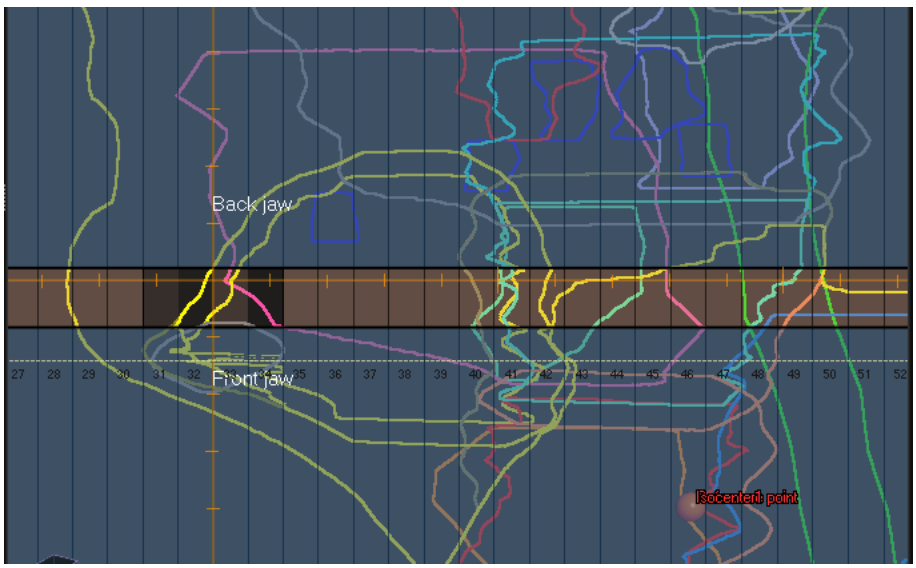
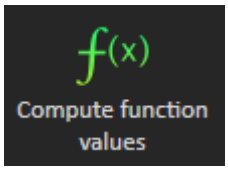


Figure 389. Leaf open times visualized in the BEV.

7.5.8 Compute function values

If an optimization function is altered after an optimization is run the value for the changed function can be updated by clicking the **Compute function values** button in the toolbar.



7.5.9 The evaluation views

Dose Volume Histogram (DVH)

The DVH view presents the cumulative dose volume histograms of the ROIs selected in the ROI List. The dose can be displayed as **absolute** or **relative [%]**. It is also possible to manually set the reference value for the relative scale. For a further description of the DVH view, see *section 3.7.1 Dose Volume Histogram (DVH) on page 78*.

The Biological Response graph

The **Biological Response** graph indicate how the biological response would change if the dose per fraction is scaled, and the number of fractions held constant. In the Plan optimization module, the dose scaling refers to the optimized beam set dose of the active plan.

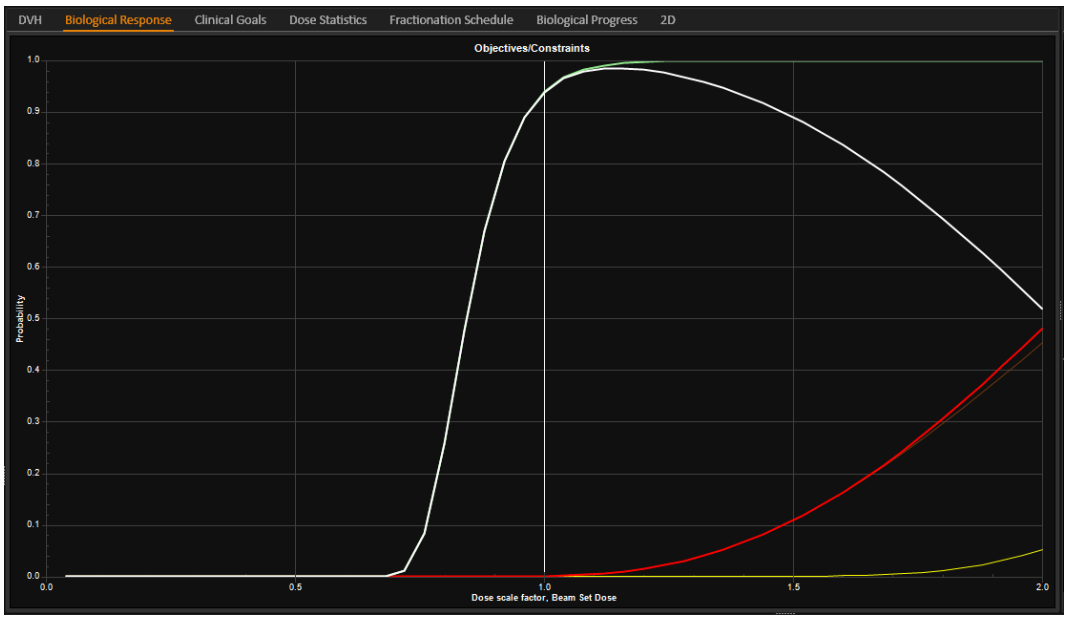


Figure 390. The Biological response graph.

Use mouse over on a response curve to see legend information about that response curve. The biological response curve legend show: Optimization function description (Plan name): [dose scale factor, probability].

Right-click in the response graph to see right-click options that allows for zooming in the response graph.

The TCP bounds of the biological constraints is displayed in the biological response graph as an arrow at the dose scale factor 1.0 (unscaled dose), pointing up at the value of the bound.

The NTCP bounds of the biological constraints is displayed in the biological response graph as an arrow at the dose scale factor 1.0 (unscaled dose), pointing down at the value of the bound.

It is possible to modify the value of a bound by dragging the arrow up and down on the final fraction line.

The biological response graph is not populated from the clinical goals, but from the optimization functions.

Clinical goals

The clinical goals functionality makes it possible to define evaluation criteria for specific ROIs and POIs. The result (pass/fail) is easy-to-read in a single column. For more information about the clinical goals functionality, see *section 3.7.3 Clinical goals on page 81*.

Biological clinical goals are described in *Biological clinical goals on page 744*.

Note: *The clinical goals will not affect the optimization.*

Dose statistics

The dose statistics view lists ROI dose information. For more information, see *section 3.7.2 Dose statistics table on page 79*.

Fractionation schedule

The **Fractionation schedule** tab displays a fractionation schedule for the active plan. The fractionation schedule in Plan Optimization module is similar to the nominal fractionation schedule in the Biological Evaluation module. See*section 8.2.3 The fractionation schedule on page 763* for detailed information.

Note: *The biological models depend both on the dose distribution and number of fractions (or dose per fraction). Repair and repopulation models depend on the time of delivery of the fractions and in this case it is important to use the correct fractionation schedule when evaluating the biological functions.*

Biological Progress

The **Biological Progress** graph displays the progress of treatment of the ROI based response functions and the composite objective functions. The biological progress graph displays the time in days on the x-axis (in decimal number where zero is midnight day 1 in the fractionation schedule, 0.5 is 12.00 the first day, 0.75 is 18.00 the first day and 1 is 0.00 day 2 in the fractionation schedule and so on.) and the probability of response [0,1] on the y-axis. Each dot in the graph represents a fraction. The time of day will be displayed in decimal number

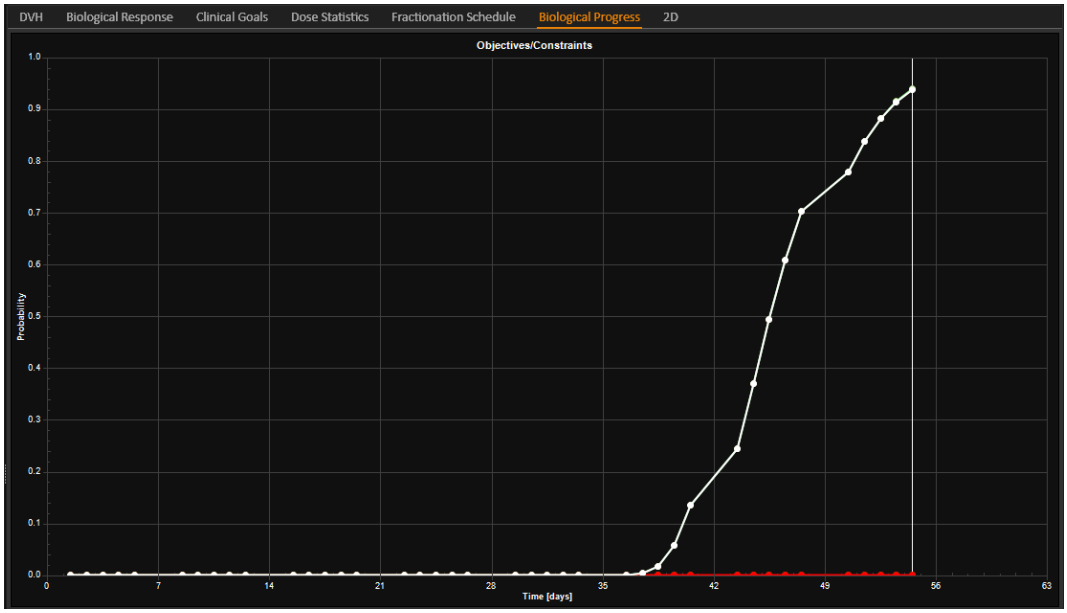


Figure 391. The Biological Progress graph.

The TCP bounds of the biological constraints is displayed in the biological progress graph as an arrow at the final fraction line, pointing up at the value of the bound.

The NTCP bounds of the biological constraints is displayed in the biological progress graph as an arrow at final fraction line, pointing down at the value of the bound.

It is possible to modify the value of a bound by dragging the arrow up and down on the final fraction line.

The biological progress graph is not populated from the clinical goals, but from the optimization functions.

7.5.10 Biological optimization workflow

A basic biological optimization workflow consists of the following steps:

1. **Define the optimization problem**.

    a. Add optimization functions for one or more of the ROIs specified for the patient and plan and specify their parameter values.

    - Add a biological objective function (described in *Adding a biological objective function on page 695*)
    - Add a biological constraint function (optional) (described in *Adding a biological constraint function on page 697*) or a physical objective function (described in *Add objectives and constraints on page 524*)
    - Add a physical constraint (optional) (described in *Adding a physical (dose) constraint on page 699*)

    b. Set the maximum number of iterations and the tolerance level for the optimization (described in *section 7.1.5 Specify optimization and segmentation settings on page 530*).

2. **Run the optimization** (described in *section 7.1.12 Running the optimization on page 549*).

    The optimization may be stopped (and reset) at any time during the optimization. Once stopped, new optimization functions may be added to the optimization problem, existing optimization function parameters may be edited and existing optimization functions may be deleted.

    a. Edit an existing objective or constraint (In order to change the function type, biological model and/or associated ROI the function must be deleted and a new one added) (described in *Editing existing objectives and constraints on page 699*)

    b. Delete an existing objective and constraint (described in *Deleting existing objectives and constraints on page 699*).

    It is recommended that the optimization is reset when new functions are added to the problem.

3. **Evaluate the plan** (described in *section 7.5.11 Evaluating the plan – assessing plan quality on page 710*).

    - If satisfied: Proceed with the next step.
    - If not satisfied: **Change the optimization problem** (and reset and restart the optimization) until an acceptable plan quality is achieved.

        The optimization may be changed (and hopefully improved) as a result of the following actions:

        a. Add new optimization functions.

        b. Edit existing optimization function parameters

        c. Change the maximum number of iterations/tolerance level.

4. **Compute dose**.

7.5.11 Evaluating the plan – assessing plan quality

An optimized treatment plan may be evaluated in terms of dose and/or in terms of estimated biological response using biological response functions. It must be pointed out that plan quality assessment cannot be based only on the predictions of the biological models, the dose distribution needs to be evaluated by conventional dose-volume based methods too. Biological models are used to calculate the TCPs and NTCPs for the dose distribution in question (resulting from biological or a combination of physical and biological treatment goals optimization) and these estimated response values are a complement to the radiation oncologist's experience in evaluating the dose distribution and the DVHs.

In Biological Optimization the calculation of TCP and NTCP for the different ROIs is based on the Poisson-LQ or LKB models together with parameter values that have been 'calibrated' against clinical data (see *Appendix A Definitions* for detailed description of the models).

7.6 ROBUST OPTIMIZATION

This section describes robust optimization for photon plans and for ion plans (Pencil Beam Scanning and Line Scanning) in the Plan Optimization module and the Multi Criteria Optimization module.

The robust optimization computes a plan which is robust according to user selections specified in the **Robustness Settings** dialog.

Setup and range uncertainties represent bounds on the magnitude of errors that the plan should be robust against. Organ motion uncertainties can be taken into account by selecting additional image sets to include in the optimization.

The errors are discretized into a number of scenarios, where each scenario represents a shift of the beam isocenters and/or a scaling of the patient densities for one of the selected image sets. Scenarios are created to take into consideration all combinations of setup errors, density errors, and image sets. The optimization minimizes the worst objective value over the scenarios.

For more details about robust optimization, refer to *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual*.

In this section

This section contains the following sub-sections:

7.6.1	Robust optimization functions	p. 712
7.6.2	Specify robustness settings	p. 714

7.6.1 Robust optimization functions

When an optimization function is added, it is possible to set the function as robust by checking the **Robust** checkbox in the **Add Optimization Function** dialog.

It is not possible to define an optimization function as robust if the function relates to beam set + background dose or to physical ion dose. It is also not possible to define an optimization function that is an Objective as robust in the Multi Criteria Optimization module.

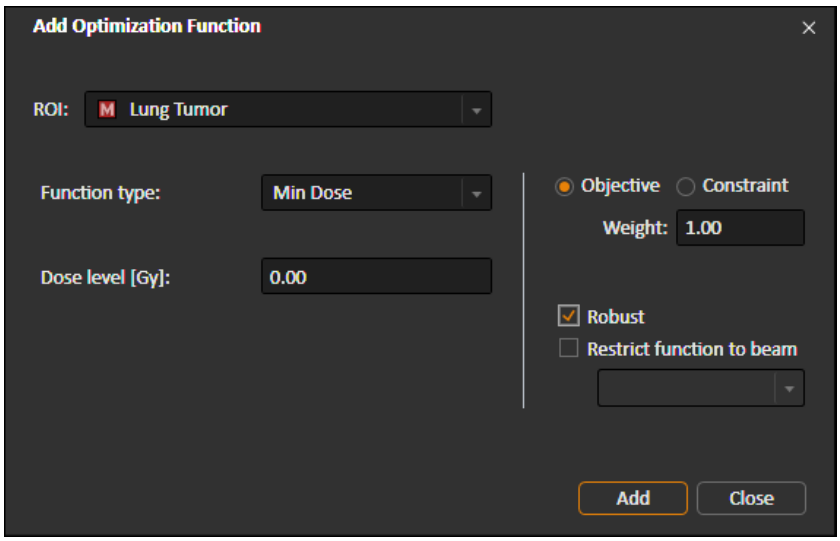


Figure 392. The **Add Optimization Function** dialog.

Robust optimization is supported for all types of physical optimization functions except for Dose Fall-Off and Uniformity Constraint. Robust optimization is not supported for any kind of biological optimization functions.

In the Optimization function list there is a column (**Robust**) to indicate the functions that are defined to take robustness into consideration.

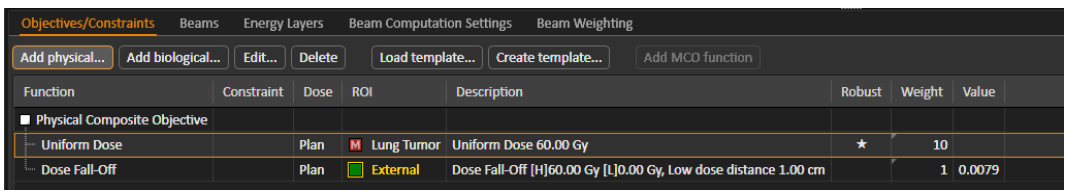


Figure 393. The Optimization function list where an asterisk in the Robust column indicates a function where robustness is taken into account.

WARNING!

Conflicting robust optimization functions. Robust optimization functions (e.g., a robust minimum dose function to a target and a maximum dose function to an OAR) may be in conflict also when applied to ROIs that are not overlapping, because of the different scenarios. This may lead to over- or underdosage. (115551)

WARNING!

Robust optimization functions may be in conflict with non-robust optimization functions. A robust constraint may, for example, be in conflict with the mimic dose function during the creation of a deliverable plan in the Multi Criteria Optimization module. The optimization may prioritize the non-robust functions over the robust functions, leading to reduced robustness. (370077)

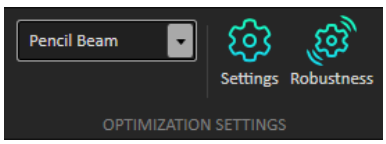
Note: *For robust optimization functions, the objective values are only displayed during and after an optimization. After a clinical dose computation, no value is displayed due to that the clinical scenario doses are not computed.*

Note: *After a robust optimization dose statistics, clinical goals and DVH:s are all based on dose computed on the planning CT only.*

Note: *Independent beams cannot be used in combination with beam split. To use independent beams for targets larger than the field size, the user must manually add beams.*

7.6.2 Specify robustness settings

To edit robustness settings, click the **Robustness** button. The button is only enabled if there are robust optimization functions defined.



This opens the Robustness settings dialog.

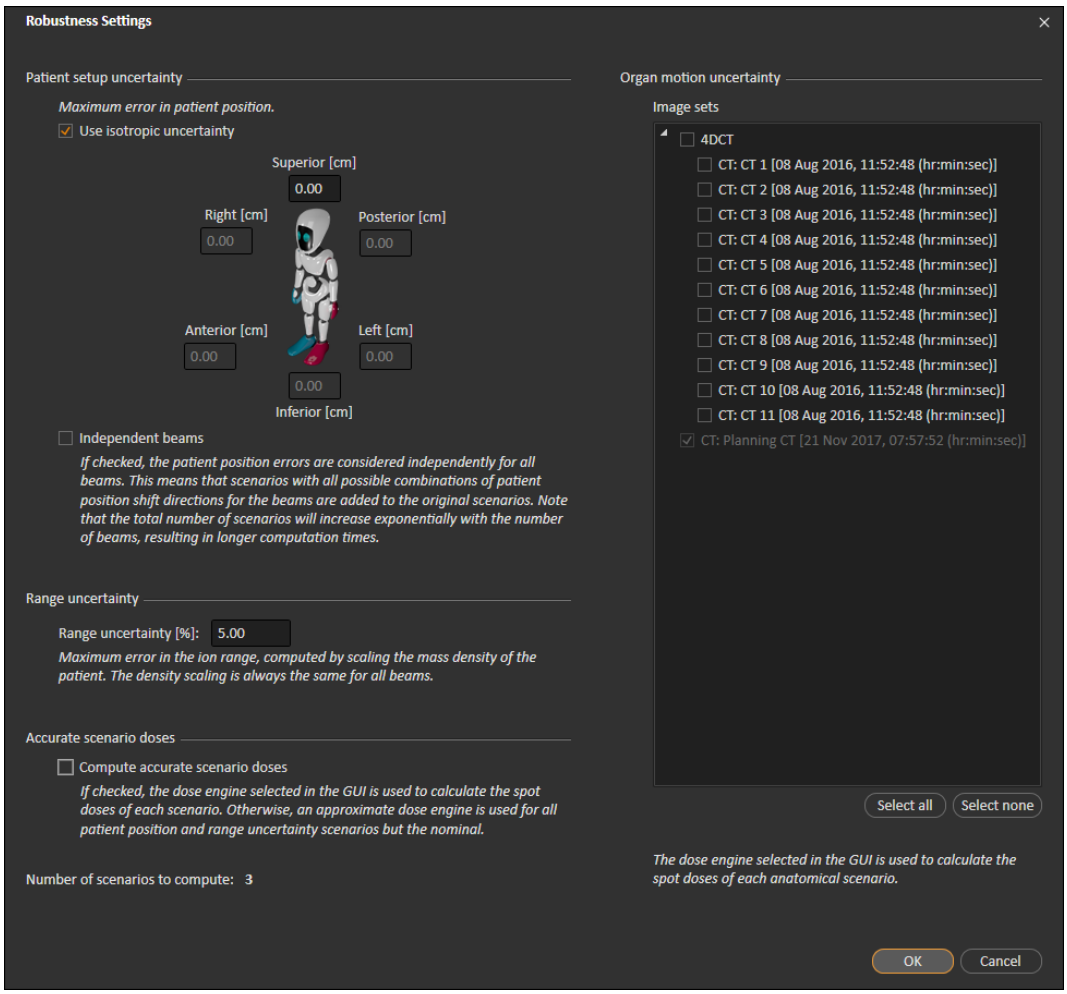

Robustness Settings
Patient setup uncertainty
Maximum error in patient position.
Use isotropic uncertainty
Superior [cm]
0.00
Right [cm]
0.00
Posterior [cm]
0.00
Anterior [cm]
0.00
Left [cm]
0.00
0.00
Inferior [cm]
Independent beams
If checked, the patient position errors are considered independently for all beams. This means that scenarios with all possible combinations of patient position shift directions for the beams are added to the original scenarios. Note that the total number of scenarios will increase exponentially with the number of beams, resulting in longer computation times.
Range uncertainty
Range uncertainty [%]: 5.00
Maximum error in the ion range, computed by scaling the mass density of the patient. The density scaling is always the same for all beams.
Accurate scenario doses
Compute accurate scenario doses
If checked, the dose engine selected in the GUI is used to calculate the spot doses of each scenario. Otherwise, an approximate dose engine is used for all patient position and range uncertainty scenarios but the nominal.
Number of scenarios to compute: 3
Organ motion uncertainty
Image sets
4DCT
CT: CT 1 [08 Aug 2016, 11:52:48 (hr:min:sec)]
CT: CT 2 [08 Aug 2016, 11:52:48 (hr:min:sec)]
CT: CT 3 [08 Aug 2016, 11:52:48 (hr:min:sec)]
CT: CT 4 [08 Aug 2016, 11:52:48 (hr:min:sec)]
CT: CT 5 [08 Aug 2016, 11:52:48 (hr:min:sec)]
CT: CT 6 [08 Aug 2016, 11:52:48 (hr:min:sec)]
CT: CT 7 [08 Aug 2016, 11:52:48 (hr:min:sec)]
CT: CT 8 [08 Aug 2016, 11:52:48 (hr:min:sec)]
CT: CT 9 [08 Aug 2016, 11:52:48 (hr:min:sec)]
CT: CT 10 [08 Aug 2016, 11:52:48 (hr:min:sec)]
CT: CT 11 [08 Aug 2016, 11:52:48 (hr:min:sec)]
CT: Planning CT [21 Nov 2017, 07:57:52 (hr:min:sec)]
Select all
Select none
The dose engine selected in the GUI is used to calculate the spot doses of each anatomical scenario.
OK
Cancel

Figure 394. The Robustness settings dialog.

The user can edit the following robustness settings:

Parameter	Description
Patient setup uncertainty	The patient setup uncertainty relates to the maximum error of setup position.
Use isotropic uncertainty	If checked, the same uncertainty will be used in all dimensions.
Independent beams	If checked, the patient setup errors are considered independently for all beams. This means that scenarios with all possible combinations of patient setup shift directions for the beams are added to the original scenarios.
Range uncertainty	Only for ions. Maximum error in the ion range.
Accurate scenario doses	Only for ions. If checked, the dose engine selected in the GUI is used to calculate the spot doses of each scenario. ***Note:*** *This option is required for carbon ion plans.*
Organ motion uncertainty	Scenarios are computed for all selected image sets. This part of the dialog is only visible if the case includes multiple image sets.

During optimization, a number of scenario doses are computed and the optimizer minimizes the worst objective value over all scenarios. The number of scenarios scales with the size of the uncertainty and the number of image sets: larger uncertainties and more selected image sets results in a larger number of scenarios. Also note that by selecting independent beams, the number of scenarios will increase and the optimization time will increase.

The Robustness settings are just like Optimization settings; they are applied on the subsequent optimizations. In other words, a dose that has been obtained by an optimization will not be affected if the user later edits an image set that was selected in the Robustness settings.

WARNING!

Evaluate the dose after robust optimization. After a robust optimization has been performed, the user is strongly advised to evaluate the dose using the perturbed dose tool in the Plan Evaluation module to verify that the dose is robust as intended. (114973)

WARNING!

Fallback plans will not take robustness into consideration during mimic dose optimization. If the original plan was optimized using robust optimization functions and a fallback plan is created, the fallback plan will try to mimic the dose of the original plan without taking robustness into consideration. (115556)

Note: *If robust optimization functions are added from a template (see section 7.1.4 Optimization function list templates on page 529) the robustness settings will not be updated, i.e., the robustness settings are not a part of the template.*

Note: *Positioning errors are in the Robustness Settings dialog specified in term of shifts of the setup position, whereas dose perturbations are specified in terms of shifts of the isocenter position in the Compute Perturbed Dose dialog (see section 8.1.7 Compute perturbed dose on page 735). A shift of the patient relative to the isocenter is equivalent to the corresponding shift of the isocenter relative to the patient with the sign reversed. Robustness against, for example, a maximum positioning error of 5 mm in the right direction should therefore be evaluated by isocenter shifts of up to 5 mm in the left direction (the positive X direction in IEC coordinates).*

8 PLAN EVALUATION

The Plan Evaluation planning activity contains the modules Plan Evaluation and Biological evaluation. The Plan Evaluation module provides various tools for dose evaluation, both for individual plans and for comparison of rival plans. The Biological Evaluation module includes functionality for biological plan evaluation using radiobiological models.

In this chapter

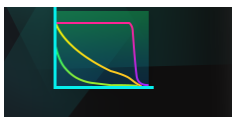
This chapter contains the following sections:

8.1	The Plan Evaluation module	p. 718
8.2	The Biological Evaluation module	p. 758

8.1 THE PLAN EVALUATION MODULE

The Plan Evaluation module provides various tools for dose evaluation, both for individual plans and for comparison of rival plans. The Plan Evaluation module includes features such as:

- side-by-side comparison of dose distributions from rival plans
- dose statistics, DVH and dose summation
- dose computation including perturbation of the dataset – for evaluation of robustness
- dose computation on additional, secondary, image sets
- dose deformation, i.e. the ability to "project" dose calculated on an additional image set, back to the original image set
- plan approval



In this section

This section contains the following sub-sections:

8.1.1	Plan Evaluation user interface	p. 723
8.1.2	Doses	p. 725
8.1.3	Single plan evaluation	p. 727
8.1.4	Plan comparison	p. 728
8.1.5	The evaluation graphs	p. 731
8.1.6	Dose summation	p. 733
8.1.7	Compute perturbed dose	p. 735
8.1.8	Compute dose on additional image sets	p. 736
8.1.9	Deform dose	p. 737
8.1.10	Define or modify prescription	p. 739
8.1.11	Export DVH curves to ASCII file	p. 740
8.1.12	Export line doses	p. 741
8.1.13	Update ROI voxel volumes	p. 742
8.1.14	Biological evaluation	p. 743
8.1.15	Plan approval	p. 748
8.1.16	Create fallback plans	p. 755

Precautions

WARNING!

System checks at approval. Be aware that the following checks before approval are only performed for planning doses:

- Beam entry validation.
- A Bolus ROI geometry exists.
- A Support ROI geometry exists.
- A Fixation ROI geometry exists.
- The Dose grid resolution is smaller than 5 mm in all directions.

For evaluation doses, the user is responsible for performing these checks.

Note that having a planning dose grid which encloses the External ROI, support ROIs, fixation ROIs and bolus ROIs does not guarantee that all relevant regions are included for dose computation on additional datasets. (26694)

WARNING!

Approximate dose is only intended for intermediate treatment planning steps. Approximate dose has lower accuracy compared to the dose displayed as "Clinical" and it must not be used for clinical decisions. A plan with approximate dose cannot be approved or exported. (126034)

WARNING!

Interpolated dose values are shown in the patient views. Interpolated dose values are shown in the patient views by default. Ensure that an appropriate dose grid resolution for the specific treatment planning situation is used. (7289)

WARNING!

Display of total dose. It is always the total dose for all planned fractions that is displayed in the patient views, the DVH graph, the dose statistics and in the clinical goals list.

Exceptions are the QA module, where the dose is displayed for one fraction, and the Dose Tracking module, where the user can select different scales of displayed dose. (7291)

WARNING!

Biological model parameters. The biological model parameters are only valid if the correct reference volume is outlined when creating the ROI. (98329)

WARNING!

Always evaluate physical dose. Biological functions can be used as auxiliary tools to evaluate a treatment plan, but the physical dose distribution must always be evaluated. (97716)

WARNING!

Biological models. When using biological models, carefully review the selection of model parameters before clinical use. (96233)

WARNING!

Factory default biological models. The database of factory default biological model parameters comes from published clinical and pre-clinical studies. Still, this is an evolving field of science and more recent studies may provide evidence for other biological model parameters that are more suitable for clinical use.

The user shall always review the literature and base their usage of biological model parameters on the current state of knowledge in the field and clinic-specific treatment techniques. (96234)

Note: *The isocenter coordinates in the beam list in plan evaluation will always refer to the isocenter coordinates in the original plan.*

8.1.1 Plan Evaluation user interface

Workspaces

In the Plan Evaluation module, the user can choose between four different workspaces; one is designed for single plan evaluation, two are for comparison of two plans, and the fourth is for evaluation and comparison of three plans.

For TomoHelical plans there is a **Leaf Open Times** view that displays a histogram for the leaf open time of all leaves and of all projections.

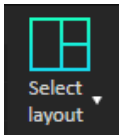
All of the workspaces contain at least one 2D patient view, DVHs, dose statistics, clinical goals, and the line dose graph. The workspaces for two plan comparison also have a 2D patient view for visualization of dose difference – the Dose difference view. 2D patient views are titled **Current**, **Compare 1** and **Compare 2** respectively.

Note: *The dose difference is only displayed if the two plans are based on the same image set or if their image sets are registered.*

Note: *In the dose difference view, the patient always will be displayed according to the treatment position of the currently active plan.*

Figure 395. The Plan Evaluation module.

Workspace selection is done via the **Select workspace layout** button to the left in the toolbar.



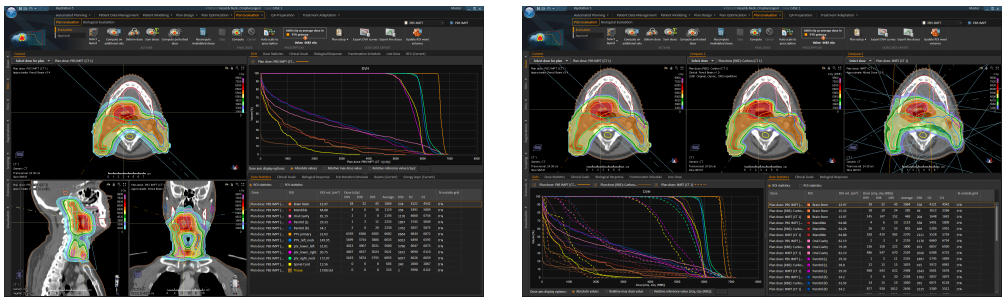


Figure 396. The workspace layout for evaluation of one dose (left) and for evaluation of three doses (right).

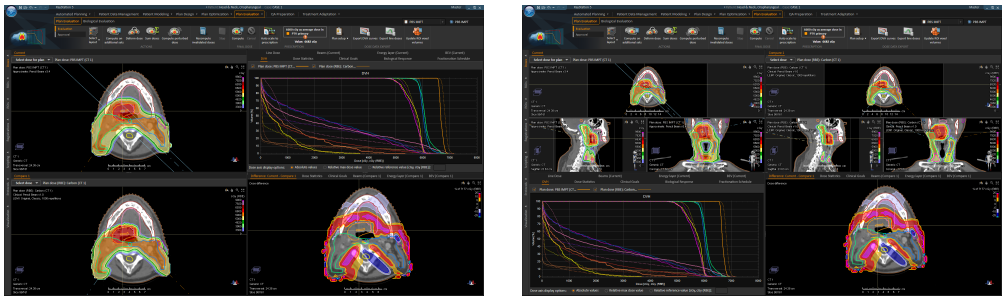


Figure 397. Two different workspaces for evaluation and comparison of two doses.

The dose list

All available doses are listed in the Dose List tool page. The tool panel is expanded /contracted by clicking the panel tab headers to the left.

A 2D patient view can be populated with a dose in two ways:

- Drag a dose in the Dose List tool page, and drop it in the view to populate
- Click the **Select dose** menu button, in the upper left corner of the view to populate, and select the dose in the list Changing dose in one 2D patient view updates all views where this dose is displayed, i.e. DVH, dose statistics etc.

Plan approval

The plan approval workspace is launched from the **Approval** tab in the toolbar. Plan approval is further described in *section 8.1.15 Plan approval on page 748*.

8.1.2 Doses

The dose list in the **Doses** tab presents all available doses for the current patient case. Available doses are either planning doses with dose calculated on the planning image set, or evaluation doses computed in the Plan Evaluation module.

Planning doses

Plan dose – the complete planned treatment dose, calculated on the planning image set. Use the plan to see the total dose for the planned treatment.

Beam set dose – a planned beam configuration, calculated on the planning image set. Use the beam set dose to see the beam set's contribution to the planned treatment.

Beam dose – use the beam dose to see the total dose for an individual beam.

Evaluation doses

Beam set dose on additional image set – the planned beam set (beam configuration) with dose calculated on an additional, registered, image set. For more information, see *section 8.1.8 Compute dose on additional image sets on page 736*.

Deformed dose – dose calculated on an additional image set mapped back to the original planning image set. For more information, see *section 8.1.9 Deform dose on page 737*.

Perturbed dose – dose computed including a perturbation of the dataset, for evaluating robustness. For more information, see *section 8.1.7 Compute perturbed dose on page 735*.

Dose summation – an arbitrary summation of doses (computed on the same image set). For more information, see *section 8.1.6 Dose summation on page 733*.

It is possible to see constituent parts of evaluation doses (summed doses, perturbed doses, doses on additional datasets) by holding the mouse over the dose label or the dose icon in the dose list.

An evaluation dose can be deleted by right-clicking on it in the dose list and selecting **Delete dose**.

An evaluation dose can be exported by right-clicking on it in the dose list and selecting **Export**. The DICOM Export dialog opens and the dose can be exported as a deformed dose.

Note: *The beam list for evaluation doses will display isocenter coordinates corresponding to the original plan.*

Planning and evaluation doses for Carbon ions

For carbon ions it is specified in the dose list if the dose is a physical ion dose or an RBE dose:

Physical ion dose (PHY) – the delivered dose.

Relative Biological Effectiveness dose (RBE) – the physical ion dose weighted with the relative biological effectiveness.

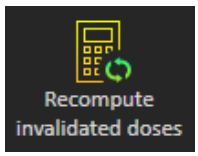
The physical ion dose (**PHY**) is presented as a sublevel to the RBE dose for **Perturbed dose**, **Plan dose** with one beam set, **Beam set dose on additional image set** and **Beam set dose**.

Recompute invalidated doses

If the treatment plan is changed, evaluation doses for that plan will be invalidated. An invalidated dose can be recomputed in two ways;

- by clicking the related pocket calculator icon in the dose list

- or by clicking the **Recompute invalidated doses** button in the toolbar, which will recompute all invalidated doses.



Note: *If a dose is not possible to compute, there is no notification when using the Recompute invalidated doses button. If a dose is still invalid (indicated with a pocket calculator in the dose tree), click the pocket calculator to get information about why the dose computation failed.*

8.1.3 Single plan evaluation

Click the **Select workspace layout** button and select the single plan evaluation workspace from the menu.

Figure 398. The workspace layout for single dose evaluation.

Select the dose to evaluate, either by dragging it from the dose list in the tool page, or by selecting it from the **Select dose** menu button in the upper left corner of the 2D patient view.

The dose distribution can then be reviewed in the 2D patient views. The dose can be further analyzed using the DVH, with ROI dose statistics, by using dose lines and clinical goals.

When a beam set dose or a beam dose is selected, beam properties can be reviewed in the beam and control point lists, and in the BEV.

Note: *Only doses related to the currently active beam set can be selected, that is the total plan, the current beam set itself, beam doses of the current beam set, and evaluation doses, and beam doses, for the current beam set.*

8.1.4 Plan comparison

To compare multiple plans and doses, select one of the dose comparison workspaces from the **Select workspace layout** menu button.

Figure 399. Workspace layouts for plan comparison.

Select the doses to evaluate, either by dragging them from the dose list in the tool page and dropping them in the view to populate, or by selecting dose from the **Select dose** menu button in the upper left corner of each 2D patient view (or group of views).

The dose distributions can then be reviewed and compared using the 2D patient views, including the dose difference view. The dose can be further analyzed using the DVH, with ROI dose statistics, by using dose lines and clinical goals.

For carbon ions it is also possible to visualize the RBE factor in the **Difference** view. For instructions on how to visualize the RBE factor, see *section 7.3.17 RBE factor visualization on page 647*.

When beam set doses or beam doses are selected, beam properties can be reviewed and compared using the beam and control point lists, and using the BEV.

When comparing doses computed on the same image set, or doses computed on registered image sets, the views are synchronized in a way that the same image positions are displayed for all doses (Dose 1, Dose 2, etc.). Example: scrolling in the transversal view for Dose 1 also scrolls the transversal view for Dose 2 to the corresponding image slice. When moving the mouse cursor over the image data for one of the doses a red plus symbol is displayed at the corresponding location in the other, synchronized dose views. This makes it possible to compare dose values at specific positions in multiple doses at the same time - the dose value at the cursor position is reported in the upper left corner of each patient view. The view synchronization when comparing doses computed on the same image set. When moving the mouse cursor over the image data for one of the doses a red plus symbol is displayed at the corresponding location in the other, synchronized dose views.

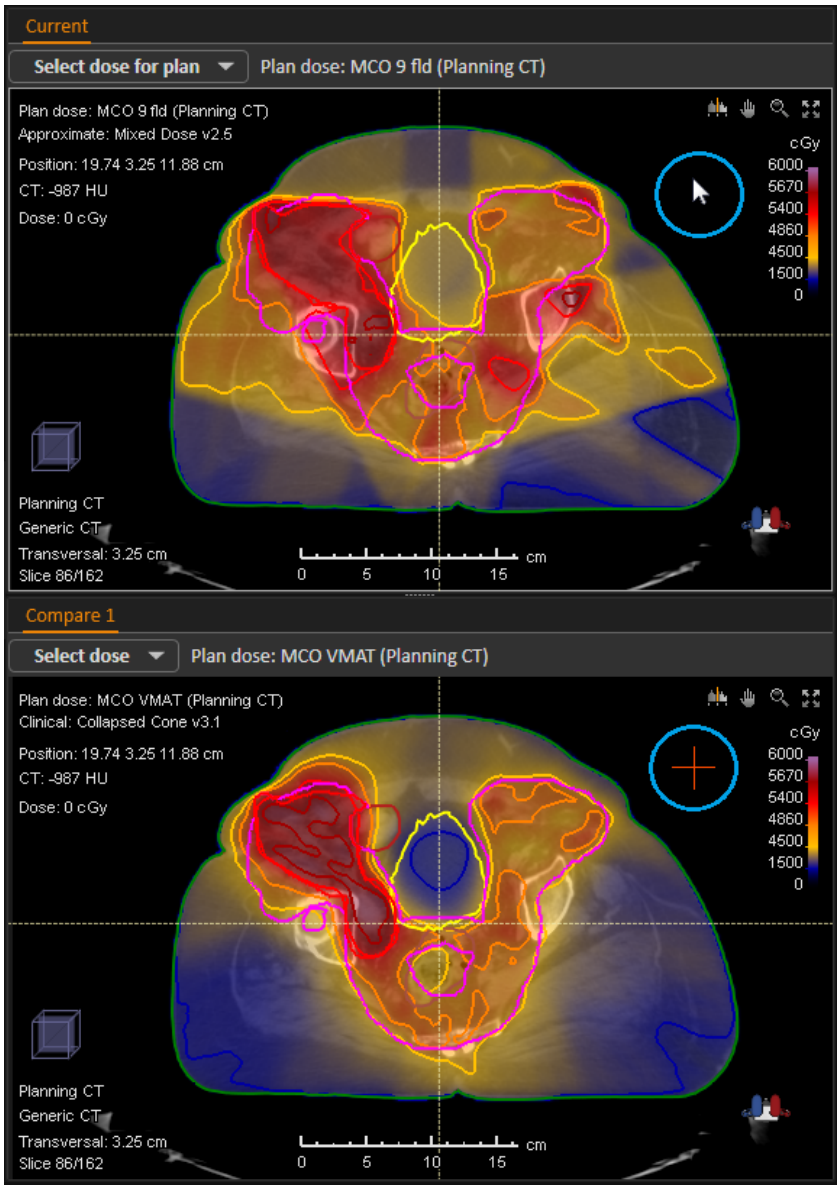


Figure 400. The view synchronization when comparing doses computed on the same image set. When moving the mouse cursor over the image data for one of the doses a red plus symbol is displayed at the corresponding location in the other, synchronized dose views.

Note: *Only doses related to the currently active beam set can be selected for the Dose 1 view(s), that is the total plan, the current beam set itself, beam doses of the current beam set, and evaluation doses, and beam doses, for the current beam set.*

Note: *Due to discrete window coordinates (pixels) the accuracy of the positioning of the haircross, when doing dose comparison, is dependent of the zoom level of the window. This may lead to a small discrepancy in positioning, causing a non 100% synchronization of the views. Positions may differ a bit, and dose difference may differ a bit. The actual position and dose reported in each view will be consistent within the view.*

Note: *When comparing two image sets or plans, the secondary image set might need a slight rotation in order to match the primary image set. The primary image set always will be fixed. If there is an image registration with a rotation this will be indicated in the view by an asterisk in conjunction to the patient plane direction. "* Transversal" will for example denote that this is a rotated view based on a transversal patient view, i.e., the reference view is transversal but the image registration between the reference image set and the shown image set may rotate the image data in the view so that it is not transversal. The same applies to the coronal and the sagittal patient views.*

8.1.5 The evaluation graphs

Dose Volume Histogram (DVH)

The DVH view presents the cumulative dose volume histograms of the ROIs selected in the ROI List. The dose can be displayed as absolute or relative [%]. It is also possible to manually set the reference value for the relative scale.

The DVH shows dose data from all doses selected for evaluation. Above the curve area each dose is presented with a unique line style and a checkbox for visibility selection, making it possible to select which doses to show in the DVH.

The ROIs displayed in the patient views, DVH, and Dose statistics are all selected from the ROI list checkboxes.

For more information about the DVH view, see *section 3.7.1 Dose Volume Histogram (DVH) on page 78*.

Dose statistics

The dose statistics view lists ROI dose information for each dose selected for evaluation. See *section 3.7.2 Dose statistics table on page 79* for more information.

Clinical goals

The clinical goals functionality makes it possible to define evaluation criteria for specific ROIs or POIs. The result (pass/fail) per plan is easy-to-read in a single column.

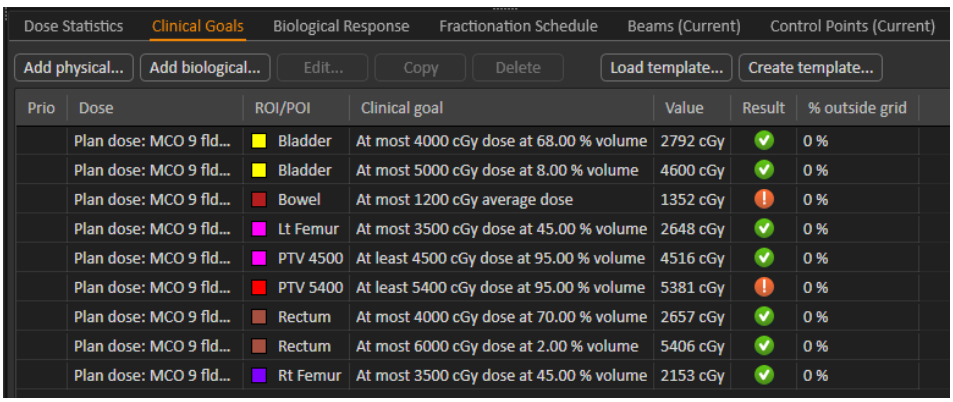

Dose Statistics
Clinical Goals
Biological Response
Fractionation Schedule
Beams (Current)
Control Points (Current)
Add physical...
Add biological...
Edit...
Copy
Delete
Load template...
Create template...
Prio
Dose
ROI/POI
Clinical goal
Value
Result
% outside grid
Plan dose: MCO 9 fld... Bladder At most 4000 cGy dose at 68.00 % volume 2792 cGy 0 %
Plan dose: MCO 9 fld... Bladder At most 5000 cGy dose at 8.00 % volume 4600 cGy 0 %
Plan dose: MCO 9 fld... Bowel At most 1200 cGy average dose 1352 cGy 0 %
Plan dose: MCO 9 fld... Lt Femur At most 3500 cGy dose at 45.00 % volume 2648 cGy 0 %
Plan dose: MCO 9 fld... PTV 4500 At least 4500 cGy dose at 95.00 % volume 4516 cGy 0 %
Plan dose: MCO 9 fld... PTV 5400 At least 5400 cGy dose at 95.00 % volume 5381 cGy 0 %
Plan dose: MCO 9 fld... Rectum At most 4000 cGy dose at 70.00 % volume 2657 cGy 0 %
Plan dose: MCO 9 fld... Rectum At most 6000 cGy dose at 2.00 % volume 5406 cGy 0 %
Plan dose: MCO 9 fld... Rt Femur At most 3500 cGy dose at 45.00 % volume 2153 cGy 0 %

Figure 401. The **Clinical goals** tab.

The biological response of the clinical goals is displayed in the **Biological Response** tab. See *Biological Response on page 746* for more information.

For a detailed description of the clinical goals functionality, see *section 3.7.3 Clinical goals on page 81*.

Line dose

Right-click in a patient view and select **Add/edit dose line** from the context menu. The dose line is placed by clicking somewhere in the view, moving the mouse and release the mouse button where the line should end – the dose line's profile is displayed in the **Line dose** tab (located in the same area as the BEV and Dose statistics). For more information, see *section 3.7.4 Line dose on page 88*.

8.1.6 Dose summation

Note: *For carbon ions: Instructions on how to sum doses can be found in section 7.3.19 Sum carbon ion doses on page 651.*

To sum doses:

1. Click the **Sum doses** button in the toolbar.

This opens the Sum doses dialog.

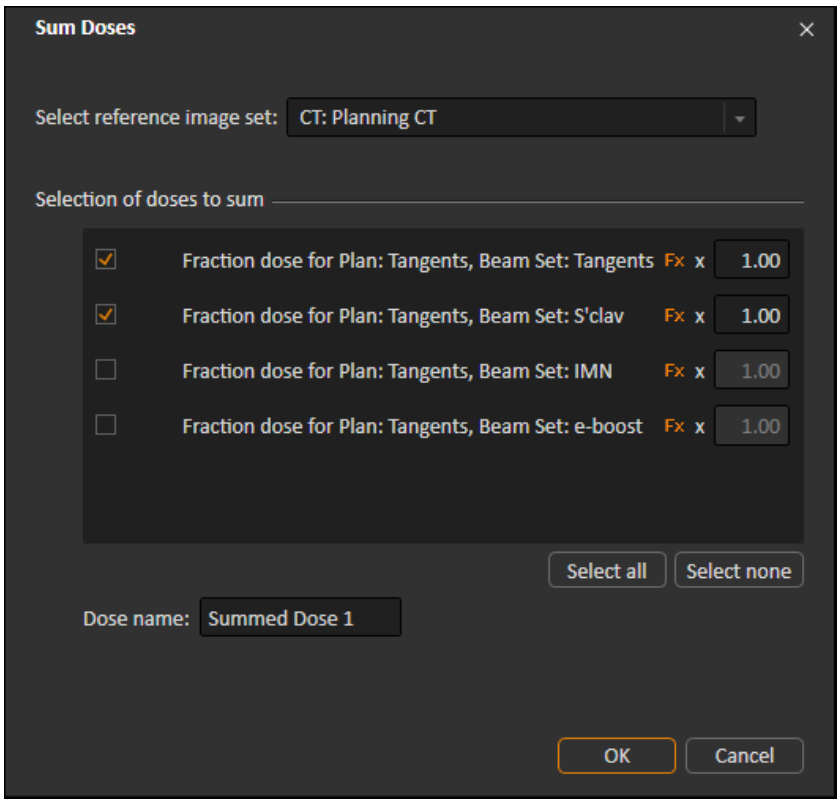


Figure 402. The Sum doses dialog.

2. Select **Reference image set**. Note that only doses calculated on the same image sets can be summed.
3. Select the doses to be summed by checking the corresponding checkboxes in the **Selection of doses to sum** list. It is possible to scale each dose by specifying the number of fractions to

use in the summation - just enter a value in the x field to the right of each fraction dose in the list.

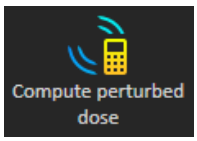
4. Enter a **Dose name** for the summation.
5. Click **OK**. Now the summed dose appears in the dose list, and from there it can be dragged into a view in the workspace.

8.1.7 Compute perturbed dose

For evaluation of robustness, doses can be computed including a perturbation of the dataset. Perturbations are specified as a scaling of densities (in %) and/or a shift of the isocenter in x, y and/or z (IEC, cm) direction.

To compute a perturbed dose:

1. Click the **Compute perturbed dose** button.



This opens the Compute Perturbed Dose dialog.

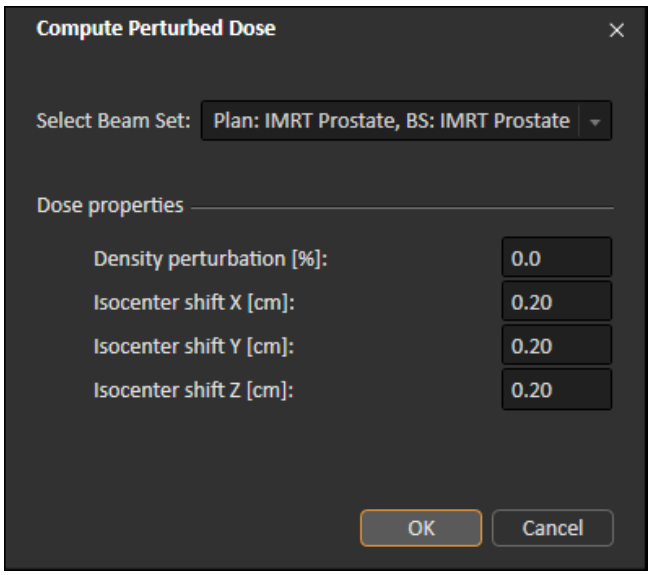


Figure 403. The Compute perturbed dose dialog.

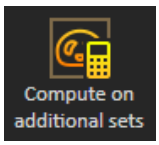
2. Select **Beam set**.
3. Enter dose properties; **Density perturbation**, **Isocenter shift X**, **Isocenter shift Y** and **Isocenter shift Z**.
4. Click **OK**.

   The perturbed dose becomes available in the list of doses after calculation. The dose name describes what perturbation was applied.

8.1.8 Compute dose on additional image sets

In RayStation dose can easily be computed for a specific beam set on an additional CT image set that is registered with the planning image set. To compute dose on additional image sets:

1. Click the **Compute on additional sets** button.



This opens Compute dose on additional image sets dialog.

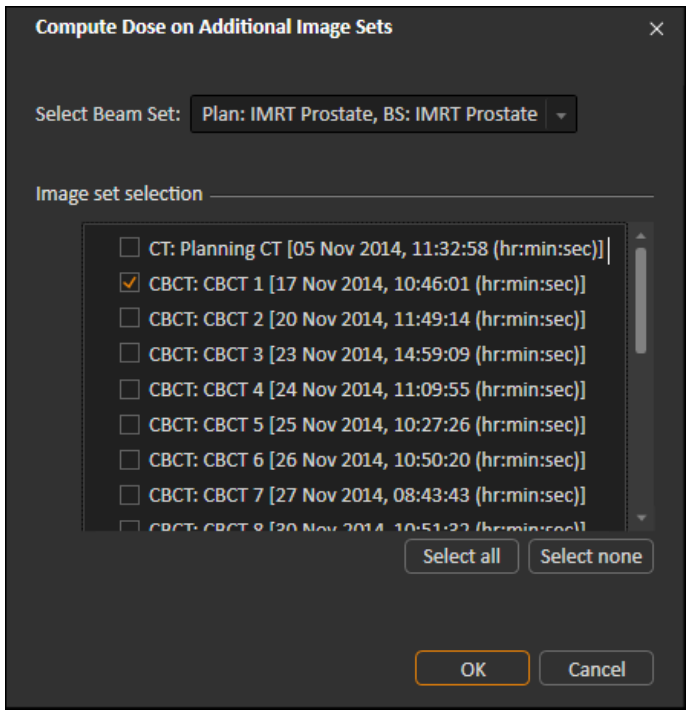

Compute Dose on Additional Image Sets
Select Beam Set:
Plan: IMRT Prostate, BS: IMRT Prostate
Image set selection
CT: Planning CT [05 Nov 2014, 11:32:58 (hr:min:sec)]
CBCT: CBCT 1 [17 Nov 2014, 10:46:01 (hr:min:sec)]
CBCT: CBCT 2 [20 Nov 2014, 11:49:14 (hr:min:sec)]
CBCT: CBCT 3 [23 Nov 2014, 14:59:09 (hr:min:sec)]
CBCT: CBCT 4 [24 Nov 2014, 11:09:55 (hr:min:sec)]
CBCT: CBCT 5 [25 Nov 2014, 10:27:26 (hr:min:sec)]
CBCT: CBCT 6 [26 Nov 2014, 10:50:20 (hr:min:sec)]
CBCT: CBCT 7 [27 Nov 2014, 08:43:43 (hr:min:sec)]
Select all
Select none
OK
Cancel

Figure 404. The Compute dose on additional image sets dialog.

2. Select a beam set to compute dose for, in the **Select Beam Set** drop-down list.
3. In the **Image set selection** list, select the image set(s) to compute dose on.
4. Click **OK**. This starts the dose computation.

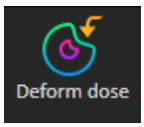
The dose computation will use the same dose grid as the one used for the planning image set. The new doses become available in the list of doses after calculation.

8.1.9 Deform dose

Dose deformation in RayStation is always performed in the direction from the target image set to the reference image set. Therefore, in order to deform dose computed on image set B to image set A, a deformable registration with A as reference image set and B as target image set must have been created. The dose deformation is performed through an interpolation procedure. Given a point in the reference image set, the displacement field and the rigid registration is applied in order to find the corresponding point in the target image set. The dose on the target image set is then tri-linearly interpolated and mapped back to the reference image set. If any of the doses selected for deformation is not fully covered by the deformation grid, the grid will be automatically expanded. The expansion will be smoothly extended from the boundary and finally padded by zero deformation vectors to cover the dose.

To calculate the deformed dose:

1. Click the **Deform dose** button.



This opens the Deform dose dialog.

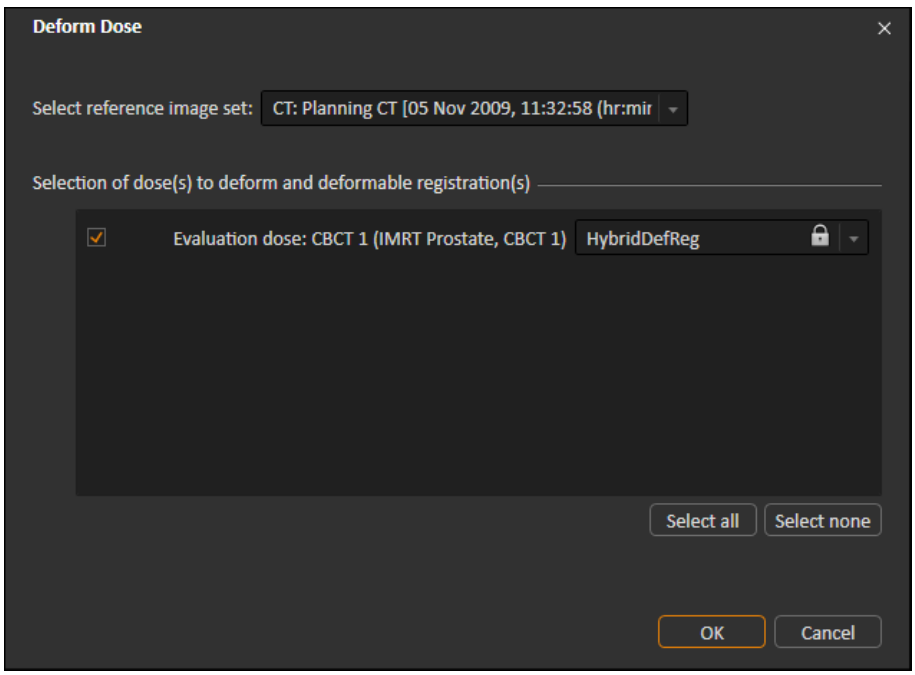


Figure 405. The Deform dose dialog.

Note: *For carbon ions: In the dialog, it is stated if the dose is an RBE dose or a physical ion dose.*

2. Select **Reference image set**.
3. Select a dose and a deformable registration from the **Selection of dose(s) to deform and deformable registration(s)** list by checking the corresponding checkbox.
4. Click **OK**.

The new doses become available in the list of doses after calculation.

8.1.10 Define or modify prescription

For instructions on how to to define or modify a dose prescription, see *section 6.1.12 Define or modify prescription on page 343*.

8.1.11 Export DVH curves to ASCII file

The DVH data can be exported to a text file.

Click the **Export DVH curves** button in the toolbar. In the Save as dialog, select a directory, type a name for the file, and click **OK**.

The following parameters are exported; PatientName, PatientId. For each displayed dose, Dosename and for each ROI in the patient, ROI name and the two vectors specifying dose level (in cGy) and relative volume (in %). An example of the exported data is displayed below:

#PatientName:Patient
#PatientId:20010101
#Dosename:Plan dose1
#RoiName:GTV
0.000 100.000
…
#Dosename:Plan dose2
#RoiName:GTV
0.000 100.000
…

Carbon ions

For carbon ions, there may now be additional information written to the file. The first two lines are as before:

#PatientName:Vx1mm_non-human_1
#PatientId:Vx1mm

For each displayed dose, in case it is of RBE type, an example of the new output is like this:

#Dosename:Plan dose (RBE): dose1
#RBE model:LEM-I Original, Classic, 1000 repetitions
#RoiName:GTV
#Roi volume fraction outside grid: 0%
#Dose unit: cGy (RBE)
0.000 100.000
…

The additional information is the new line "RBE model" and the suffix (RBE) added to the dose unit. For physical ion doses the output looks like before.

8.1.12 Export line doses

Any added line doses can be exported to a csv file.

To export line doses:

1. Click the **Export line doses** button in the toolbar.

2. In the Save As dialog that opens, select a directory, type a name for the file, and click Save.

For more information about the file format, see *Appendix G Line dose export*.

8.1.13 Update ROI voxel volumes

When a new ROI is created, or an existing ROI has been edited after dose computation, it will be visible in the **Dose statistics** list and the **Clinical goals** list, but the corresponding dose fields will be empty. To get the dose updated for the new ROI, click the update symbol next to "**Dose statistics missing**" (visible when applicable in e.g., the **DVH** tab and the **Dose Statistics** tab).

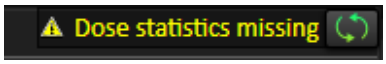


Figure 406. "**Dose statistics missing**" followed by an update symbol will be visible when applicable in for example the **DVH** tab and the **Dose Statistics** tab.

Note: *The dose is invalidated for all beams if editing the external ROI or an ROI with a density assigned.*

8.1.14 Biological evaluation

It is possible to compare treatment plans biologically in the Plan Evaluation module by using biological clinical goals.

A license for biological evaluation is required.

Note: *Biological evaluation is not supported for carbon ions.*

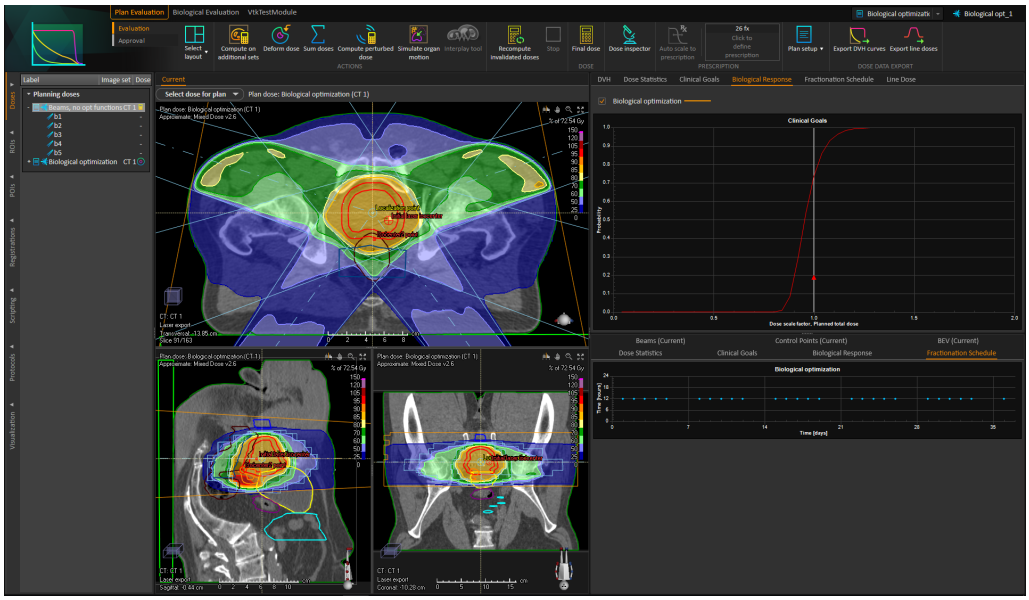


Figure 407. Biological evaluation of a single dose in the Plan Evaluation module.

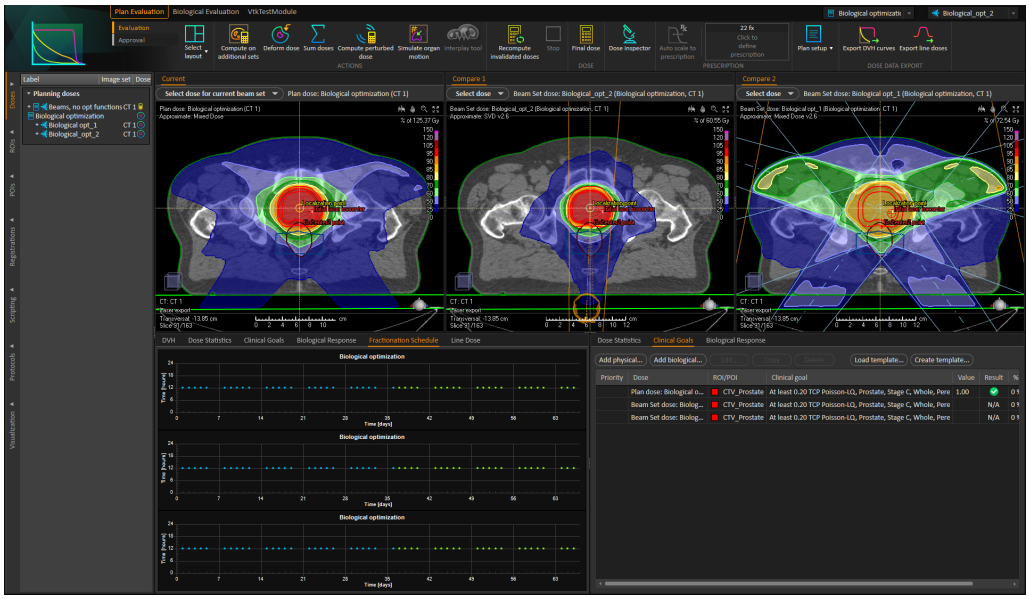


Figure 408. Biological evaluation of three doses in the Plan Evaluation module.

Biological clinical goals

To add a biological clinical goal:

1. Click the **Clinical goals** tab.
2. Click the **Add biological…** button. This opens the **Add biological clinical goal** dialog.

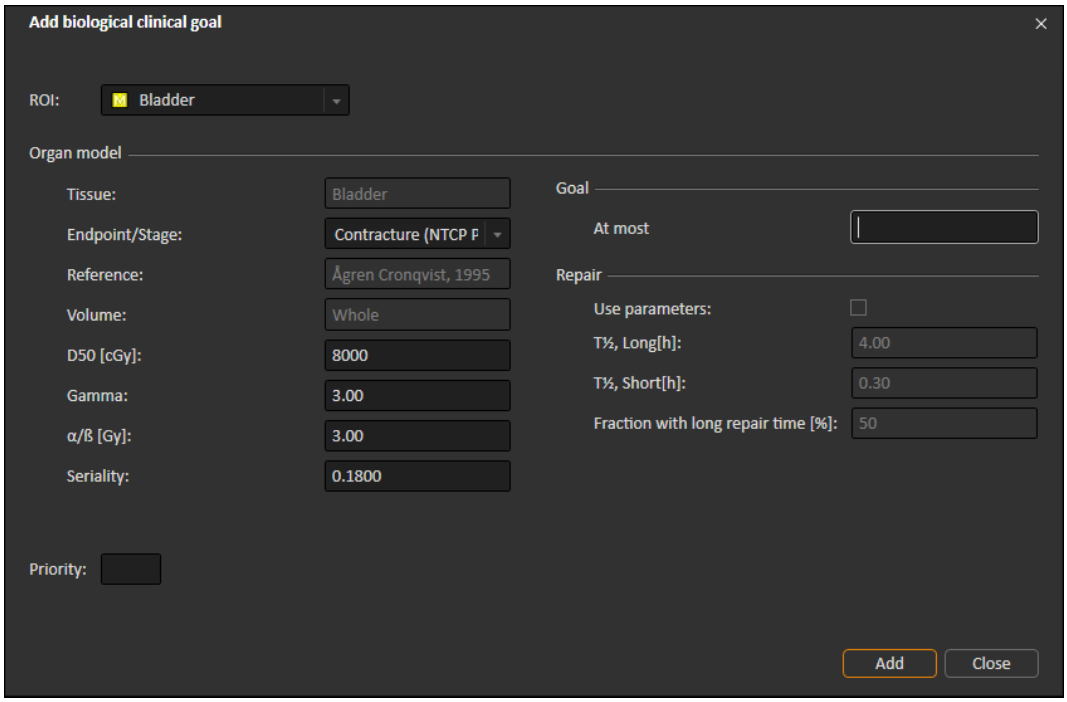


Figure 409. The **Add biological clinical goal** dialog.

3. Select the desired **ROI** from drop-down list.

   Adding a biological evaluation function for an ROI with organ type OAR will automatically result in a NTCP function while adding one for a target structure will result in a TCP function.

   Note: *Make sure that the correct organ type and tissue type are defined in the ROI Properties dialog, see section 3.4.1 The ROI list on page 54.*

4. Select **Endpoint/stage** (using the drop-down menu) if more than one endpoints/stages exists.

   Editable parameter values from the model parameter database are automatically added for the selected model. If any of the model parameters (D50, Gamma, etc.) are modified by the user, the reference will be set to **User defined**.

   WARNING!

   Biological model parameters. The biological model parameters are only valid if the correct reference volume is outlined when creating the ROI. (98329)

5. Enter the NTCP or TCP **Goal** that the ROI should receive **At most** or **At least**.

6. Optionally, enable a repair model by checking the **Use Parameters** checkbox under **Repair**. Edit the parameters as desired.

   Note: *When using a repair model, make sure that the fractionation schedule is correct because the repair model depends on the recovery time between fractions.*

7. Optionally, enable a repopulation model (only possible for TCP functions) by clicking the **Use Parameters** checkbox under **Repopulation**. Edit the parameters as desired.

   Note: *When using a repopulation model, make sure that the total treatment time is correct because the repopulation model depends on the time of delivery of the last fraction.*

8. Click **Add** to add the clinical goal to the list.

Refer to *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual* for information about the models and their parameters.

Clinical goals are described in detail in *section 3.7.3 Clinical goals on page 81*.

Note: *Selecting a repair model does not set the Reference to User defined since it does not modify the underlying model, whereas selecting a repopulation model does.*

Note: *If neither repair nor repopulation are used the model is independent of time of delivery, but it depends of the dose and the number of fractions. In this case, moving fractions in the fractionation schedule will not change the response value.*

Biological Response

The **Biological Response** graph displays the biological response as a function of scaled total planned dose. If multiple beam sets are used, all beam sets are scaled. In case of an adaptive plan, the dose of the delivered fractions is not scaled.

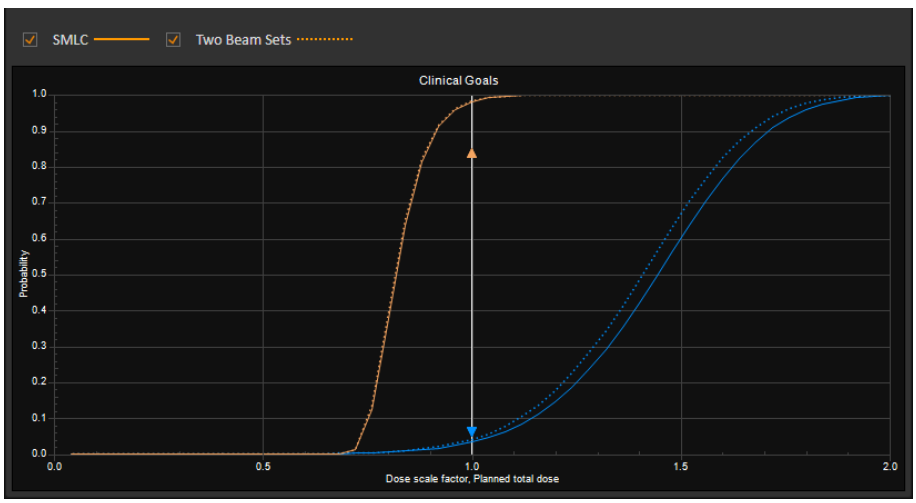


Figure 410. The Biological Response graph.

To avoid a cluttered response graph, deselect less important ROIs from the ROI list. The deselected ROIs will be removed from the response graph but will still be visible in the clinical goals list.

Note: *The arrows in the graph cannot be edited.*

Note: *The Clinical Goals tab is present in several modules, but the biological response graph of the clinical goals is only displayed in the Plan Evaluation module.*

Fractionation Schedule

A fractionation schedule is automatically created from a five fractions per week default pattern when adding a beam set. The **Fractionation Schedule** tab displays the (nominal) fractionation schedule of the loaded treatment plan. If more than one treatment plan is selected for comparison, fractionation schedules for each plan will be displayed. The fractionation schedule in combination with the dose distributions delivered for each fraction are needed when analyzing the result of a biological evaluation, especially if time dependent models to account for repair and accelerated repopulation are used.

Note: *The biological models depends both on the dose distribution and number of fractions (or dose per fraction). Repair and repopulation models depends on the time of delivery of the fractions and in this case it is important to use the correct fractionation schedule when evaluating the biological functions.*

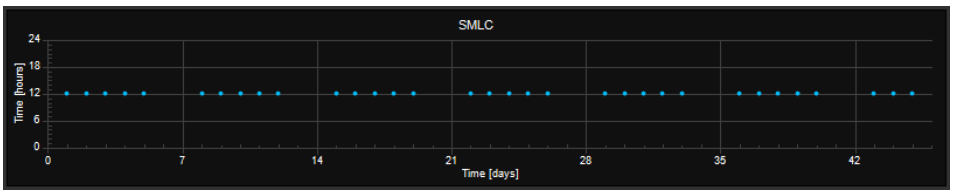


Figure 411. The Fractionation schedule tab.

The nominal fractionation schedule of the active plan can be edited by drag and drop, but the schedules of the comparative plans are locked. Click on a fraction and drag and drop it to a desired position in the fractionation schedule.

The fractionation schedule of the active plan in the Plan Evaluation module is similar to the nominal fractionation schedule in the Biological Evaluation module. See *section 8.2.3 The fractionation schedule on page 763* for detailed information.

8.1.15 Plan approval

The final treatment plan, i.e., the plan that is intended to be used for actual patient treatment, must be approved in RayStation. Before approval, a final accurate dose shall be computed, and the plan shall be properly evaluated.

If the plan contains multiple beam sets, each beam set has to be approved separately. For instructions, see *Approve a plan with multiple beam sets on page 752*.

For carbon ions there are some prerequisites before the plan can be approved for clinical use. These are described in *Plan approval prerequisites on page 640*.

When a plan is approved, it becomes read-only and the structure set will be locked. The approved status will be set in the DICOM file at export. The only way to unlock the structure set is to unapprove the plan or to delete all approved plans referring to that specific structure set.

Precautions

WARNING!

System checks at approval. Be aware that the following checks before approval are only performed for planning doses:

- Beam entry validation.
- A Bolus ROI geometry exists.
- A Support ROI geometry exists.
- A Fixation ROI geometry exists.
- The Dose grid resolution is smaller than 5 mm in all directions.

For evaluation doses, the user is responsible for performing these checks.

Note that having a planning dose grid which encloses the External ROI, support ROIs, fixation ROIs and bolus ROIs does not guarantee that all relevant regions are included for dose computation on additional datasets. (26694)

The approval toolbar

The **Approval** tab displays approval information for the current plan. For approved plans the approver's name as well as the date and time of the approval are displayed.

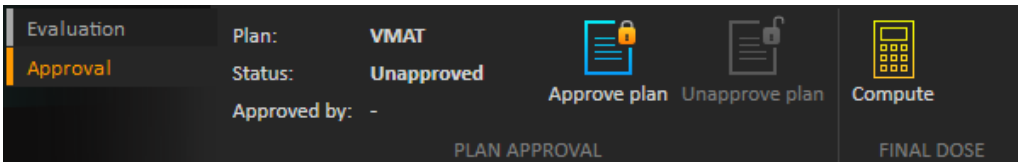
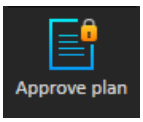


Figure 412. The Approval tab in the Plan Evaluation module.

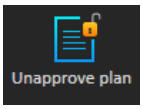
To make a final review and approve the current plan, click the **Approve plan** button to open the Approve plan workspace. It is only possible to approve a plan for which a final accurate dose computation has been done.



Note: *For electron, proton and carbon plans: The dose grid resolution must be smaller than or equal to 0.3 cm per voxel or in order to get a clinical dose. Otherwise, the plan cannot be approved.*

Note: *For carbon ions: Only the RBE dose is shown when approving a plan.*

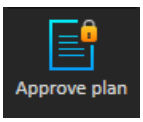
To unapprove the current plan, click the **Unapprove plan** button.



For plans containing multiple beam sets, each beam set has to be approved separately. See *Approve a plan with multiple beam sets on page 752* for more information.

The Approve plan workspace

The **Approve plan** workspace is accessed by clicking the **Approve plan** button.



The **Approve plan** workspace opens in a window on top of the main RayStation 7 window. This workspace presents an overview of the plan to be approved. To the left is the tool panel with one page for Plan information, one page for the ROI list and one page for the POI list.

Workspace itself consists of six views. There are four image data views; three of them are 2D patient views (transversal, coronal, and sagittal), and the fourth can be switched between the BEV and the

3D view. To the right are the evaluation views; DVH, dose statistics and clinical goals. For more information about the evaluation views, see *section 3.7 Common graphs, tables and tools on page 77*.

At the bottom of the view are the tabs; Beams, Control points and Beam dose specification point.

The Approve plan workspace always displays the total dose, i.e. the dose for all fractions of the planned treatment.

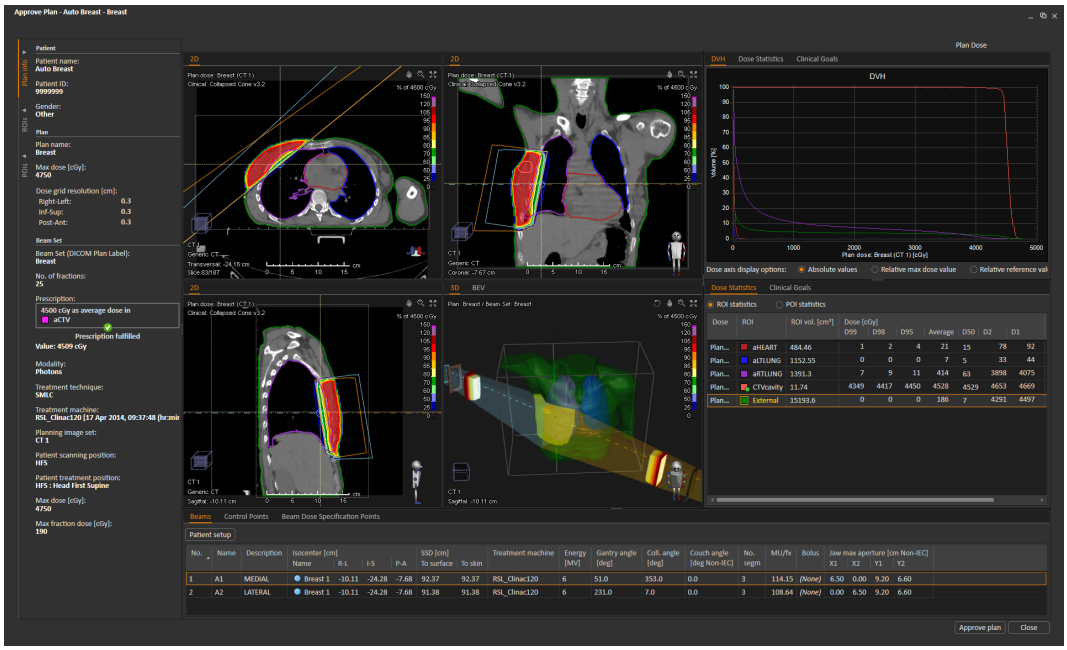
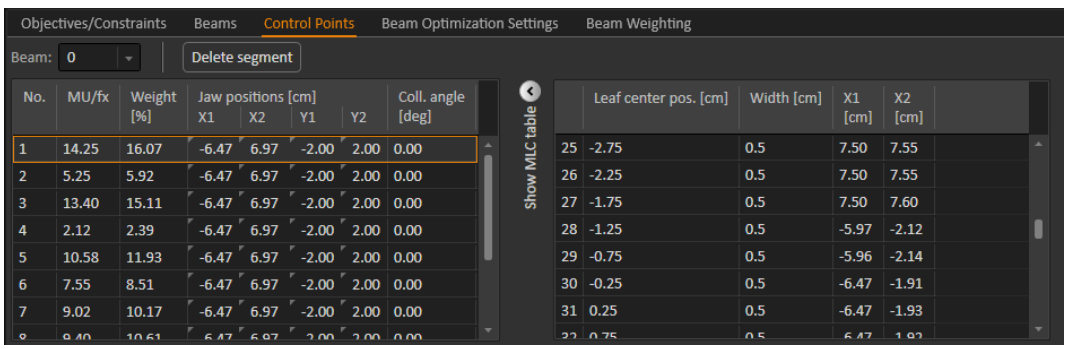


Figure 413. The Approve plan workspace.

Control points and MLC positions

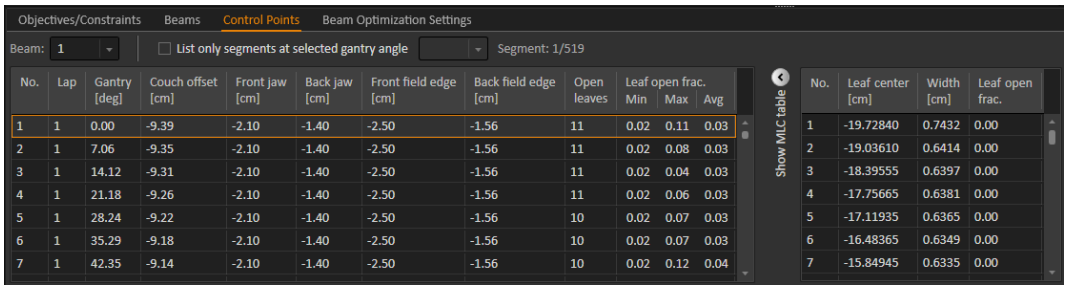
The **Control points** tab lists all segments and corresponding MLC positions for a selected beam.



No.	MU/fx	Weight [%]	Jaw positions [cm] X1	X2	Y1	Y2	Coll. angle [deg]
1	14.25	16.07	-6.47	6.97	-2.00	2.00	0.00
2	5.25	5.92	-6.47	6.97	-2.00	2.00	0.00
3	13.40	15.11	-6.47	6.97	-2.00	2.00	0.00
4	2.12	2.39	-6.47	6.97	-2.00	2.00	0.00
5	10.58	11.93	-6.47	6.97	-2.00	2.00	0.00
6	7.55	8.51	-6.47	6.97	-2.00	2.00	0.00
7	9.02	10.17	-6.47	6.97	-2.00	2.00	0.00

	Leaf center pos. [cm]	Width [cm]	X1 [cm]	X2 [cm]
25	-2.75	0.5	7.50	7.55
26	-2.25	0.5	7.50	7.55
27	-1.75	0.5	7.50	7.60
28	-1.25	0.5	-5.97	-2.12
29	-0.75	0.5	-5.96	-2.14
30	-0.25	0.5	-6.47	-1.91
31	0.25	0.5	-6.47	-1.93

Figure 414. The **Control points** tab.



No.	Lap	Gantry [deg]	Couch offset [cm]	Front jaw [cm]	Back jaw [cm]	Front field edge [cm]	Back field edge [cm]	Open leaves	Leaf open frac. Min	Max	Avg
1	1	0.00	-9.39	-2.10	-1.40	-2.50	-1.56	11	0.02	0.11	0.03
2	1	7.06	-9.35	-2.10	-1.40	-2.50	-1.56	11	0.02	0.08	0.03
3	1	14.12	-9.31	-2.10	-1.40	-2.50	-1.56	11	0.02	0.04	0.03
4	1	21.18	-9.26	-2.10	-1.40	-2.50	-1.56	11	0.02	0.06	0.03
5	1	28.24	-9.22	-2.10	-1.40	-2.50	-1.56	10	0.02	0.07	0.03
6	1	35.29	-9.18	-2.10	-1.40	-2.50	-1.56	10	0.02	0.07	0.03
7	1	42.35	-9.14	-2.10	-1.40	-2.50	-1.56	10	0.02	0.12	0.04

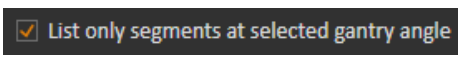
No.	Leaf center [cm]	Width [cm]	Leaf open frac.
1	-19.72840	0.7432	0.00
2	-19.03610	0.6414	0.00
3	-18.39555	0.6397	0.00
4	-17.75665	0.6381	0.00
5	-17.11935	0.6365	0.00
6	-16.48365	0.6349	0.00
7	-15.84945	0.6335	0.00

Figure 415. The **Control points** tab for TomoHelical.

Note: *Front and back jaw positions are stored in the database and sent to the machine. For usability, the front and back field edges are also presented. They represent the edges of the full width at half maximum (FWHM) of the resulting dose on the isocenter plane. The conversion between jaw positions and field edges are done using the conversion table stored in the machine model.*

The field edges are also used for jaw presentation in the graphical patient views (e.g., BEV).

For TomoHelical plans it is possible to select to only list the segments that are located at a certain gantry angle by checking the corresponding checkbox.



The approve plan procedure

To approve the plan in the Approve plan workspace:

1. Click the **Approve plan** button in the lower right corner. This opens the authentication dialog.

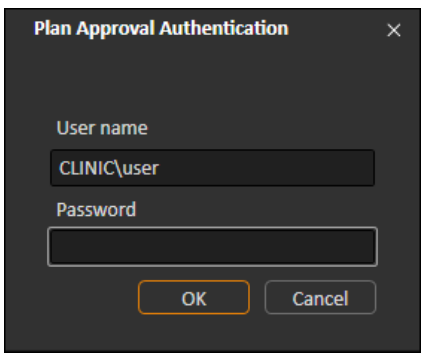


Figure 416. Authentication dialog.

2. Type **User name** (the Windows user name) and **Password**.
3. Click **OK**.

When the plan has been approved it is no longer editable and the referenced ROIs will become read-only.

Approve a plan with multiple beam sets

When approving a plan with multiple beam sets, each beam set has to be approved separately (or if one of them is imported, lock it by setting it as approved to be used for background dose planning as described in *section 6.1.20 Multiple beam set planning on page 372*).

In the Approval tool panel, select to approve one of the beam sets and its separate beam set dose.

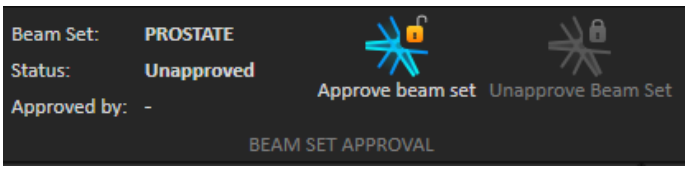
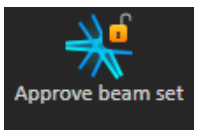


Figure 417. The Beam set approval toolbar.

1. Click the **Approve beam set** button.



This opens the Approve beam set view.

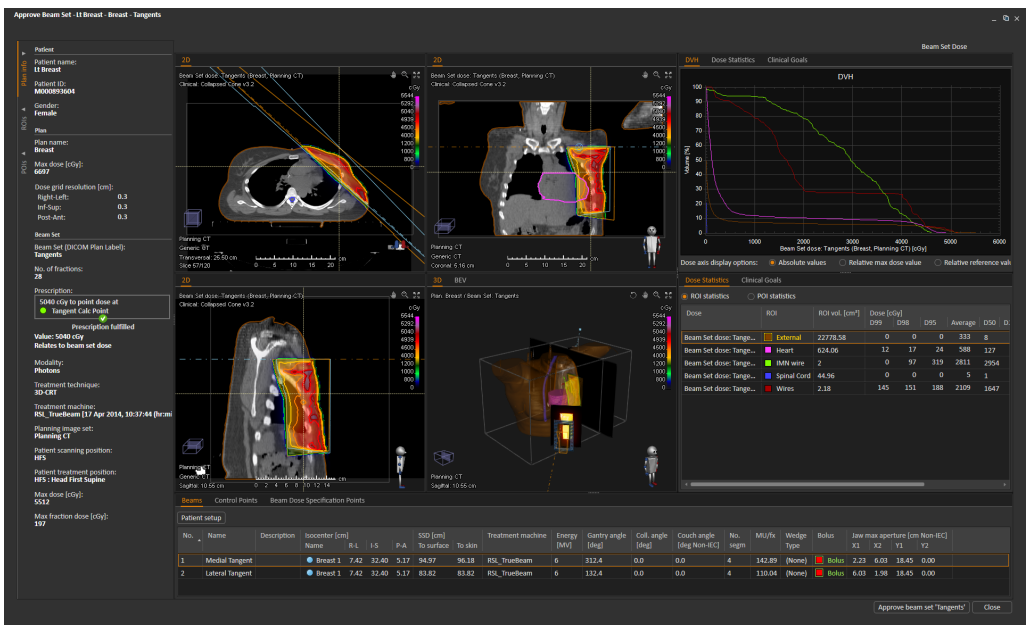


Figure 418. The Approve beam set workspace.

2. Review the beam set information and click **Approve beam set '…'**. This opens the authentication dialog.

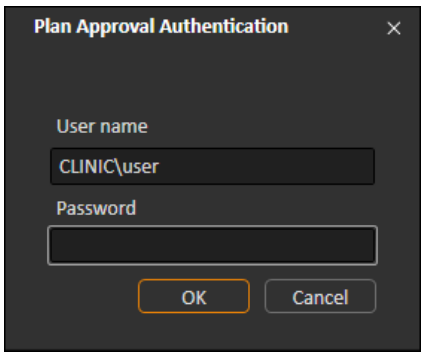
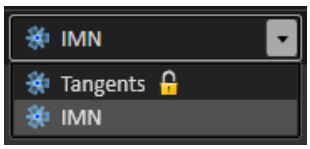
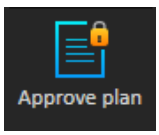


Figure 419. Authentication dialog.

3. Type **User name** and **Password**.
4. Click **OK**. The current beam set will be approved and a padlock will be displayed next to the approved beam set in the list.
5. Select the other unapproved beam set from the list at the upper right corner.



6. Click the **Approve plan** button.



This opens the Plan approval view.

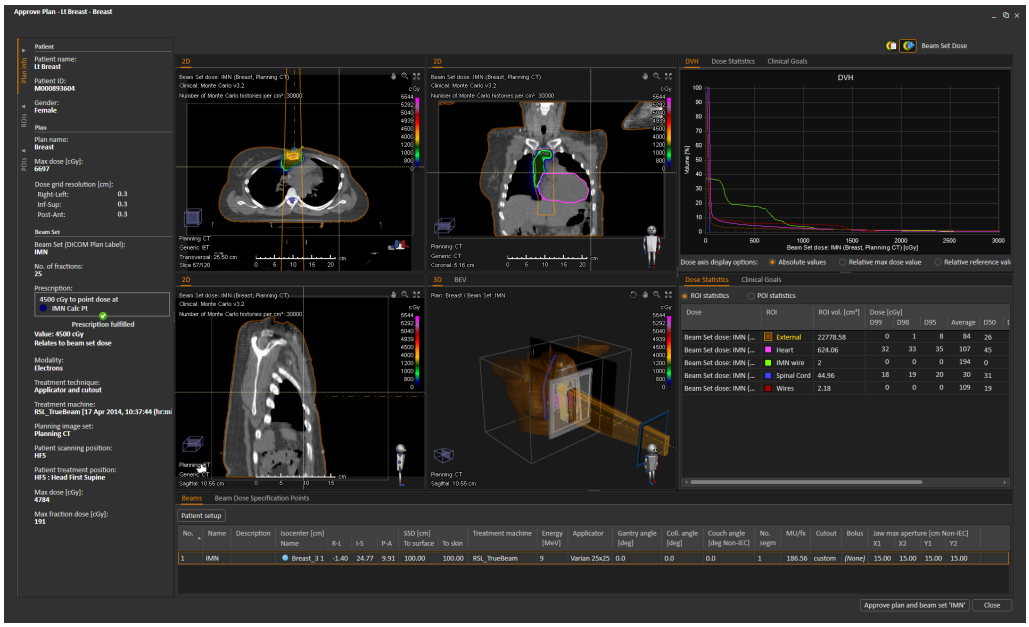


Figure 420. The approve plan dialog.

7. Select to display **Plan Dose** or **Beam Set dose** by clicking the corresponding button.
8. Review the plan information and click **Approve plan and beam set '…'**. This opens the authentication dialog.

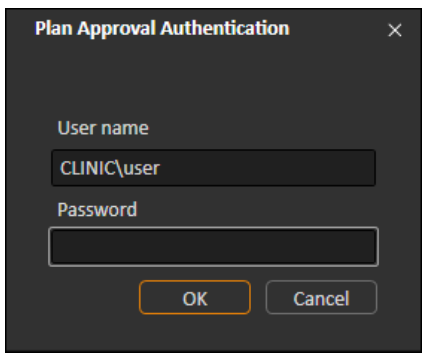


Figure 421. Authentication dialog.

Make sure to review both the separate beam set dose and the total plan dose.

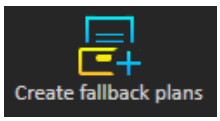
9. Type **User name** and **Password**.
10. Click **OK**. The current beam set and the whole plan will be approved. A padlock will be displayed next to the approved beam set in the list.

8.1.16 Create fallback plans

After plan approval, the user can create fallback plans using alternative machines and treatment techniques. It is recommended to create the fallback plans prior to the patient's treatment start so that they are available at any time in case of machine unavailability. For more information about fallback planning, see *chapter 10 Automated Planning*.

To create a fallback plan:

1. Click the **Create fallback plans** button.

   This opens the **Create fallback plans** dialog.

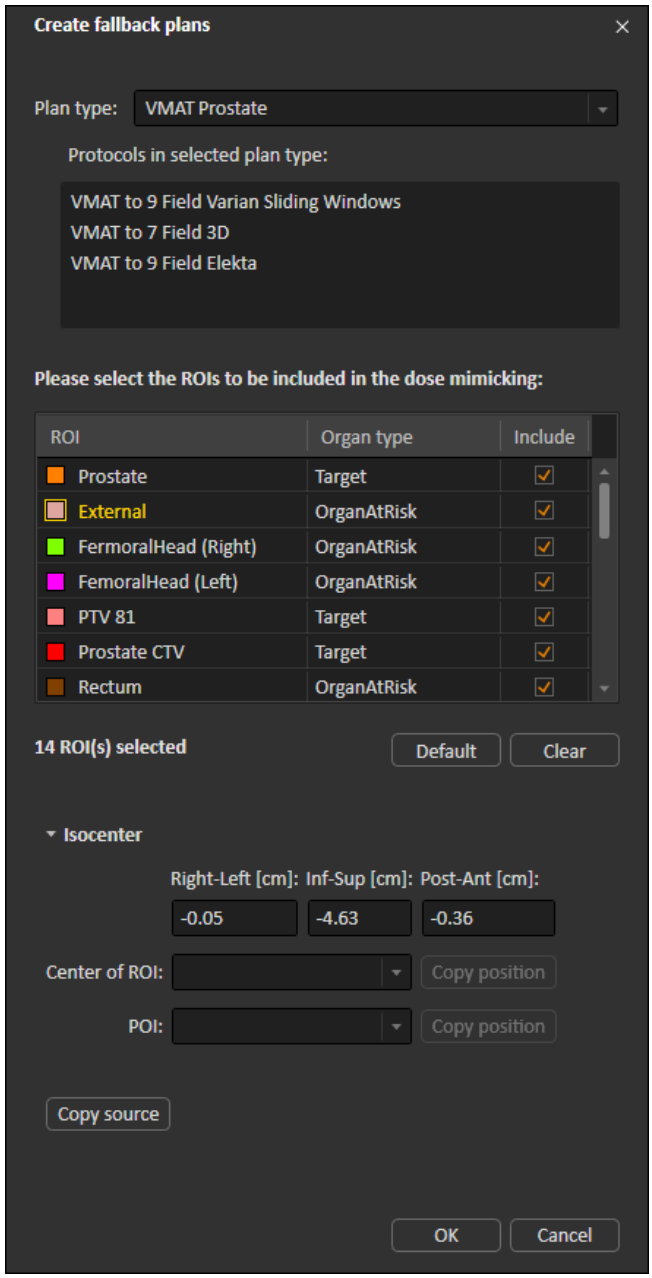


Figure 422. The **Create fallback plans** dialog.

2. Select the applicable **Plan type** for the patient. (In order for the plan types and corresponding protocols to be available in the list they have to be created in the Fallback Protocol Management

module. For instructions on how to create plan types, see *Step 1. Create a fallback plan type on page 858*.)

All existing protocols for the selected plan type will appear in the dialog.

3. Select or deselect relevant ROIs for the dose mimicking. By default, the ROIs that are used as optimization functions will be selected.
4. If desired, define an **Isocenter** shift. The default is the isocenter of the approved plan.
    - If the isocenter shall be in the center of an ROI, select an ROI from the **Center of ROI** drop-down list.
    - If the isocenter shall be in the same position as a POI position, select a **POI** from the POI drop-down list.
    - To reset the isocenter to the default value, click the **Copy source** button.
5. If the treatment machine has multiple energies, a dialog will prompt the user to select **Energy** for each protocol in the fallback plan.
6. Click **OK**.

    For each protocol of the selected plan type, the system now creates a fallback plan according to the protocol and then performs the dose mimicking to make the dose of each fallback plan mimic the dose of the original plan.

    The created fallback plans will be available in the **Fallback plans** list in the Fallback Planning module.

8.2 THE BIOLOGICAL EVALUATION MODULE

The Biological Evaluation module includes functionality for biological plan evaluation using radiobiological models. Biological evaluation of different fractionation schedules for a single treatment plan will be referred to as "**fractionation assessment**". Fractionation assessment may be used to investigate:

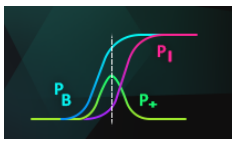
- the effect of a gap in the treatment
- how to compensate for a gap in the treatment
- the effect of changing the time of delivery of individual fractions

The RayStation 7 system presents, stores and outputs information to the user concerning the radiobiological effects of the plan evaluated according to user-specified biological models on multiple fractionation schedules.

This section describes biological evaluation and explains the individual workspace components and their possible commands. It describes a typical biological evaluation workflow for a fractionation assessment use scenario. Each workflow step has a reference to a sub-section in this section (or manual) where more information about how to perform the individual step is found.

Note: *Different plans can be compared biologically in the Plan Evaluation module using biological clinical goals.*

Note: *Biological evaluation is not supported for carbon ions.*



In this section

This section contains the following sub-sections:

8.2.1	Using biological evaluation	p. 761
8.2.2	The Biological Evaluation module user interface	p. 762
8.2.3	The fractionation schedule	p. 763
8.2.4	The response functions	p. 767
8.2.5	The evaluation views	p. 770
8.2.6	Biological evaluation workflow	p. 771

Precautions

WARNING!

Always evaluate physical dose. Biological functions can be used as auxiliary tools to evaluate a treatment plan, but the physical dose distribution must always be evaluated. (97716)

WARNING!

Biological model parameters. The biological model parameters are only valid if the correct reference volume is outlined when creating the ROI. (98329)

WARNING!

Factory default biological models. The database of factory default biological model parameters comes from published clinical and pre-clinical studies. Still, this is an evolving field of science and more recent studies may provide evidence for other biological model parameters that are more suitable for clinical use.

The user shall always review the literature and base their usage of biological model parameters on the current state of knowledge in the field and clinic-specific treatment techniques. (96234)

WARNING!

Biological models. When using biological models, carefully review the selection of model parameters before clinical use. (96233)

WARNING!

Biological evaluation and optimization for protons. The underlying biological model is based on photon survival curves. The proton dose is not scaled when performing biological evaluation and biological optimization for protons. When using biological evaluation and optimization for protons, the machine must include an RBE factor in the absolute dosimetry. (103740)

The Biological Model Library Manager

The Biological Evaluation module uses a library of biological model parameters which comes with default parameters upon installation (factory defaults). These may be edited and amended, using the RayBiology application. For more information, see *Appendix E RayBiology*.

Radiobiological models

The radiobiological models included in the Biological Evaluation module are described in *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual*.

Prerequisites

Biological Evaluation requires that a patient and plan is loaded and active in RayStation 7, that a patient record is stored in the system and contains one or more calculated treatment plans. This plan will be referred to as the "nominal" plan.

8.2.1 Using biological evaluation

Radiobiology is a complement to evaluating a treatment plan by the dose distribution and the dose volume histograms (DVHs). The estimated probabilities of the clinical outcome are evaluated in terms of TCP for the targets and NTCP for the organs at risk. These biological indices can be used to compare rival dose distributions as well as rival fractionation schedules. Given a dose distribution the radiobiological tools can be used to manually modify the fractionation schedule so that a better fractionation schedule is obtained with respect to the biological models and the individual patient geometry. It must, however, be kept in mind that the biological models of today have a limited predictive power, and that the physical dose distributions must also be inspected and found acceptable in conventional terms before approving a plan for delivery.

Note: *It is possible to define a dose grid that does not cover all structures. If such a dose grid has been defined, the DVHs that are drawn will be incorrect, as will the predictions of the biological models.*

8.2.2 The Biological Evaluation module user interface

Workspace

The biological evaluation workspace consists of several views and tables.

The **Fractionation Schedule** tab is divided into the Nominal fractionation schedule in which the fractionation schedule of the loaded plan is displayed and the Alternative fractionation schedule where an alternative fractionation schedule may be defined for the loaded treatment plan.

The **DVH** tab presents the dose volume histograms of the different ROIs, the **Biological Response** tab presents the biological response as a function of scaled beam set dose of the ROIs for which a TCP or NTCP function has been defined and the **Biological Progress** tab presents the biological response as a function of time of delivery.

The **Evaluation Functions** area allows for adding, editing, deleting, visualization and calculation of response functions.

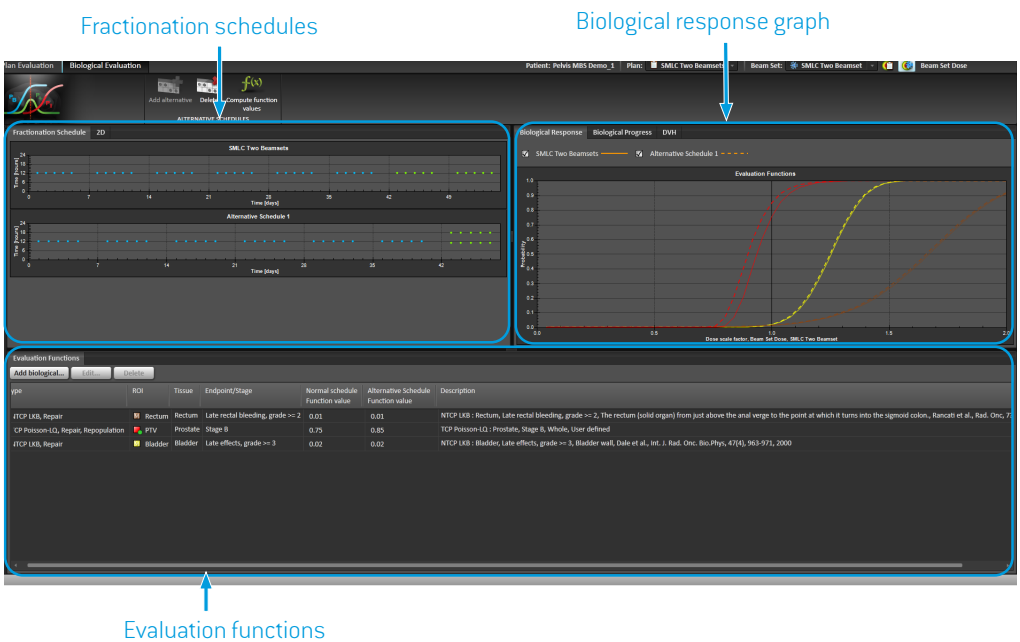


Figure 423. The Biological evaluation workspace.

8.2.3 The fractionation schedule

The **Fractionation Schedule** tab is divided into the Nominal fractionation schedule in which the fractionation schedule of the loaded plan is displayed and the Alternative fractionation schedule where an alternative fractionation schedule may be defined for the loaded treatment plan. A five fractions per week default pattern is automatically applied when a beam set is added and builds the nominal schedule displayed in Fractionation Schedule view. If multiple beam sets are used, they are by default considered to be delivered in sequence (like boost plans). The default schedule can be modified from the Fractionation Schedule view. In the Fractionation Schedule view, the time of delivery of each fraction is displayed with a symbol. Planned fractions are displayed as a small circle, and the delivered fractions as a small square. If several fractions are delivered on exactly the same time a larger circle or square is displayed around the normal symbol. Each beam set has a unique color and the delivered fractions are always red. When hoovering over a fraction the tooltip information displays fraction number, beam set name, planned or delivered, modality and time of delivery.

Note: *The biological models depends both on the dose distribution and number of fractions (or dose per fraction). Repair and repopulation models depends on the time of delivery of the fractions and in this case it is important to use the correct fractionation schedule when evaluating the biological functions.*

The weekly default pattern

When a beam set is added in the Plan Design module a 5 fractions per week default pattern is automatically created. Modifying the number of fractions will always be made with respect to this underlying weekly default pattern. If two beam sets are used the second beam set is pushed back according to its pattern if fractions are added to the first beam set, as long as its pattern has not been broken by moving a fraction. Once a fraction has been moved the fractions before the last moved fraction are considered to be without a weekly pattern, whereas the fractions after the last moved fraction are still generated from the weekly pattern.

Example: If there are two beam sets and no fraction has been moved in beam set 2, moving a fraction from beam set 1 to the middle of beam set 2 will push back all fractions in beam set 2 according to the weekly pattern so that the delivery of beam set 2 starts after the moved fraction of beam set 1. On the other hand, if a fraction has been moved in beam set 2, the time of the fractions of beam set 2 are considered to be fixed in time and the fractions are no longer pushed according to the weekly pattern if moving fractions in beam set 1.

Note: *Once a fraction in the nominal pattern is moved it is not possible to regenerate the default pattern. If the undo information is lost, the only way to recreate the original fractionation schedule is to move the fractions manually, but the weekly default pattern is lost for the moved fractions.*

Note: *The nominal schedule is the fractionation schedule of the loaded plan. Any changes to the nominal schedule is transferred to the other modules in RayStation 7.*

Note: *For the nominal schedule it is not possible to reorder the beam sets in the fractionation schedule.*

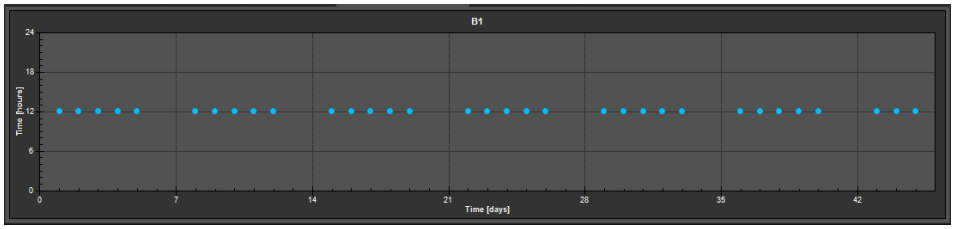


Figure 424. The fractionation schedule for a plan with one beam set and no delivered fractions as generated from the default schedule. (The y-axis displays the time of day in hours and the x-axis displays the treatment day.)

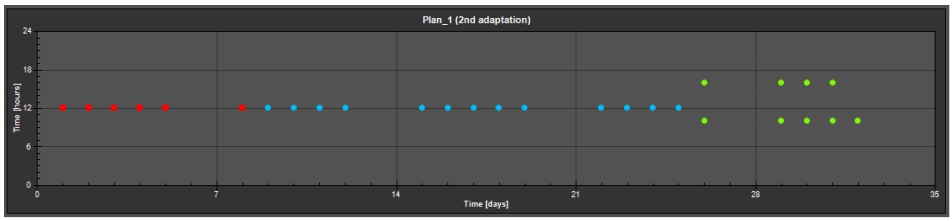


Figure 425. The fractionation schedule for an adpative plan with two beam sets and six delivered fractions. The last beam set is delivered twice a day at 10:00 and 16:00. Each beam set has a unique color. Delivered fractions are always colored red and shaped like squares.

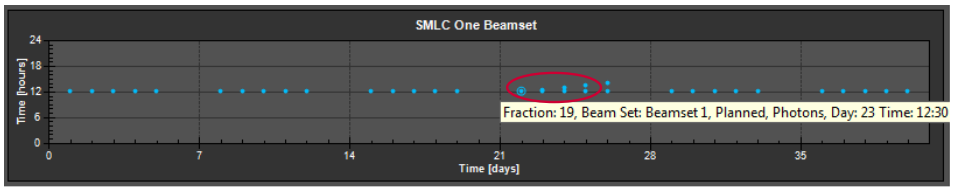


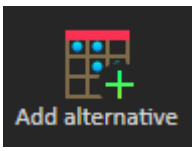
Figure 426. If fractions are delivered on exactly the same time a larger circle around the original circle is shown (day 22 in this example). Note that the larger circle is not displayed when fractions are delivered close together, but not on exactly the same time (day 23 in this example). The tooltip when hovering over a fraction symbol displays the fraction number, and it reveals if fractions are delivered close together or how many fractions are delivered on the same occasion. It is possible zoom in the fractionation schedule view.

Note: *For plans created with earlier RayStation versions, there is no default fractionation schedule. All fractions are assumed to be delivered at the same time (zero). This means that the calculated response will not be correct if repair or repopulation models are used. TCP and NTCP calculations without repair and repopulation do not depend on time and therefore these calculations are still correct.*

Adding an alternative fractionation schedule

It is possible to add an alternative fractionation schedule. The alternative fractionation schedule will be applied to the active plan (plan loaded and active in RayStation 7) only. Any modifications to an alternative schedule is isolated to the Biological Evaluation module and does not affect the fractionation schedule of the loaded treatment plan.

To add an alternative fractionation schedule, click the **Add alternative** button in the Alternative schedules toolbar. The evaluation of a biological function with respect to an alternative schedule, is based on the same dose per fraction per beam set as the nominal schedule. If the number of fractions are different in the nominal and the alternative schedules, the total dose differs and the biological function values of the alternative schedule are based on another total dose than the values of the nominal schedule. Note that only the total dose of the nominal schedule is displayed in the CT and DVH views.



The alternative schedule will be a copy of the nominal fractionation schedule. To edit the alternative fractionation schedule, see *Editing an existing fractionation schedule on page 765*.

Editing an existing fractionation schedule

It is possible to move a fraction in the fractionation schedule by clicking on a fraction and drag and drop it to desired position.

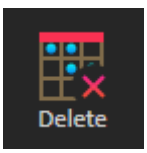
Note: *It is not possible to move a delivered fraction or move a planned fraction that is earlier than the last delivered fraction.*

Note: *In case of multiple beam sets, it is not possible to (applicable to the nominal schedule only):*

- *move a fraction from the last beam set to a time earlier than the last fraction in the previous beam set, the beam sets are always delivered in the planned sequence.*
- *move a fraction from the first beam set to a time later than the first fraction in the following beam set, the beam sets are always delivered in the planned sequence.*

Deleting an existing alternative fractionation schedule

To delete an existing alternative fractionation schedule, click the **Delete** button.



Note: *It is not possible to delete the nominal fractionation schedule.*

8.2.4 The response functions

The **Evaluation Functions** area allows for adding, editing, visualization and calculation of response functions. Added response functions and their parameters and function values are displayed in the **Evaluation Functions** list. In the description column, the model type, tissue name, endpoint/stage, reference and reference volume are displayed.

WARNING!

Biological model parameters. The biological model parameters are only valid if the correct reference volume is outlined when creating the ROI. (98329)

Note: *If any of the model parameters (D50, Gamma, etc.)are modifed by the user, the reference will be set to User defined. Otherwise, the reference is the origin of the model, i.e. the paper where the parameters were published or the reference information entered when adding the model in RayBiology.*

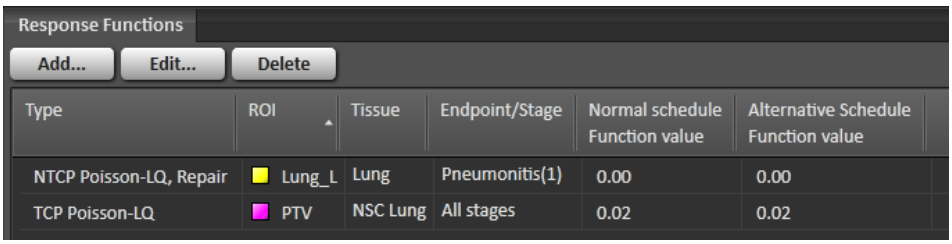


Figure 427. The Evaluation Functions tab.

More information about adding, editing and deleting biological evaluation function is found in the next sections. It is not possible to add, edit or delete evaluation functions to an approved plan.

Adding a biological evaluation function

To add a biological evaluation function:

1. Click the **Add...** button, located to the left in the **Evaluation Functions** tab.

   This opens the Add Response Function dialog.

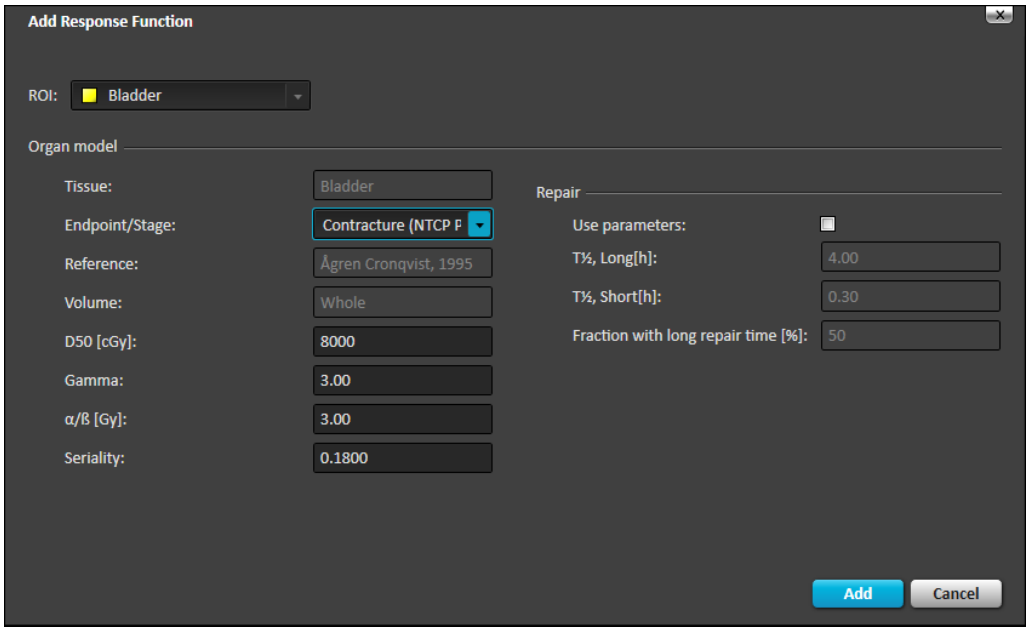


Figure 428. The Add Response Function dialog.

2. Select the desired **ROI** (using the drop-down menu) for which you want to add a biological evaluation function.

   Adding a biological evaluation function for an OAR will automatically result in a NTCP function while adding one for a target structure will result in a TCP function.

   Note: *Make sure that the correct organ type and tissue type are defined in the ROI Properties dialog, see section 3.4.1 The ROI list on page 54.*

3. Select **Endpoint/stage** (using drop down menu) if more than one endpoints/stages exists.

   Editable default parameter values are automatically added for the selected model. If any of the model parameters (D50, Gamma, etc.) are modified by the user, the reference will be set to **User defined**.

4. Optionally, enable a Repair model by checking the **Use Parameters** checkbox under **Repair**. Edit the parameters as desired.

   Note: *When using a repair model, make sure that the fractionation schedule is correct because the repair model depends on the recovery time between fractions.*

5. Optionally, enable a repopulation model (only possible for TCP functions) by clicking the **Use Parameters** checkbox under **Repopulation**. Edit the parameters as desired.

   Note: *When using a repopulation model, make sure that the total treatment time is correct because the repopulation model depends on the time of delivery of the last fraction.*

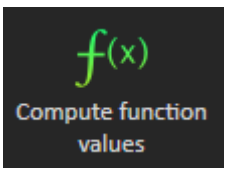
Refer to *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual* for information about the models and their parameters.

Note: *Selecting a repair model does not set the Reference to User defined since it does not modify the underlying model, whereas selecting a repopulation model does.*

Note: *If neither repair nor repopulation are used the model is independent of time of delivery, but it depends of the dose and the number of fractions. In this case, moving fractions in the fractionation schedule will not change the response value.*

Calculating the biological response

To calculate the biological response, click the **Compute function values** button.



The function values will be displayed in the **Evaluation Functions** table and plotted in the **Biological response** graph and the **Biological Progress** graph.

Editing biological evaluation functions parameters

Any response function may be edited after it has been added.

To edit an existing biological evaluation function parameter:

1. Select the function that you want to edit in the **Evaluation Functions** table.
2. Click the **Edit...** button or double-click on the desired response function directly. This opens the Edit Response Function dialog.
3. Edit the parameter values.
4. Click **OK**.

Changing the function type, biological model and/or associated ROI for an existing biological evaluation function

To change the function type, biological model and/or associated ROI, the function must be deleted and a new one added.

1. Select the function that you want to delete in the **Evaluation functions** table.
2. Click **Delete**.

For information on how to add a new biological evaluation function, refer to *Adding a biological evaluation function on page 767*.

8.2.5 The evaluation views

Note: *The dose distribution and the DVHs displayed in the Biological Evaluation module are with respect to the nominal schedule. No dose is shown for the alternative schedule. The evaluation of a biological function with respect to an alternative schedule, is based on the same dose per fraction per beam set as the nominal schedule. As long as the number of fractions are the same in the nominal and the alternative schedules the dose of the nominal schedule is identical to the dose of the alternative schedule. However, if the number of fractions is different in the nominal and the alternative schedules the total beam set doses and the total plan dose displayed are valid for the nominal schedule only.*

The 2D patient view

The 2D patient view displays the plan isodoses for a selected plan.

Refer to *section 3.6 Common views on page 71* for more information about patient views and patient view options.

Dose Volume Histogram (DVH)

The DVH view presents the cumulative dose volume histograms of the ROIs selected in the ROI List. The dose can be displayed as **absolute** or **relative [%]**. It is also possible to manually set the reference value for the relative scale. For a further description of the DVH view, see *section 3.7.1 Dose Volume Histogram (DVH) on page 78*.

Biological response graph

The **Biological Response** tab presents the biological response as a function of scaled beam set dose of the ROIs for which a TCP or NTCP function has been defined. The beam set used for scaling is displayed as an x-axis label. This beam set is the one set as active when the calculation was performed, not necessarily the current active beam set.

When opening a plan, the biological response graph will be empty until new response values are calculated.

Refer to *The Biological Response graph on page 705* for more information about biological response graph and biological response graph options.

Biological Progress graph

The **Biological Progress** tab presents the biological response as a function of time of delivery for which a TCP or NTCP function has been defined.

Refer to *Biological Progress on page 706* for more information about biological progress graph options.

8.2.6 Biological evaluation workflow

A basic fractionation assessment workflow consists of the following steps:

1. **Specify an alternative fractionation schedule** to be applied to the loaded plan (described in *Adding an alternative fractionation schedule on page 765*).
   a. Add an alternative fractionation schedule (described in *Adding an alternative fractionation schedule on page 765*).
   b. Edit an existing fractionation schedule (described in *Editing an existing fractionation schedule on page 765*).
   c. Delete an existing fractionation schedule (described in *Deleting an existing alternative fractionation schedule on page 765*).
2. **Define the biological evaluation criteria** to be applied to the active plan.
   a. Add a biological evaluation function (described in *Adding a biological evaluation function on page 767*)
3. **Calculate the biological responses** (described in *Calculating the biological response on page 769*).

   The system presents biological response and other data corresponding to the biological models chosen to evaluate the plan(s).
4. **Change/edit evaluation parameters and initiate a new calculation of biological response** (optional).
   a. Calculate the biological response (described in *Calculating the biological response on page 769*).
   b. Edit existing biological evaluation functions parameters (described in *Editing biological evaluation functions parameters on page 769*).
   c. Change the function type, biological model and/or associated ROI of an existing evaluation function (described in *Changing the function type, biological model and/or associated ROI for an existing biological evaluation function on page 769*).
5. **Evaluate the results**.
   a. Study the **Biological Response** graph to see what effect the scaling of the beam set dose would have on the response values.
   b. Study the **Biological Progress** graph to see what effect an interrupted treatment would have on the response values.

9 QA PREPARATION

The QA Preparation module is used to transfer the clinical plan to a phantom and recalculate dose. The output from the module is the QA plan and dose distribution in DICOM format. It is possible to export the DICOM data either with name and ID taken from the patient or from the QA phantom. The selection is done by setting QA Plan Identity in Clinic Settings to either Patient or Phantom. (See *section D.2.4 The DICOM tab on page 929* for more information). If Patient is selected, only RT Plan and RT Dose objects can be exported.

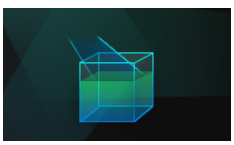
When creating the QA plan, modifications can be done including changes of the isocenter positions of the beams and changes of the gantry, collimator and treatment couch angles. It is possible to create several QA plans for each single beam set in a treatment plan.

Note: *Only Head First Supine positioned phantoms are supported. Do not try to position the phantom according to the patient, in case the patient was positioned differently.*

Note: *For carbon ions: Only the physical ion dose is shown in the QA Preparation module.*

Note: *The shortcut Ctrl+D (Compute final dose) refers to the treatment plan, not the open QA plan. Ctrl+D will trigger computation of the treatment plan dose and subsequent invalidation of the QA plan.*

Note: *The message "Old version of dose statistics" also refers to the treatment plan. Issuing the "Update ROI voxel volumes" command will trigger invalidation of the current QA plan.*



In this chapter

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9.1 THE QA PREPARATION MODULE USER INTERFACE

Workspace

The QA Preparation workspace has four image data views. Three 2D views for displaying the phantom in transversal, sagittal, and coronal directions. The fourth view can be switched between a 3D view, a BEV, a line dose view and a dose statistics view. The bottom area contains the beam list.

For TomoHelical plans there is a **Leaf Open Times** view that displays a histogram for the leaf open time of all leaves and of all projections.

The QA Preparation module has two extra tool panels; the Phantom ROI List listing the phantom ROIs and the phantom POI list listing the phantom POIs. The tool panel is expanded /contracted by clicking the panel tab headers to the left.

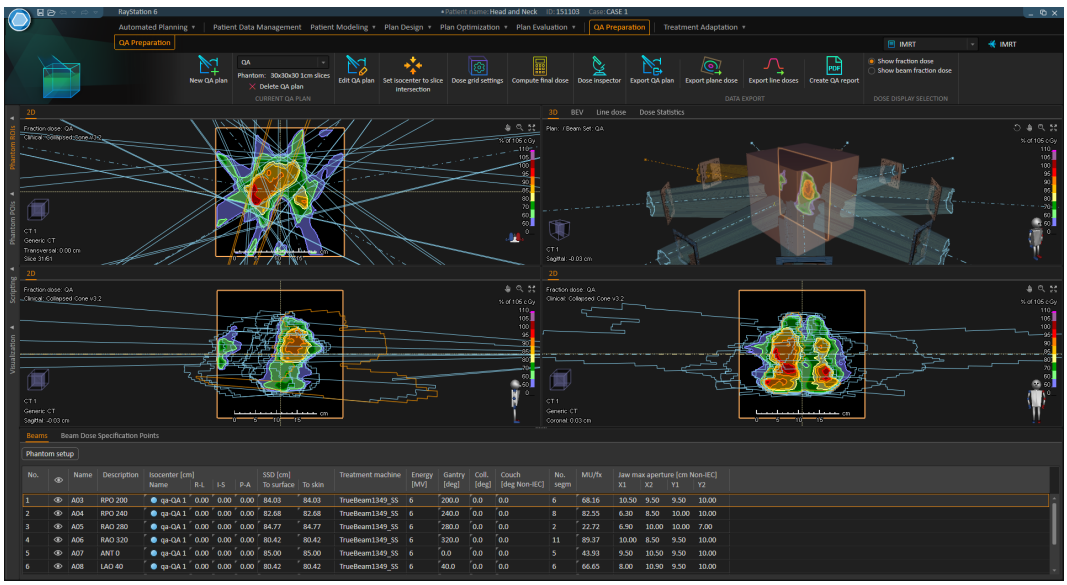


Figure 429. The QA preparation workspace.

9.2 PHANTOM IMPORT

A phantom in RayStation 7 consists of an image set and a structure set – at least one ROI defining the phantom outline is required. Once a phantom is imported it can be reused over and over again, for QA preparation of multiple patients and treatment plans. The phantom is imported from the RayPhysics application, see *RSL-D-RS-7.0-RPHY, RayStation 7 RayPhysics Manual* for more information.

Note: *An imported phantom cannot be modified in RayStation 7. To modify the phantom in RayStation 7 before importing it to the phantom library it can be imported as a patient. Then ROIs and POIs can be created using the regular tools in the Structure Definition module. Export the patient and import it to the phantom library.*

Note: *The imported phantoms are read only in the QA Preparation module. Therefore, it is not possible to move the phantom with respect to the couch when creating verification plans, which may be especially important for TomoHelical plans. It is possible to create multiple instances of a phantom with different positions in relation to the couch in the RayPhysics application.*

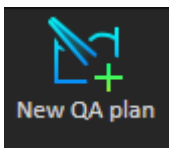
9.3 CREATE A QA PLAN FOR A BEAM SET

Before creating a QA plan for a beam set, a suitable phantom first has to be imported into the phantom library. See *RSL-D-RS-7.0-RPHY, RayStation 7 RayPhysics Manual* for more information.

Create a QA plan for a photon beam set

To create a QA plan, i.e. to apply the current plan and beam configuration onto a phantom:

1. Click the **New QA plan** button.



This opens the Create QA plan dialog.

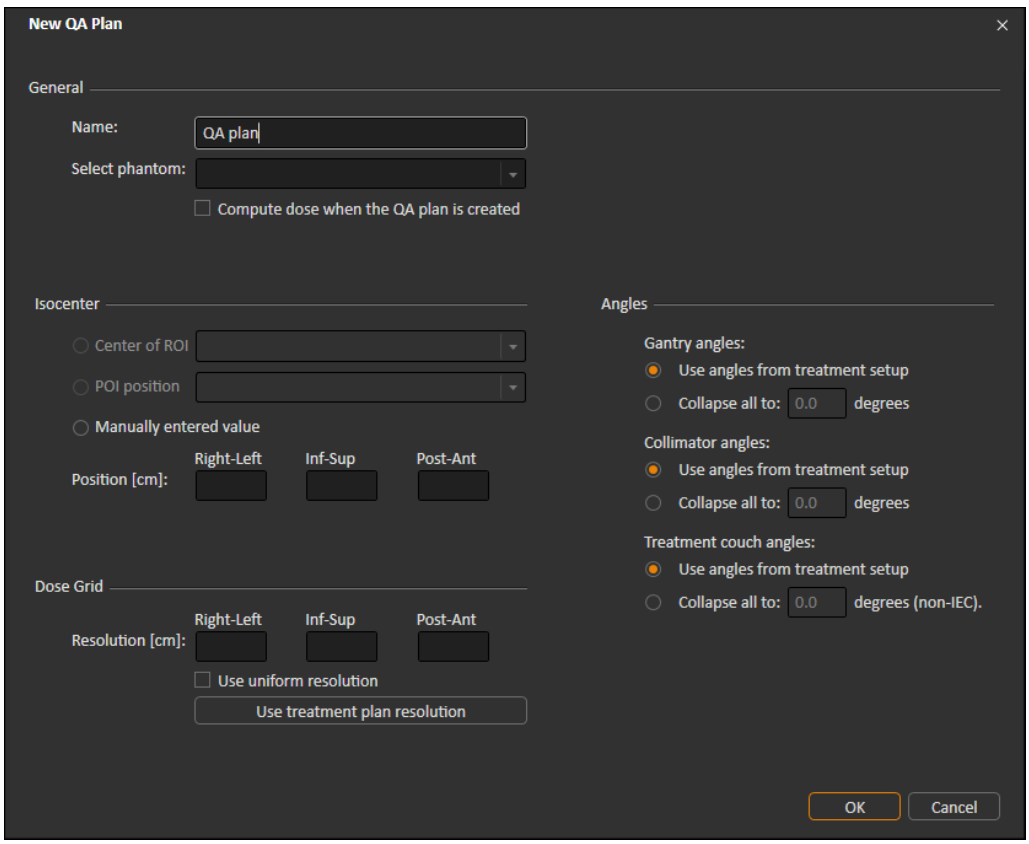


Figure 430. The Create QA plan dialog.

2. Specify a **Name** for the QA plan.

3. Select the **Phantom** to use.
4. Select to **Compute dose when the QA plan is created** by checking the corresponding checkbox.
5. Select where, in the phantom, to position the beam **Isocenter**. The isocenter may be specified as the center of an ROI, a center of a POI or by manually entering the coordinates of the isocenter.

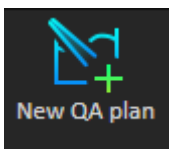
   Note: *When creating a QA plan for a plan including beams with several isocenters, all beams in the QA plan will be assigned to a new common isocenter local to the QA plan.*
6. Specify the resolution of the **Dose grid**. Select to **Use uniform resolution** by checking the corresponding checkbox. The **Use treatment plan resolution** button obtains the dose grid resolution from the treatment plan and displays the values. The dose grid is automatically generated to cover the entire external ROI of the phantom using the specified dose grid resolution.
7. The **Gantry angles** of the beams may either be preserved from the treatment plan or collapsed to a value common for all beams and control points. N/A for TomoHelical and Static Arc plans.
8. The **Collimator angles** of the beams may either be preserved from the treatment plan or collapsed to a value common for all beams. N/A for TomoHelical plans.
9. The **Treatment couch angles** of the beams may either be preserved from the treatment plan or collapsed to a value common for all beams. N/A for TomoHelical plans.
10. Click **OK**.

Note: *The QA plan always has one fraction only, regardless of the number of fractions in the treatment plan.*

Create a QA plan for an electron beam set

To create a QA plan, i.e. to apply the current plan and beam configuration onto a phantom:

1. Click the **New QA plan** button.

   This opens the Create QA plan dialog.

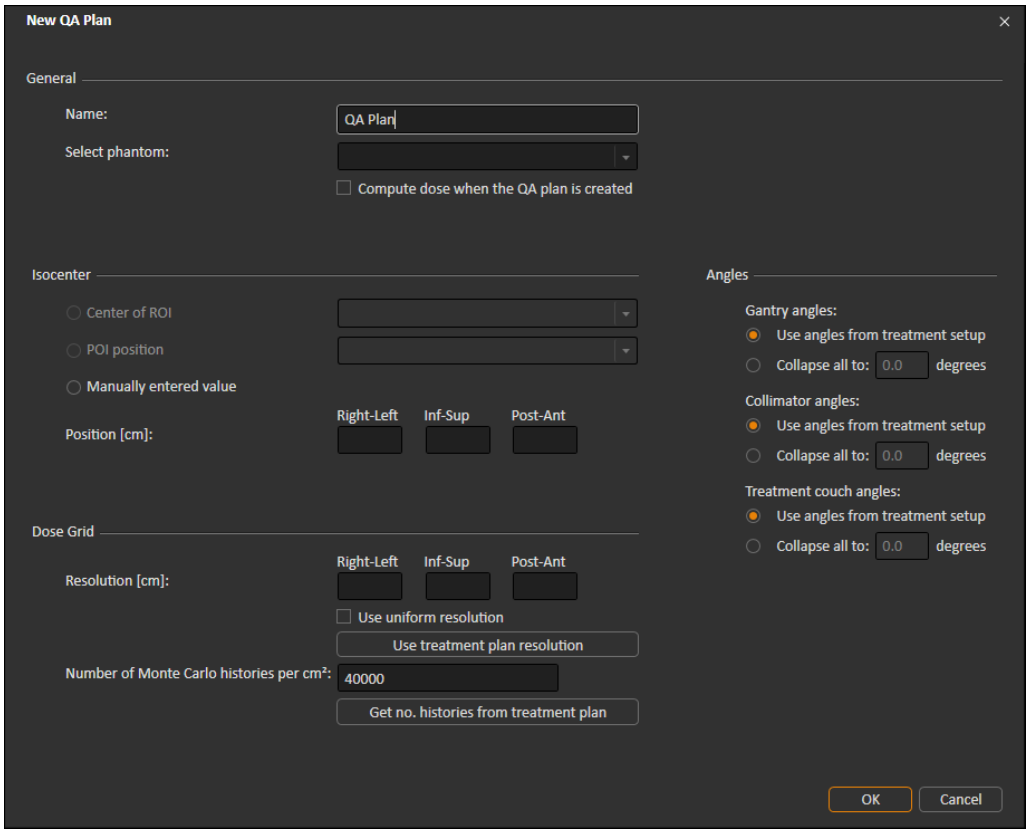


Figure 431. The Create QA plan dialog.

2. Specify a **Name** for the QA plan.
3. Select the **Phantom** to use.
4. Select to **Compute dose when the QA plan is created** by checking the corresponding checkbox.
5. Select where, in the phantom, to position the beam **Isocenter**. The isocenter may be specified as the center of an ROI, a center of a POI or by manually entering the coordinates of the isocenter.
6. Specify the resolution of the **Dose grid**. Select to **Use uniform resolution** by checking the corresponding checkbox. The **Use treatment plan resolution** button obtains the dose grid resolution from the treatment plan and displays the values. The dose grid is automatically generated to cover the entire external ROI of the phantom using the specified dose grid resolution.
7. Specify the **Number of of Monte Carlo histories per cm²**. The **Get nr. of histories from treatment plan** button obtains the histories from the treatment plan and displays the value.

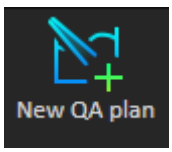
8. The **Gantry angles** of the beams may either be preserved from the treatment plan or collapsed to a value common for all beams.
9. The **Collimator angles** of the beams may either be preserved from the treatment plan or collapsed to a value common for all beams.
10. The **Treatment couch angles** of the beams may either be preserved from the treatment plan or collapsed to a value common for all beams.
11. Click **OK**.

Note: *The QA plan always has one fraction only, regardless of the number of fractions in the treatment plan.*

Create a QA plan for a proton beam set and carbon ion beam set

To create a QA plan, i.e. to apply the current plan and beam configuration onto a phantom:

1. Click the **New QA plan** button.



This opens the Create QA plan dialog.

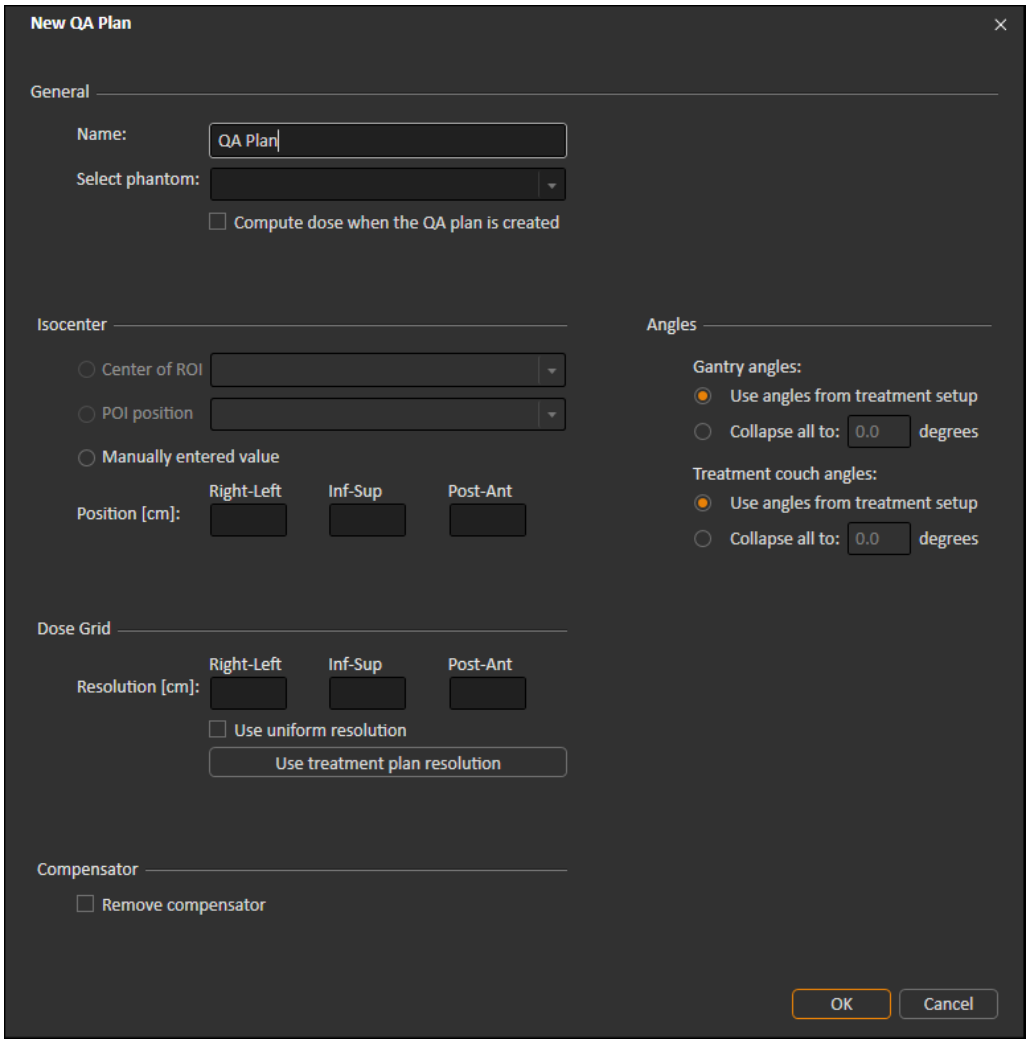


Figure 432. The Create QA plan dialog.

2. Specify a **Name** for the QA plan.
3. Select the **Phantom** to use.
4. Select to **Compute dose when the QA plan is created** by checking the corresponding checkbox.
5. Select where, in the phantom, to position the beam **Isocenter**. The isocenter may be specified as the center of an ROI, a center of a POI or by manually entering the coordinates of the isocenter.
6. Specify the resolution of the **Dose grid**. Select to **Use uniform resolution** by checking the corresponding checkbox. The **Use treatment plan resolution** button obtains the dose grid resolution from the treatment plan and displays the values. The dose grid is automatically

generated to cover the entire external ROI of the phantom using the specified dose grid resolution.

7. Select to **Remove compensator** by checking the corresponding checkbox (not applicable for proton PBS, Line Scanning and carbon ion PBS).
8. The **Gantry angles** of the beams may either be preserved from the treatment plan or collapsed to a value common for all beams.

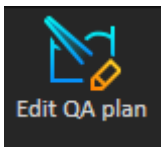
> **WARNING!**
>
> **Avoid changing beam angles in the QA plan for ion treatment machines with different beam models for different beam angles.** When creating a treatment plan using an ion treatment machine with different beam models for different beam angles, the beam model for a specific beam will be chosen from the corresponding beam angle. If the beam angles are changed in the QA plan compared to the treatment plan (e.g., by collapsing all the beam angles to a chosen beam angle), the dose computation in the QA plan will be based on a different beam model combination than in the treatment plan. The user should therefore avoid changing the beam angles in the QA plan, or if such a change is needed, carefully assess the validity of the QA plan. (149548)

9. The **Treatment couch angles** of the beams may either be preserved from the treatment plan or collapsed to a value common for all beams.
10. Click **OK**.

Note: *The QA plan always has one fraction only, regardless of the number of fractions in the treatment plan.*

Edit QA plan

To edit the QA plan information, click the **Edit QA plan** button.



Note: *When updating QA plan information using the Edit QA Plan dialog, the gantry, collimator and couch angles will be set according to the angle options selected in the dialog. This means that if a beam angle has been manually modified, it may get updated by the Edit QA Plan dialog.*

Note: *For a VMAT or Conformal Arc plan where the gantry angles have been collapsed to a common value, it's not possible to return to the original treatment plan gantry angles when editing the QA plan.*

Switch QA plan

Use the QA plan drop-down list in the **Current QA plan** toolbar to select another QA plan for the current treatment plan.

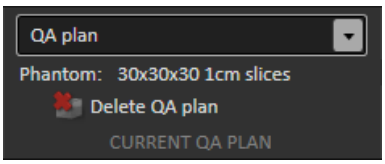


Figure 433. The Current QA plan toolbar.

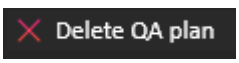
Edit QA beams

It is not possible to edit the snout position for beams with block or MLC contour or compensator. Changing the snout position for such beams will change the physical geometry of the objects such that they no longer match the treatment plan. If the gap is edited in QA, it will update the isocenter, not the snout position.

In addition, it is not possible to edit snout position of beams if the machine beam model is dependent on the snout position.

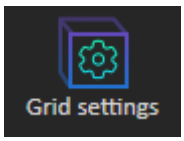
Delete QA plan

To delete the current QA plan, click the **Delete QA plan** button.



9.4 EDIT DOSE GRID

After the QA plan has been created, the dose grid used for the QA plan may be edited by clicking the **Dose grid settings** button. This opens up the **Edit Dose Grid Settings** dialog, see section *section 6.1.4 Define and edit the dose grid on page 312* for more information.

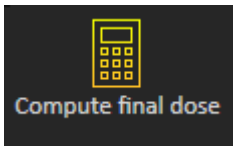


9.5 ADJUST ISOCENTER

After the QA plan has been created the isocenter may be adjusted using the white cross-hair visible in the 2D patient data views. The position of the cross-hair can be adjusted by using the mouse scroll wheel. To set the isocenter to the cross-hair position, click the **Set isocenter to slice intersection** button and select **For all beams** or **For current beam**.

9.6 COMPUTE DOSE

To compute the dose in the phantom, click the **Compute final dose** button.

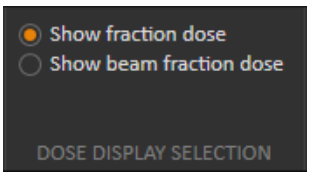


WARNING!

Independent dose calculation. Ensure that the independent dose calculation system that is used really is independent. There are systems that may appear to be suitable for independent dose calculation that are in fact not independent at all since the dose engine is manufactured by RaySearch and uses the same algorithm for photon dose computation and possibly also the same code as RayStation (e.g., Compass (IBA)). (113204)

9.7 DOSE DISPLAY - PLAN DOSE VS. BEAM DOSE

The QA Preparation module always displays the fraction dose for the beam set in the current QA plan, i.e. the dose for one fraction - either the QA plan dose (for all beams) or the beam dose (for one beam at a time).



9.8 LINE DOSE

Right-click in a patient view and select **Add/edit dose line** from the context menu. The dose line is positioned by clicking somewhere in the view, moving the mouse and release the mouse button where the line is to end – the dose line's profile is displayed in the Line dose tab (found in the same area as the BEV and Dose statistics). For more information, see *section 3.7.4 Line dose on page 88*.

9.9 BEAM DOSE SPECIFICATION POINT

A beam dose specification point can be selected for each beam in the **Beam dose specification points** tab. This point and its values can be exported and used in external systems, for example RadCalc, to verify the dose calculation. The isocenter of each beam will, by default, be used as Beam dose specification point. Once clinical dose has been computed, different information is displayed for the Beam dose specification point depending on modality and treatment technique.

- For proton and carbon beams, **Dose per fraction** and **Physical depth** are displayed in the list.
- For non-TomoHelical photon beams, values for **Dose per fraction**, **Physical depth** and **Water equivalent depth** are displayed. For VMAT, Conformal Arc and Static arc plans the **Physical depth** and the **Water equivalent depth** will be calculated as an unweighted mean over all control points. For Static arcs virtual control points are created maximum two degrees apart.
- For TomoHelical photon beams, only **Dose per fraction** is listed.
- For electron beams, **Electron density weighted depth**, which is the integrated depth from the surface weighted with the electron density relative to water, is given instead of **Water equivalent depth** in addition to **Dose per fraction** and **Physical depth**.

Create a dose specification point

Right-click in a patient view and select **Create dose specification point** from the context menu. Default point position is at the coordinates of the slice intersection.

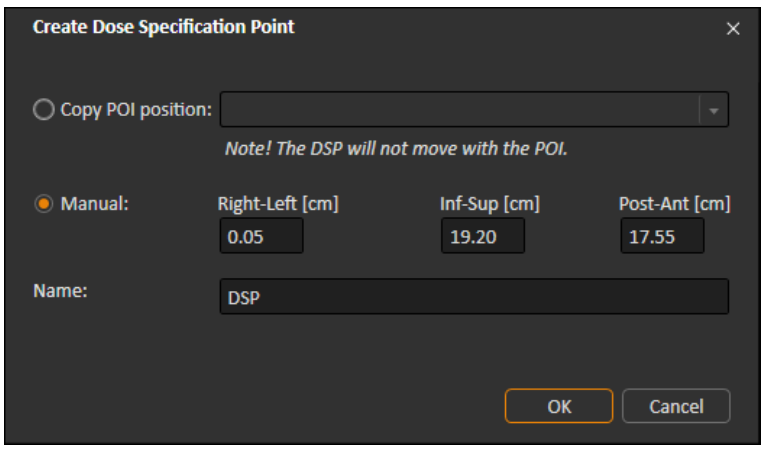


Figure 434. The Create Dose Specification Point dialog.

Note: *Ensure that the beam dose specification points are placed in a region where dose is not close to zero and where the dose gradient is low.*

Note: *For VMAT, Conformal Arc and Static arc plans, SSDs will be generated from the beam angle of the first segment of each beam.*

Move a dose specification point

Right-click in a patient view to access the Context menu. Select **Move dose specification point**. Drag and drop the dose specification point to a desired position. Right-click again and deselect **Move dose specification point** to exit edit mode.

Select beam dose specification point

A beam dose specification point can be selected directly from the **Beam dose specification points** list. The beam dose specification point will be set to isocenter if no other point is selected.

Beams | Beam Dose Specification Points

Beam no.	Beam	Point	Dose per fraction [cGy]	Physical depth [cm]	Water equivalent depth [cm]
1	Ant	*Isocenter*	71.1	10.25	13.55
2	Left	*Isocenter*	61.2	14.62	15.04
3	Post	*Isocenter*	76.7	10.02	10.45
4	Right	*Isocenter*	60.4	15.22	15.52

Figure 435. The Beam dose specification points tab.

9.10 QA DETAILS

Detailed information on the QA plan and its setup is available in the lower part of the screen. The **Beams** tab shows beam setup data for the QA plan. The **Beam Dose Specification Points** tab shows dose and location of each beam's dose specification point.

Data on the phantom setup geometry is presented in a separate window shown by clicking the **Phantom setup** button which is available when the **Beams** tab is selected. This view shows three axial views of the phantom plan with the localization point. It also gives information about setting up the phantom relative to an external reference system such as in room laser lines.

Note: *To be able to open the Phantom setup window, the phantom must have a localization point.*

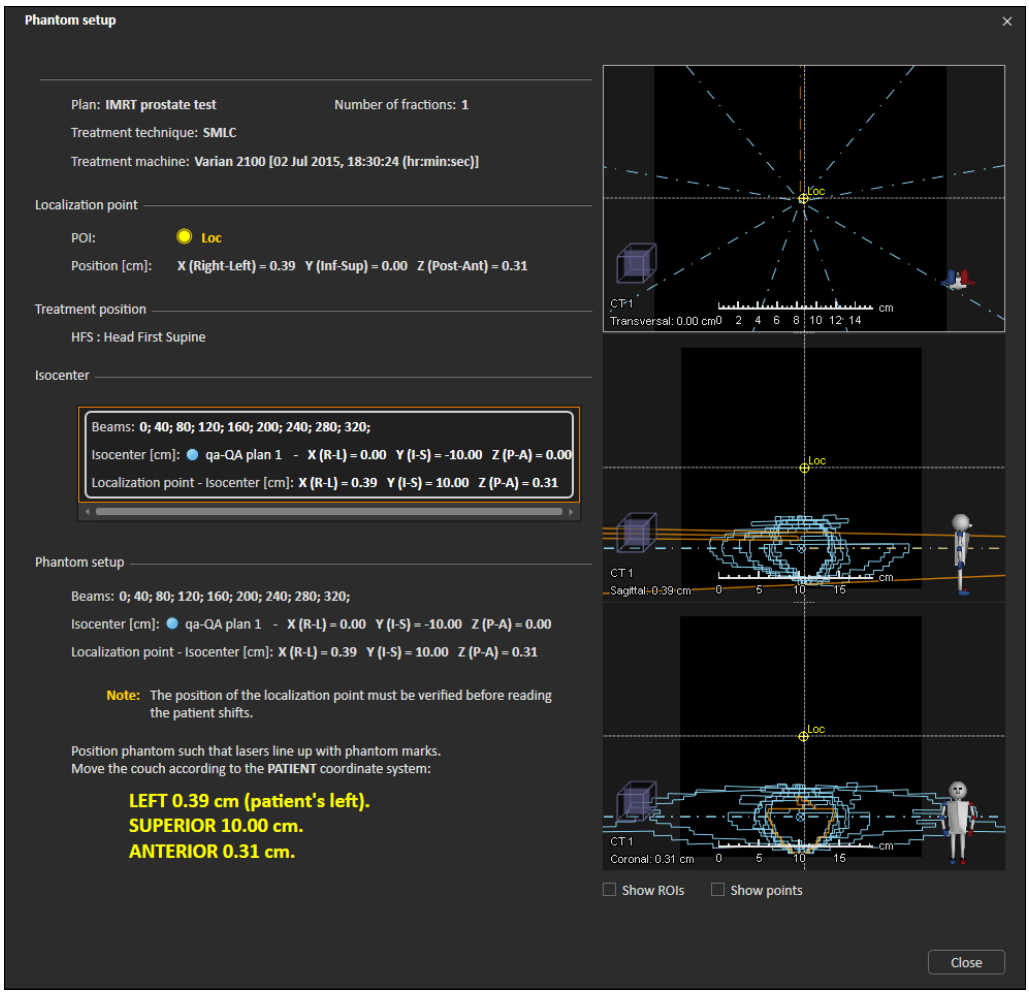
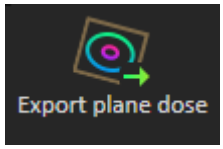

Phantom setup
Plan: IMRT prostate test
Number of fractions: 1
Treatment technique: SMLC
Treatment machine: Varian 2100 [02 Jul 2015, 18:30:24 (hr:min:sec)]
Localization point
POI: Loc
Position [cm]: X (Right-Left) = 0.39 Y (Inf-Sup) = 0.00 Z (Post-Ant) = 0.31
Treatment position
HFS : Head First Supine
Isocenter
Beams: 0; 40; 80; 120; 160; 200; 240; 280; 320;
Isocenter [cm]: qa-QA plan 1 - X (R-L) = 0.00 Y (I-S) = -10.00 Z (P-A) = 0.00
Localization point - Isocenter [cm]: X (R-L) = 0.39 Y (I-S) = 10.00 Z (P-A) = 0.31
Phantom setup
Beams: 0; 40; 80; 120; 160; 200; 240; 280; 320;
Isocenter [cm]: qa-QA plan 1 - X (R-L) = 0.00 Y (I-S) = -10.00 Z (P-A) = 0.00
Localization point - Isocenter [cm]: X (R-L) = 0.39 Y (I-S) = 10.00 Z (P-A) = 0.31
Note: The position of the localization point must be verified before reading the patient shifts.
Position phantom such that lasers line up with phantom marks.
Move the couch according to the PATIENT coordinate system:
LEFT 0.39 cm (patient's left).
SUPERIOR 10.00 cm.
ANTERIOR 0.31 cm.
Loc
CT 1
Transversal: 0.00 cm
Sagittal: 0.39 cm
Coronal: 0.31 cm
Show ROIs
Show points
Close

Figure 436. The Phantom setup dialog.

9.11 PLANE DOSE EXPORT

To export the dose in a single plane to an image:

1. Click the **Export plane dose** button.



This opens the dialog for dose plane export.

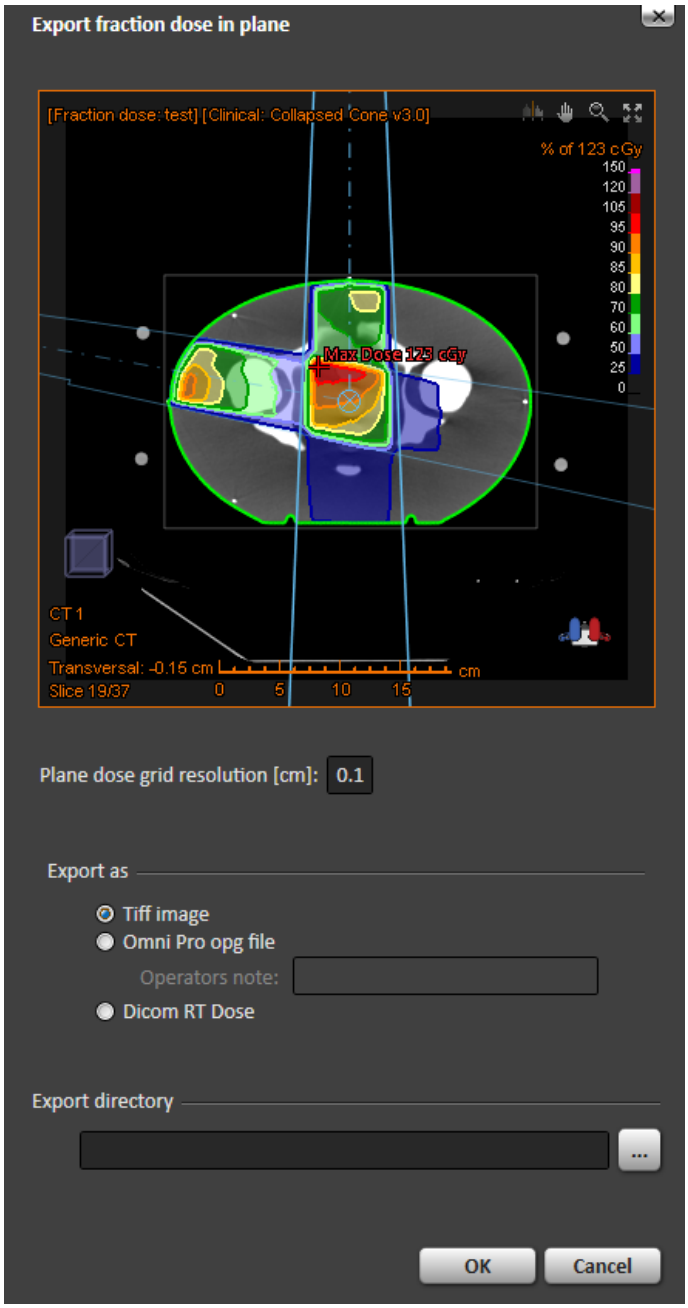


Figure 437. The Export fraction dose in plane dialog.

2. By scrolling with the mouse wheel and using the **Patient direction** option in the context menu it is possible to select the plane to be exported.
3. Specify the resolution for the exported image in the **Plane dose grid resolution** field.
4. Select export format. The planar dose can be exported as a **Tiff image** (16-bit TIFF format), with the grayscale values proportional to the dose, as an **Omni Pro opg file** or as a **2D RTDose DICOM file**.
5. Click the **...** button and select **Export directory**.
6. Click **OK**. The image is exported.

Note: *The exported files will be saved in a folder tree in the selected directory, with subfolder names identifying the treatment plan, the beam set and the verification plan.*

Note: *It is only possible to export the 2D RTDose to file, not to a PACS server.*

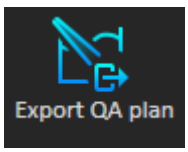
9.12 DICOM EXPORT

The QA plan and its related data can be exported in DICOM format.

It is possible to export the DICOM data either with name and ID taken from the patient or from the QA phantom. The selection is done by setting **QA Plan Identity** in Clinic Settings to either **Patient** or **Phantom**. (See *section D.2.4 The DICOM tab on page 929*.) If Patient is selected, only RT Plan and RT Dose objects can be exported.

To export the QA plan:

1. Click the **Export QA plan** button.

   This opens the **QA Plan Export** dialog.

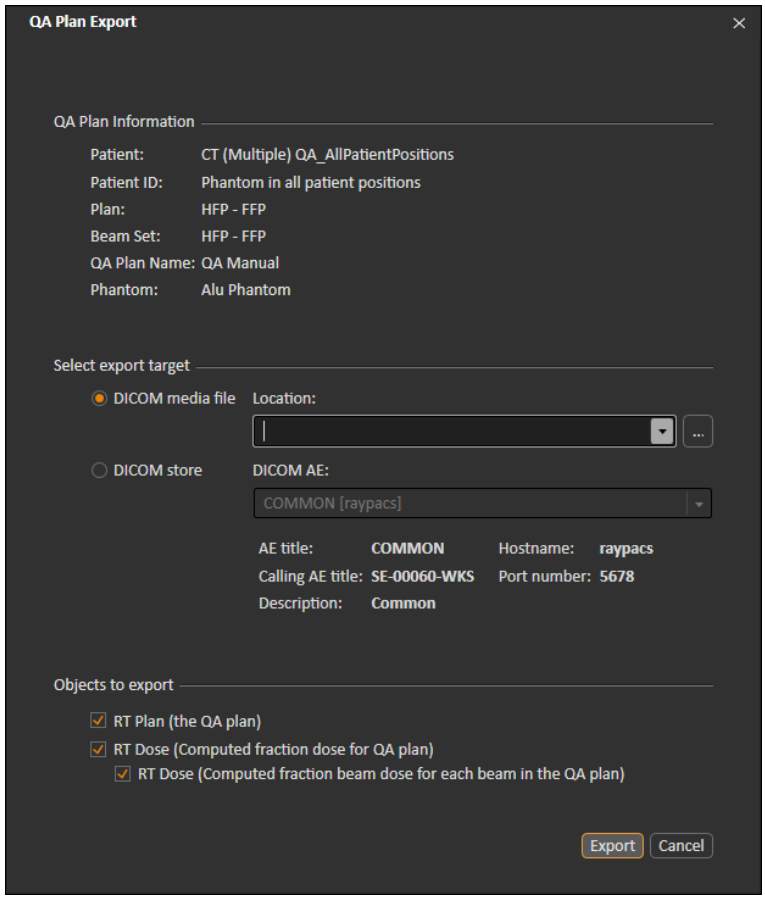


Figure 438. The **QA Plan Export** dialog.

2. Select export target.
3. Select **Objects to export**. If **QA Plan Identity** is set to **Patient**, only RT Plan and RT Dose objects can be exported.
4. Click **Export**.

For more information about how to export DICOM data, see *section 4.4 Export patient data on page 132*.

Note: *In RayStation 7, it is possible to unapprove phantoms used for verification plans in the RayPhysics Beam 3D Modeling module. However, to be able to DICOM export a verification plan with QA plan patient identity set to Phantom, the phantom can not be deleted from RayPhysics.*

Note: *When exporting a VMAT or Conformal Arc plan where the gantry angles have been collapsed to a common value, the gantry angles in the exported plan will be collapsed. To do QA measurements with rotating gantry, the treatment plan must be used. An exported collapsed VMAT or Conformal Arc plan which is imported back into RayStation will be interpreted as a DMLC plan.*

WARNING!

Use the exported treatment plan for plan verification. Using the treatment plan for QA measurements provides an opportunity to detect errors in data transfer. It is recommended to only use the QA plan for computing QA dose and to perform QA measurements using the treatment plan. (53986)

WARNING!

Collapse of gantry angles for arc beam QA. Collapse of gantry angles to a single angle for arc beams (VMAT and Conformal Arc) in the QA Preparation module is intended for QA with a detector mounted perpendicular to the treatment beam and rotating with the gantry. The dose computed in the QA Preparation module can be used, but the QA delivery shall be performed with a rotating gantry to detect any delivery problems related to gantry rotation. For details about dose computation for arc beams and collapsed arc beams, refer to the *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual*. (369355)

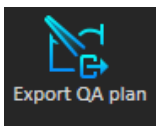
9.13 DICOM EXPORT TO IDMS

The QA plan can be exported to iDMS. In order for the export to work there are a few preconditions:

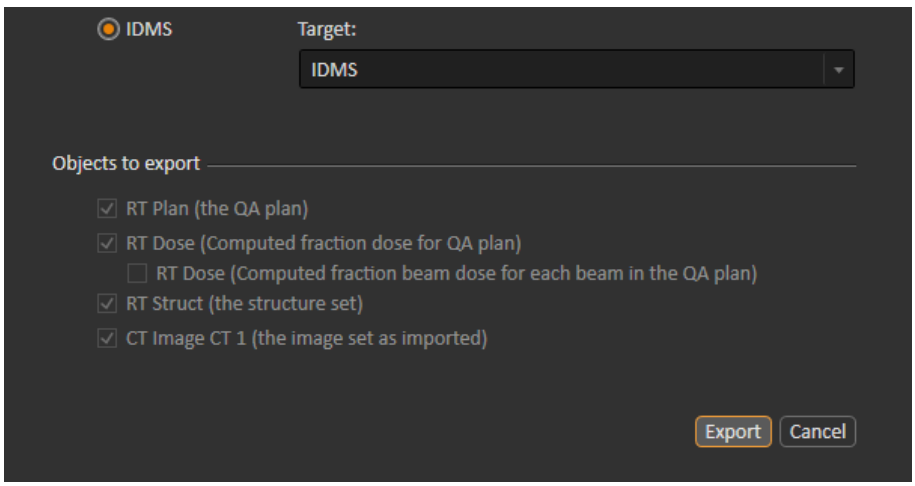
- A RayGateway connection must be set up in Clinic Settings.
- The Plan must be based on the TomoHelical treatment technique.
- The treatment plan that the QA plan is based on must first be exported to iDMS through the treatment plan **DICOM Export** dialog.
- The treatment plan cannot be modified between the first export and the QA plan export.

To export the QA plan to iDMS:

1. Make sure that the preconditions listed above have been fulfilled.
2. Click the **Export QA plan** button. This opens the **QA Plan Export** dialog.



3. Select "IDMS" as export target.


IDMS
Target:
IDMS
Objects to export
RT Plan (the QA plan)
RT Dose (Computed fraction dose for QA plan)
RT Dose (Computed fraction beam dose for each beam in the QA plan)
RT Struct (the structure set)
CT Image CT 1 (the image set as imported)
Export
Cancel

4. Click **Export**.

Note: *When exporting to iDMS the user cannot manually select the objects to export or QA Plan Identity. This is because iDMS requires certain data in a certain format.*

9.14 EXPORT LINE DOSES

Any added line doses can be exported to a csv file.

To export line doses:

1. Click the **Export line doses** button in the toolbar.

2. In the Save As dialog that opens, select a directory, type a name for the file, and click Save.

For more information about the file format, see *Appendix G Line dose export*.

10 AUTOMATED PLANNING

The Automated Planning activity contains the following modules:

- **Plan Explorer** - provides tools for generating a set of Exploration plans and to filter out the most suitable plan based on clinical goals and treatment machines.
- **Automated Breast Planning** - provides tools for automated planning of tangential breast IMRT using heuristic optimization
- **Fallback Planning** - provides tools for evaluating an automatically generated fallback plan, as well as tools for promoting a fallback plan to a treatment plan
- **Fallback Protocol Management** - provides tools for definition of fallback protocols, which controls how the fallback plans are created

Fallback planning in RayStation is a tool for creating additional plans to be used in a contingency situation, enabling a patient to be treated on another machine, possibly with a different modality and/or treatment technique, in case the original machine is unavailable.

Fallback planning is performed in several modules, including the Fallback Planning module and the Fallback Protocol Management module. A suggested workflow for the entire fallback planning process is described in *section 10.3 The Fallback Planning workflow on page 843*.

Note: *For carbon ions: Only the RBE dose is shown in the Automated Planning activity.*

Note: *Fallback planning is not supported for carbon ions.*

In this chapter

This chapter contains the following sections:

10.1	The Plan Explorer module	p. 803
10.2	The Automated Breast Planning module	p. 829
10.3	The Fallback Planning workflow	p. 843
10.4	The Fallback Planning module	p. 849
10.5	The Fallback Protocol Management module	p. 856

Precautions

WARNING!

Fallback Planning. Be aware that any user may edit fallback plan types and protocols. These changes affect all other users at the clinic. (97458)

WARNING!

Automated Planning. Since there is less user involvement in plan creation when using automatic tools, extra care needs to be taken to manually verify the plan quality in the Plan Approval workspace. (117826)

WARNING!

Fallback Planning for protons. When using fallback plans for protons, the machine must include an RBE factor in the absolute dosimetry. A photon fallback plan created from a proton plan, requires that the proton beam model includes the RBE scaling factor in order to make the doses from the photon and proton plans equivalent. (252951)

10.1 THE PLAN EXPLORER MODULE

The Plan Explorer module provides tools to automatically generate multiple plans and quickly select the most suitable plan(s) based on clinical goals and hardware properties.

The Plan Explorer module fully supports photon plans with treatment techniques SMLC, DMLC and VMAT. Plans of other treatment modalities and treatment techniques can be copied to Plan Explorer for plan comparison.

The module includes features such as:

- automatic optimization with the objective to fulfill clinical goals
- generating plans in parallel using a High Performance Computing (HPC) cluster
- plan filtering with respect to fulfillment of clinical goals
- plan filtering with respect to treatment machines and treatment setup parameters
- fast plan comparison using clinical goals radar charts
- detailed side-by-side comparison of plans

In this section

This section contains the following sub-sections:

10.1.1	The Plan Explorer module user interface	p. 804
10.1.2	Exploration plan thumbnails	p. 807
10.1.3	Radar chart in the Exploration plan thumbnails	p. 808
10.1.4	High Performance Computing (HPC) cluster	p. 813
10.1.5	Plan Explorer algorithm	p. 814
10.1.6	Plan Explorer specific clinical goals	p. 815
10.1.7	Plan Explorer workflow	p. 816
10.1.8	Set up Plan Exploration	p. 818
10.1.9	Generate Exploration plans	p. 820
10.1.10	Filter Exploration plans	p. 822
10.1.11	Compare filtered plans and copy to Plan list	p. 825
10.1.12	Create Plan Exploration template	p. 826

10.1.1 The Plan Explorer module user interface

There are three different workspaces in the Plan Explorer module: the Setup workspace, the Explore workspace and the Compare workspace.

The upper part of all three workspaces contains the toolbar.

The Setup workspace

The left part of the main window in The Setup workspace contains information about the selected Exploration, such as **Name**, **Description**, **Planning image set**, **Planned by** and **Number of exploration plans**.

The right part of the main window contains the **Clinical goals** list.

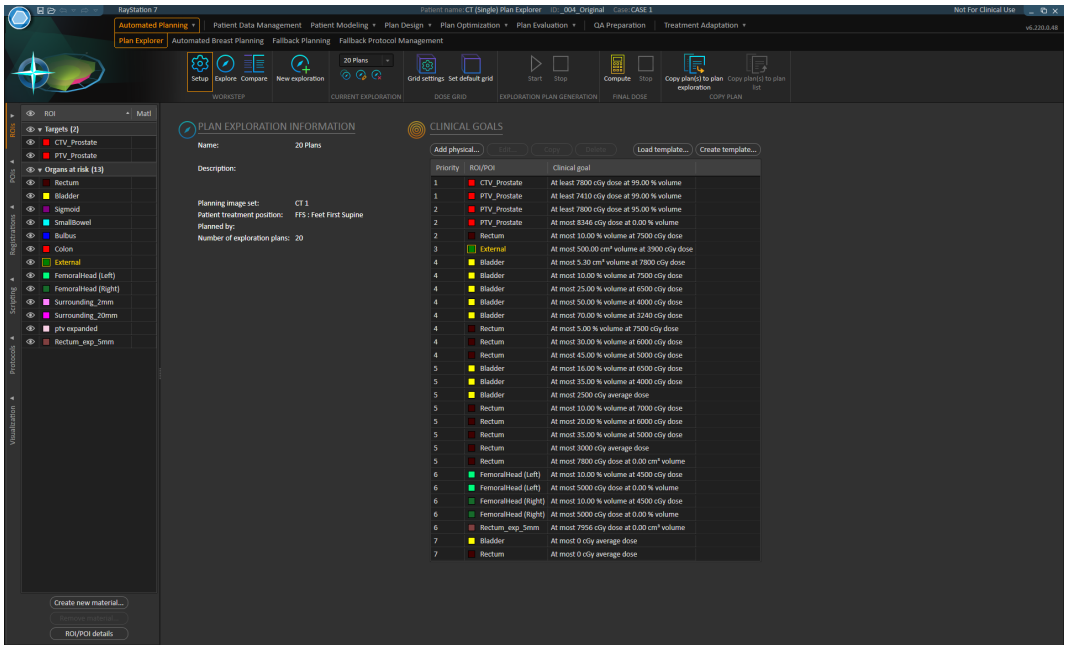

RayStation 7
Automated Planning
Patient Data Management
Patient Modeling
Plan Design
Plan Optimization
Plan Evaluation
QA Preparation
Treatment Adaptation
Plan Explorer
Automated Breast Planning
Fallback Planning
Fallback Protocol Management
Setup
Explore
Compare
New exploration
20 Plans
Grid settings
Set default grid
Start
Stop
Compute
Stop
Copy plan(s) to plan exploration
Copy plan(s) to plan list
WORKSTEP
CURRENT EXPLORATION
DOSE GRID
EXPLORATION PLAN GENERATION
FINAL DOSE
COPY PLAN
ROI
Matl
Targets (2)
CTV_Prostate
PTV_Prostate
Organs at risk (13)
Rectum
Bladder
Sigmoid
SmallBowel
Bulbus
Colon
External
FemoralHead (Left)
FemoralHead (Right)
Surrounding_2mm
Surrounding_20mm
ptv expanded
Rectum_exp_5mm
Create new material...
ROI/POI details
PLAN EXPLORATION INFORMATION
Name: 20 Plans
Description:
Planning image set: CT 1
Patient treatment position: FFS : Feet First Supine
Planned by:
Number of exploration plans: 20
CLINICAL GOALS
Add physical...
Load template...
Create template...
Priority
ROI/POI
Clinical goal
1 CTV_Prostate At least 7800 cGy dose at 99.00 % volume
1 PTV_Prostate At least 7410 cGy dose at 99.00 % volume
2 PTV_Prostate At least 7800 cGy dose at 95.00 % volume
2 PTV_Prostate At most 8346 cGy dose at 0.00 % volume
2 Rectum At most 10.00 % volume at 7500 cGy dose
3 External At most 500.00 cm³ volume at 3900 cGy dose
4 Bladder At most 5.30 cm³ volume at 7800 cGy dose
4 Bladder At most 10.00 % volume at 7500 cGy dose
4 Bladder At most 25.00 % volume at 6500 cGy dose
4 Bladder At most 50.00 % volume at 4000 cGy dose
4 Bladder At most 70.00 % volume at 3240 cGy dose
4 Rectum At most 5.00 % volume at 7500 cGy dose
4 Rectum At most 30.00 % volume at 6000 cGy dose
4 Rectum At most 45.00 % volume at 5000 cGy dose
5 Bladder At most 16.00 % volume at 6500 cGy dose
5 Bladder At most 35.00 % volume at 4000 cGy dose
5 Bladder At most 2500 cGy average dose
5 Rectum At most 10.00 % volume at 7000 cGy dose
5 Rectum At most 20.00 % volume at 6000 cGy dose
5 Rectum At most 35.00 % volume at 5000 cGy dose
5 Rectum At most 3000 cGy average dose
5 Rectum At most 7800 cGy dose at 0.00 cm³ volume
6 FemoralHead (Left) At most 10.00 % volume at 4500 cGy dose
6 FemoralHead (Left) At most 5000 cGy dose at 0.00 % volume
6 FemoralHead (Right) At most 10.00 % volume at 4500 cGy dose
6 FemoralHead (Right) At most 5000 cGy dose at 0.00 % volume
6 Rectum_exp_5mm At most 7956 cGy dose at 0.00 cm³ volume
7 Bladder At most 0 cGy average dose
7 Rectum At most 0 cGy average dose

Figure 439. The Setup workspace in the Plan Explorer module.

The Explore workspace

The main window in the Explore workspace contains the Exploration plans. It is possible to change the size of the plan thumbnails by adjusting the slider in the lower left part of the workspace. The displayed plan information depends on the size of the thumbnail. Details about the current Exploration (e.g., number of plans, number of filtered plans) is found in the lower right part of the workspace.

In the Explore workspace it is possible to create **New** Exploration plans as well as to **Edit**, **Copy** and **Delete** existing Exploration plans. A set of Exploration plans containing representative treatment setups and segmentation setups can be stored as a template.

The rightmost part of the workspace contains the **Filters** tab. A filter can be applied to find a subset of the Exploration plans that fulfill the property specified by the filter. There are filters for all the clinical goals that have been added to the Exploration. There are also filters for treatment machines, SMLC parameters, DMLC parameters and VMAT parameters.

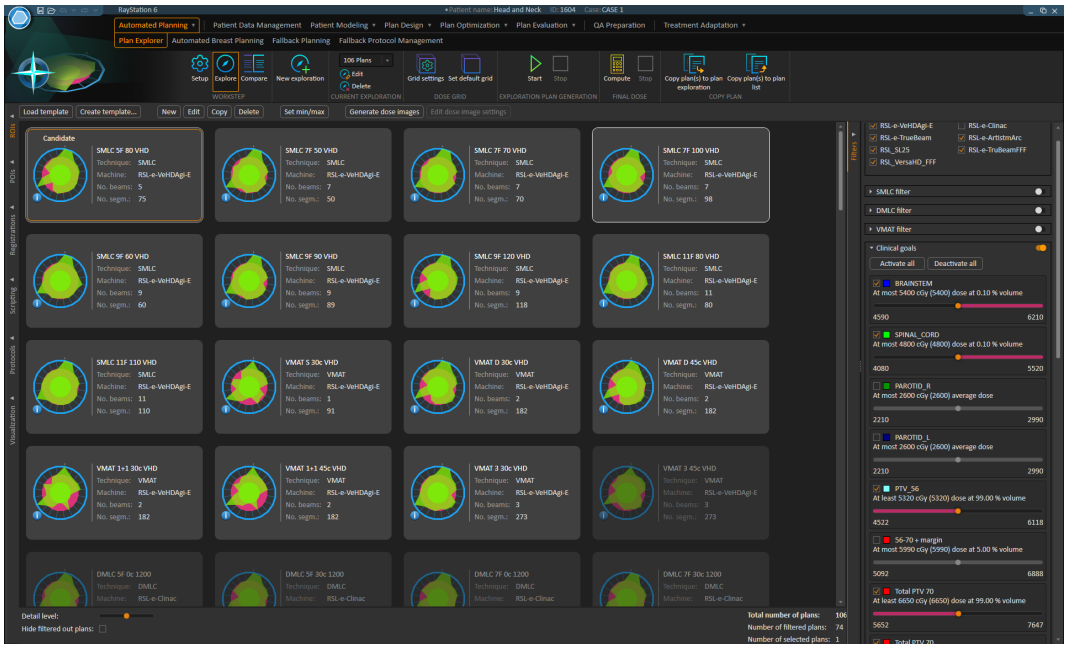


Figure 440. The Explore workspace in the Plan Explorer module.

The Compare workspace

The lower part of the Compare workspace contains the Exploration plans that have not been discarded (filtered out) by the user in the Explore workspace. In this workspace, the plans can be compared side-by-side in detail and plan(s) can be selected and copied to the ordinary Plan list.

Figure 441. The Compare workspace in the Plan Explorer module.

Plan selection

There are a number of ways to select or deselect plans in the Explore workspace and the Compare workspace:

- Click on a plan to select it.
- Hold down the Ctrl key while clicking on a selected plan to deselect it.
- Hold down the Ctrl key while clicking on several plans to select multiple plans.
- Press Ctrl + a to select all the plans that have not been filtered out.
- Hold down the SHIFT key while clicking on one plan and then another to select the two plans as well as all plans in-between them.

10.1.2 Exploration plan thumbnails

In the Explore workspace and in the Compare workspace, Exploration plans are represented with Exploration plan thumbnails. The thumbnail view contains information about some of the most important aspects of the plan.

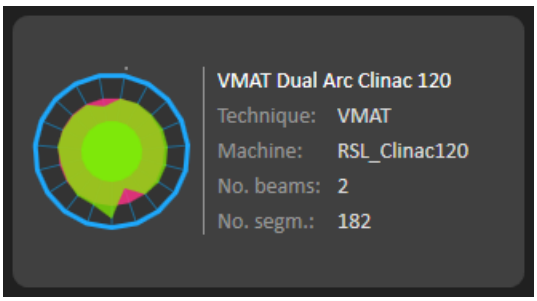


Figure 442. An example of a plan thumbnail with 19 clinical goals.

The following plan information is shown in the plan thumbnail:

- **Plan** (name)
- **Treatment technique**
- **Machine**
- **Number of beams**
- **Number of segments**
- **Clinical goals radar chart** (illustration)

10.1.3 Radar chart in the Exploration plan thumbnails

The Exploration plan thumbnail contains a radar chart that illustrates the plan quality in terms of fulfillment of the clinical goals.

For each clinical goal there is a corresponding axis connecting the inner and outer perimeters. The point on each axis that is in-between the magenta and black regions in the chart represents the acceptance level of the corresponding clinical goal.

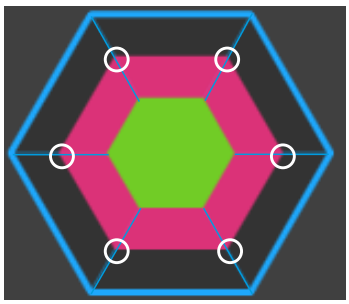


Figure 443. Radar chart showing the point on each axis that represents the acceptance level of the corresponding clinical goal.

The part of the axis that is embedded in the inner magenta region represents values where the clinical goal is not fulfilled and the closer to the inner perimeter, the worse the plan is in terms of fulfillment of the clinical goal.

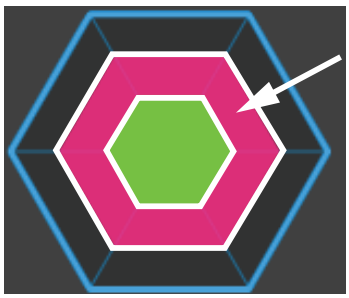


Figure 444. Radar chart showing the inner magenta region.

The part of the axis that is embedded in the outer black region represents values where the clinical goal is fulfilled and the closer to the outer perimeter, the better the plan is in terms of fulfillment of the clinical goal.

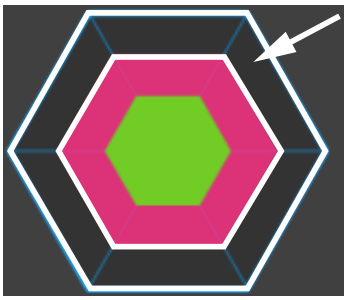


Figure 445. Radar chart showing the outer black region.

The points of the resulting clinical goal values (optimization and dose calculation) are connected and the interior forms a green surface in the radar chart.

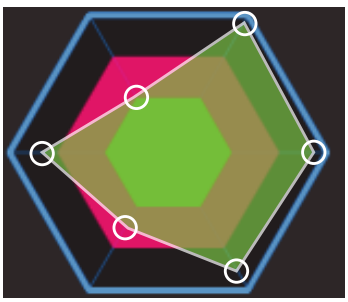


Figure 446. Radar chart showing the connected points and the inner green surface.

Therefore, if the green surface completely covers the magenta region in the radar chart, all clinical goals are fulfilled. On the other hand, if the green surface is restricted within the magenta region, none of the clinical goals are fulfilled. For the more realistic case where some of the clinical goals

are fulfilled and some are not, it is straightforward to conclude from the chart which are not by studying the axes where magenta appear.

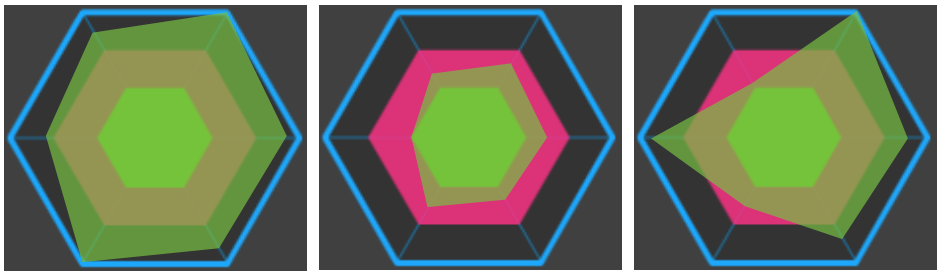


Figure 447. Radar chart where all the clinical goals are fulfilled (left), radar chart where no clinical goals are fulfilled (middle) and a radar chart where some clinical goals are fulfilled (right).

When hovering over each clinical goal line, more information about that specific clinical goal is displayed.

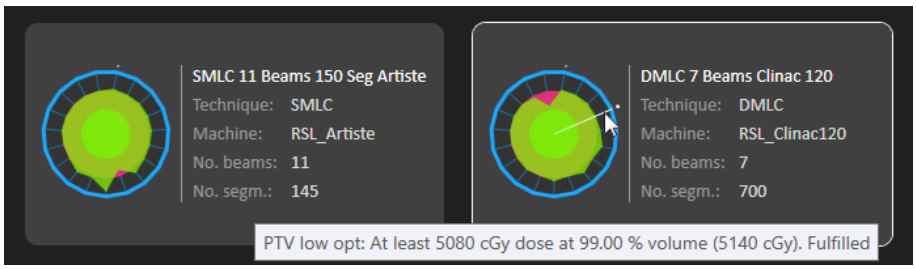

SMLC 11 Beams 150 Seg Artiste
Technique: SMLC
Machine: RSL_Artiste
No. beams: 11
No. segm.: 145
DMLC 7 Beams Clinac 120
Technique: DMLC
Machine: RSL_Clinac120
No. beams: 7
No. segm.: 700
PTV low opt: At least 5080 cGy dose at 99.00 % volume (5140 cGy). Fulfilled

Figure 448. A plan thumbnail with the mouse cursor hovering over a specific clinical goal.

Clinical goals' order in the radar chart

The clinical goals' axes in the radar chart are arranged according to their priority. The clinical goals are clock-wise ordered with the clinical goal with the highest priority on the first axis that appears clock-wise of the 12 o'clock position. If several clinical goals have the same priority, these are arranged clock-wise in the order they were added.

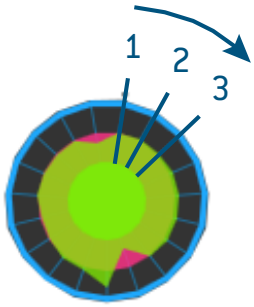


Figure 449. The clinical goals' order in the radar chart. This example has 19 clinical goals in total.

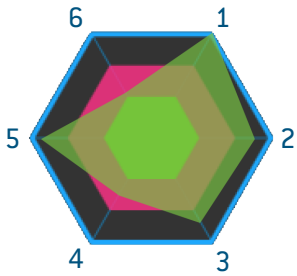


Figure 450. The illustration shows a radar chart with six clinical goals after optimization. The clinical goals 1, 2, 3, 4 and 6 are fulfilled and clinical goal 5 is not fulfilled.

How to interpret the radar chart

The clock-wise ordering of the clinical goals with respect to priority facilitates a quick assessment of the plan by studying the radar chart. By assessing if the green surface covers the most important clinical goals, then it can be concluded if a plan is a relevant candidate or not.

When comparing two radar charts (that represent two different plans evaluated over the same set of clinical goals), a plan where the green surface covers the upper right part is the better plan with respect to the most important clinical goals.

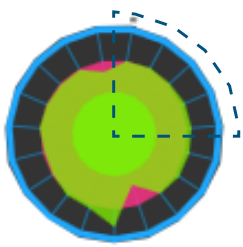


Figure 451. The illustration shows a radar chart where the green surface covers the upper right part of the chart.

Scale in the radar chart

As default, the minimum and maximum displayed values for each clinical goal line is +/- 15% of the clinical goal.

To make is easier to compare a few plans that are very similar with respect to fulfilment of clinical goals, it is possible to rescale the minimum and maximum values for a number of selected plans by clicking the **Set min/max** button.

The rescaling will for each selected plan and each clinical goal:

- Set the minimum displayed value to the minimum value of the minimum of the clinical goal evaluated over all the selected plans and the value of the corresponding filter. In case the resulting value is greater than the acceptance level, the minimum displayed value is not set.
- Set the maximum displayed value to the maximum value of the maximum of the clinical goal evaluated over all the selected plans and the value of the corresponding filter. In case the resulting value is smaller than the acceptance level, the maximum displayed value is not set.

Note: *The boundaries of the clinical goal filters are synchronized with the boundaries of the radar chart. Thus rescaling the radar chart will also update the boundaries of the filters.*

Clipped values in the radar chart

If a radar chart axis is scaled so that the value of a clinical goal is not within the range of displayed values, the goal will be plotted on the edge of the chart (inner or outer perimeter dependent on the goal type). Whenever this happens, an information icon will be displayed to notify the user.

When hovering over the information sign (visible only if any clipped clinical goals exists), more information about the clipped value(s) is displayed.

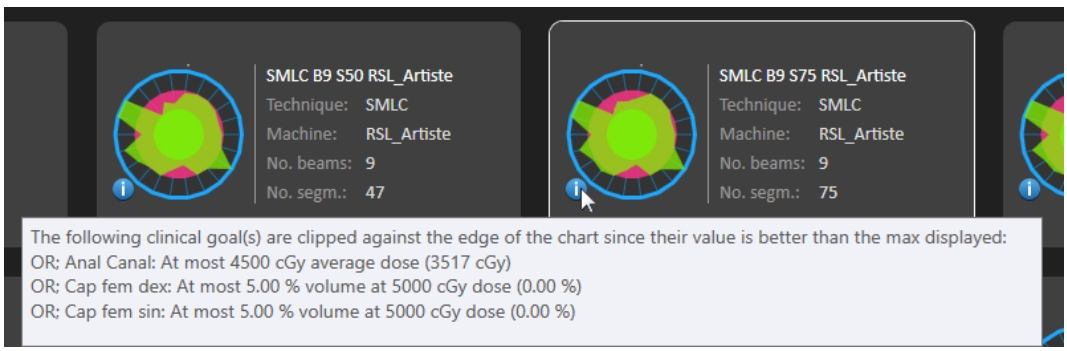

SMLC B9 S50 RSL_Artiste
Technique: SMLC
Machine: RSL_Artiste
No. beams: 9
No. segm.: 47
SMLC B9 S75 RSL_Artiste
Technique: SMLC
Machine: RSL_Artiste
No. beams: 9
No. segm.: 75
The following clinical goal(s) are clipped against the edge of the chart since their value is better than the max displayed:
OR; Anal Canal: At most 4500 cGy average dose (3517 cGy)
OR; Cap fem dex: At most 5.00 % volume at 5000 cGy dose (0.00 %)
OR; Cap fem sin: At most 5.00 % volume at 5000 cGy dose (0.00 %)

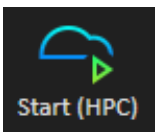
Figure 452. The illustration shows an example of information about the clipped value(s).

10.1.4 High Performance Computing (HPC) cluster

Plan Explorer includes a feature called High Performance Computing (HPC). HPC enables high-speed optimization calculations as the calculations are run in parallel across a cluster of computers. Because of the parallelism, the time to evaluate all the solutions is a lot shorter than if only one computer is used.

HPC is an add-on to Plan Explorer, which needs to be set up and configured by IT together with RaySearch. When the hardware is in place, HPC is configured from the ClinicSettings application and the tab called **HPC - High-Performance-Computing**. The normal user name and password is used to schedule optimization jobs to run on the cluster.

When the configuration is in place, it is possible to select have two start buttons in the Plan Explorer toolbar, one for optimizing exploration plans locally, **Start**, and another button for optimizing exploration plans on the HPC cluster, **Start (HPC)**.



Selecting two start buttons is done by checking the **Show both local and HPC buttons** option in the ClinicSettings application. If this is unchecked, the ordinary **Start** button will schedule work on the HPC cluster if it is correctly configured and available, but otherwise schedule work on the local node. The first time the **Start (HPC)** button is used, the system will prompt for user name and password. The rest is automatic.

For information on how to configure the HPC computation cluster in the ClinicSettings application, see *section D.2.7 HPC on page 937*.

10.1.5 Plan Explorer algorithm

Given a list of clinical goals and a plan setup, the Plan Explorer algorithm will generate a treatment plan. By clicking the **Start**/**Start (HPC)** button in Plan Explorer, the algorithm will start generating a treatment plan for the given setup. The treatment plan is created in order to fulfill the clinical goals in priority order. In order for the algorithm to work, certain inputs are needed from the user.

Inputs needed from the user

The user should provide one or more setup plans that each contains one of the treatment techniques supported by the algorithm (SMLC, DMLC or VMAT).

The plan properties that are taken into account by the algorithm are displayed and editable in the **Edit Exploration Plan** dialog. That includes the treatment setup, beam optimization settings and segmentation settings. If a plan would include optimization settings, clinical goals or optimization functions, the algorithm will ignore these and always use the goals specified in the Plan Explorer setup.

In order to create a good plan, the algorithm needs a list of clinical goals set up in priority order. It is important to note that the algorithm works strictly according to these priorities, i.e., it will never slack a goal of higher priority in order to fulfill a goal of lower priority if the goals are in conflict. Therefore, the list of clinical goals needs to be setup with great care. Note that the algorithm only supports clinical goals of the following types: DoseAtVolume, DoseAtAbsoluteVolume, AverageDose, VolumeAtDose and AbsoluteVolumeAtDose.

About the algorithm

The algorithm uses methods inspired by lexicographic optimization in order to find a treatment plan for the given inputs. It will try different optimization function setups in order to fulfill as many goals as possible according to their priorities.

The progress bar that can be seen in the Plan Explorer module shows in percent how many of the clinical goals that have been taken into account by the algorithm when creating the plan.

The generated plan

The plan generated by the algorithm can be copied to the plan list. This enables the user to see the plan in Plan Optimization or Plan Evaluation, which makes it possible for the planner to continue working on the plan if desired. The plan can also be directly evaluated in Plan Explorer using the **Compare** view. The plan will contain a set of optimization functions with dose function parameters and weights calculated by the algorithm.

10.1.6 Plan Explorer specific clinical goals

There are two types of clinical goals that are specific for the Plan Explorer module; **Reduce average dose** and **Dose Fall-Off**.

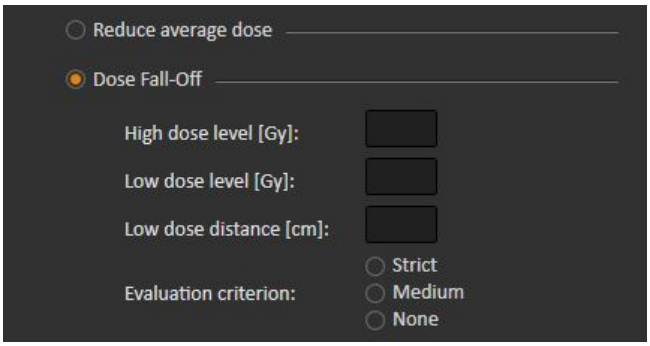


Figure 453. The clinical goals specific for the Plan Explorer module.

Both these goals are handled separately by Plan Explorer and the plan generation algorithm. They are used only as input to the algorithm and are not included in the radar charts or in the goal **Filters** tab, hence cannot be evaluated.

The **Reduce average dose** goal will give the algorithm input to try to lower the average dose to the organ at risk specified in the goal. It can be added to any priority group except for the first one. The algorithm will take the formerly achieved dose and gradually try to reduce it while keeping goals of higher priority fulfilled.

The **Dose Fall-Off** goal will add a dose fall-off function to the specified ROI using the high dose level, low dose level and low dose distance declared in the goal. This type of goal can either be applied to a target or to an organ at risk. If it is applied to an organ at risk, the goal must be the only goal of its priority. The clinical goal must specify if the evaluation criterion of the goal should be Strict, Medium or None. This will indicate the importance of the conformity and the dose fall-off.

- If choosing "Strict", the algorithm will try to tighten the conformity as much as possible using the given dose fall-off function, and will not allow it to be slacked in order to fulfill goals of lower priority.
- If choosing "Medium", the algorithm will allow some slack in the conformity on behalf of goals of lower priority, but not very much.
- If choosing "None", the algorithm will add the dose fall-off function and have it present during the optimization, but it will not slack lower prioritized goals in order to keep the achieved conformity.

10.1.7 Plan Explorer workflow

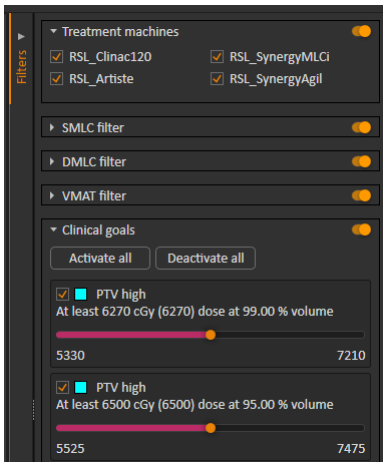
The Plan Explorer workflow consists of the following steps:

1. **Copy an existing Plan Exploration or set up a new Plan Exploration.** It is possible to copy an existing Plan Exploration by clicking the **Copy plan exploration** button. It is also possible to create a new Plan Exploration by following the instructions in *section 10.1.8 Set up Plan Exploration on page 818*.

   To delete a plan exploration, click the **Delete** button.

2. **Define clinical goals and generate Exploration plans**. For a new Plan Exploration, clinical goals and Exploration plans must be defined. For instructions, see *section 10.1.9 Generate Exploration plans on page 820*.

3. **Filter Exploration plans**. For instructions, see *section 10.1.10 Filter Exploration plans on page 822*.



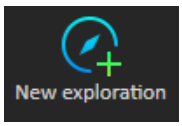
4. **Compare filtered plans and copy to plan list**. For instructions, see *section 10.1.11 Compare filtered plans and copy to Plan list on page 825*.

10.1.8 Set up Plan Exploration

To set up a Plan Exploration:

1. Click the **Setup** button to go to the Setup workspace.

2. Click the **New exploration** button.



This opens the **New Plan Exploration** dialog.

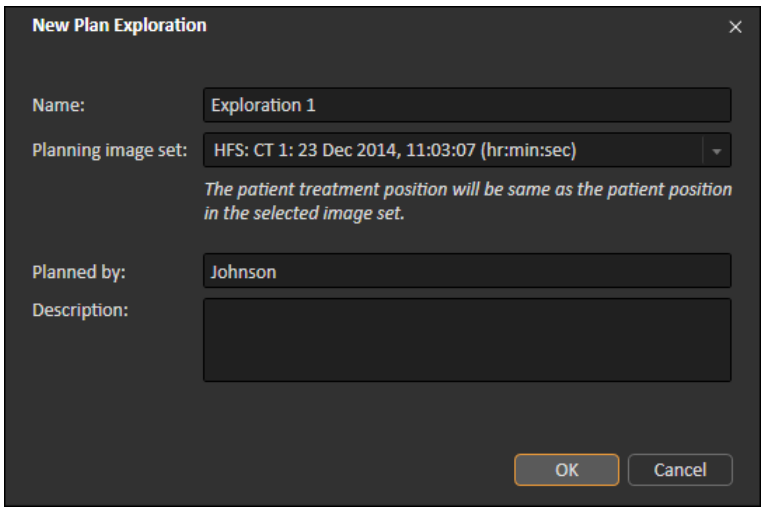


Figure 454. The **New Plan Exploration** dialog.

3. In the **New Plan Exploration** dialog:
   a. Enter a **Name** of the exploration.
   b. Select **Planning image set**.
   c. Enter information in the **Planned by** field (optional).
   d. Enter a **Description** in free text (optional).
   e. Click **OK**.

4. A default dose grid will be set when creating the new Plan Exploration. If desired, it is also possible to edit the dose grid. For more information, see *section 6.1.4 Define and edit the dose grid on page 312*.

5. Add the clinical goals from a template by clicking the **Load template** button, or add them manually by clicking the **Add physical...** button. For more information about adding or editing clinical goals, see *section 3.7.3 Clinical goals on page 81*.

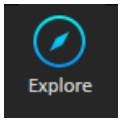
   Note that there are two additional types of clinical goals that are specific for the Plan Explorer module; **Reduce average dose** and **Dose Fall-Off**. For more information about these clinical goals, see *section 10.1.6 Plan Explorer specific clinical goals on page 815*.

6. Make sure to add a priority for each clinical goal in the list. The Exploration plan generation is dependent on the priority order of the clinical goals.

10.1.9 Generate Exploration plans

To generate a set of Exploration plans:

1. Click the **Explore** button to go to the Explore workspace.



2. Click the **Load template** button to open the **Load Template** dialog.

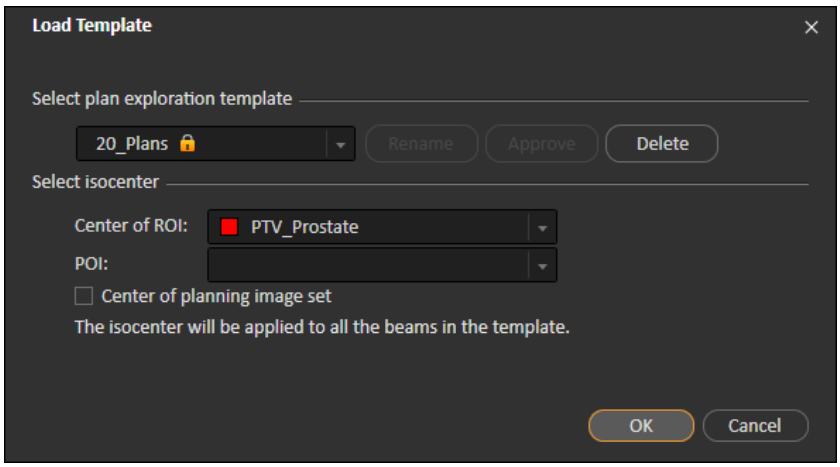


Figure 455. The **Load Template** dialog.

3. In the **Load Template** dialog:

   a. Select an existing Plan Exploration template, containing the plans with the desired treatment techniques and treatment setups, in the drop-down list. If no such template exists, create a template according the instructions in *section 10.1.12 Create Plan Exploration template on page 826*.

   To rename the selected template, click **Rename** and enter a new name for the template. To delete the selected template, click **Delete**.

   To approve a template, click **Approve**. Only admin users can approve a template. Approved templates have a padlock next to the template name. If a non-approved template is loaded, a warning will be displayed. These warnings can be disabled in Clinic Settings. For more information on template approval, see *Approval of templates on page 43*.

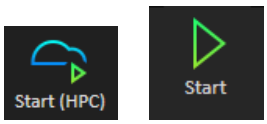
   b. Define the isocenter position for the beams:

      - If the isocenter shall be in the center of an ROI, select an ROI from the **Center of ROI** drop-down list.

- If the isocenter shall be in the same position as a POI position, select a POI from the **POI** drop-down list.
- If the isocenter shall be in the center of the planning image set, select the **Center of planning image set** checkbox.

c. Click **OK**.

4. In order for the algorithm to work, provide input according to *Inputs needed from the user on page 814*.
5. Select the plans that should be included in the exploration. If all of the plans should be included, press Ctrl + A.
6. To start the optimization and dose calculation for the selected plans, click the **Start (HPC)** button or the **Start** button. Both start buttons can be visible, the visibility depends on the HPC configuration in the Clinic Settings application. For information about HPC, see *section 10.1.4 High Performance Computing (HPC) cluster on page 813*.



When the plan generation has completed, the generated plans have segments and clinical dose. The quality of the plan with respect to fulfillment of the clinical goals can be assessed using the radar charts in the plan thumbnails.

How to interpret the radar chart in the Exploration plan thumbnail is described in *section 10.1.2 Exploration plan thumbnails on page 807* and *section 10.1.3 Radar chart in the Exploration plan thumbnails on page 808*.

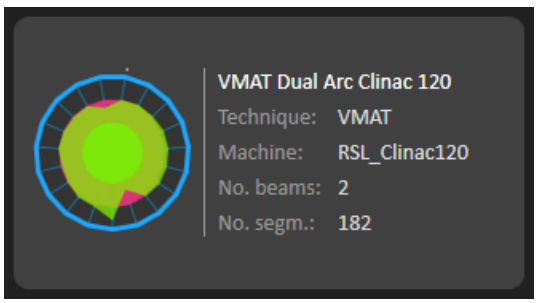


Figure 456. Exploration plan thumbnail.

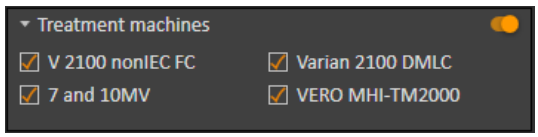
7. After the automatic plan generation has completed, the next step is to find the smallest set of plans that shall be evaluated in detail (*section 10.1.10 Filter Exploration plans on page 822*).

10.1.10 Filter Exploration plans

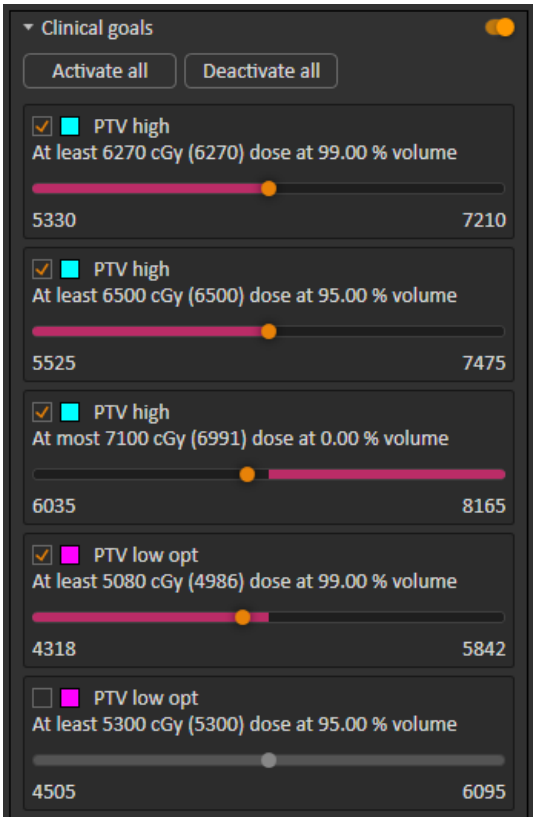
When Exploration plans are available it is possible to find a subset of the Exploration plans that fulfill specific properties using filters. Filters for the treatment techniques SMLC, DMLC and VMAT will be available when such plans are present.

To filter the Exploration plans:

1. Go to the Explore workspace and the **Filters** tab.
2. Filter out plans based on treatment machines:
    a. Activate the **Treatment machines** filter by toggling the slider button in the upper right corner.
    b. Check checkboxes of the machine(s) of interest. The plans using the unchecked machines will be filtered out.



3. Filter out plans based on the value of a clinical goal:
    a. Activate the **Clinical goals** filter by toggling the slider button in the upper right corner.
    b. Check the checkboxes of the clinical goals of interest.
    c. Set the slider to the acceptance level value for each selected clinical goal. The plans that do not fulfill the acceptance level will be filtered out.



4. Filter out plans based on treatment technique parameters for SMLC, DMLC and/or VMAT:
   a. Activate the filter by toggling the slider button in the upper right corner.
   b. Check the checkboxes of the parameter(s) of interest.
   c. Set the slider to the desired threshold value for each parameter.

   Treatment technique parameters for SMLC (when applicable):

   - **Max number of beams**
   - **Max number of segments**
   - **Max total MU**

   Treatment technique parameters for DMLC and VMAT (when applicable):

   - **Max number of beams**
   - **Max total MU**

5. If desired, alter the tuning parameters in the lower left part of the workspace:
   - Check the **Hide filtered out plans** checkbox to hide all plans that have been filtered out.
   - Change the **Detail level** for the Exploration plans by using the corresponding slider.
6. If desired, scale the min/max values of the clinical goals in the plan thumbnails by clicking the **Set min/max** button. For more information see, *Scale in the radar chart on page 812*. Only SMLC, DMLC och VMAT are supported.

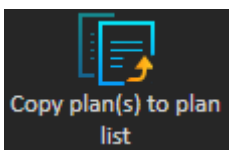
10.1.11 Compare filtered plans and copy to Plan list

To compare the filtered Exploration plans in detail and to copy the best plan(s) to the Plan list in order to be able to use them for treatment planning in RayStation:

1. Click the **Compare** button to go to the Compare workspace.

2. Set a suitable plan (the plan that from a first assessment of the radar charts seems to be the best plan) as the Candidate plan by selecting it and clicking the **Set candidate plan** button in the lower part of the workspace. The Candidate plan appears as the left plan in the side-by-side view. The thumbnail of the Candidate plan is highlighted with a solid orange line.
3. Set a plan as the Challenger plan by selecting it and clicking the **Set challenger plan** button in the lower part of the workspace. The Challenger plan appears as the right plan in the side-by-side view. The thumbnail of the Challenger plan is highlighted with a dotted orange line.
4. Select a plan to compare the challenger plan with by clicking the plan and then the **Set challenger plan** button in the lower part of the workspace.
5. Study the plans side-by-side and compare the necessary information such as Clinical Goals, Dose Statistics, DVH curves, Beams, Control points and the BEV. For more information, see the *section 8.1.5 The evaluation graphs on page 731*.

   In the Plan Explorer Compare workspace, each plan has a separate Clinical goals list to simplify plan comparison.
6. Compare the rest of the challenger plans with the candidate plan. Always set the best plan as the candidate plan.
7. If desired, it is also possible, for comparison only, to copy plans of other treatment modalities than photons and other treatment techniques than SMLC, DMLC and VMAT. All plans but carbon ion plans can be imported for comparison.
8. When the best plan(s) have been selected, they need to be copied to the Plan list by clicking the **Copy plan(s) to plan list** button. Once the plan(s) have been copied to the Plan list, they will be available in the rest of the RayStation modules.



10.1.12 Create Plan Exploration template

In the Plan Explorer module it is possible to create a Plan Exploration template that contains a number of Exploration plans with representative treatment setups. The Exploration plans should also have representative segmentation settings since this affects the outcome of the automatic plan generation.

To create a Plan Exploration template:

1. Set up a Plan Exploration in Plan Explorer according to the instructions in *section 10.1.8 Set up Plan Exploration on page 818*.
2. In order for the algorithm to work, provide input according to *Inputs needed from the user on page 814*.
3. Go to the Explore workspace.
4. Click the **New** button to open the **New Exploration Plan** dialog.

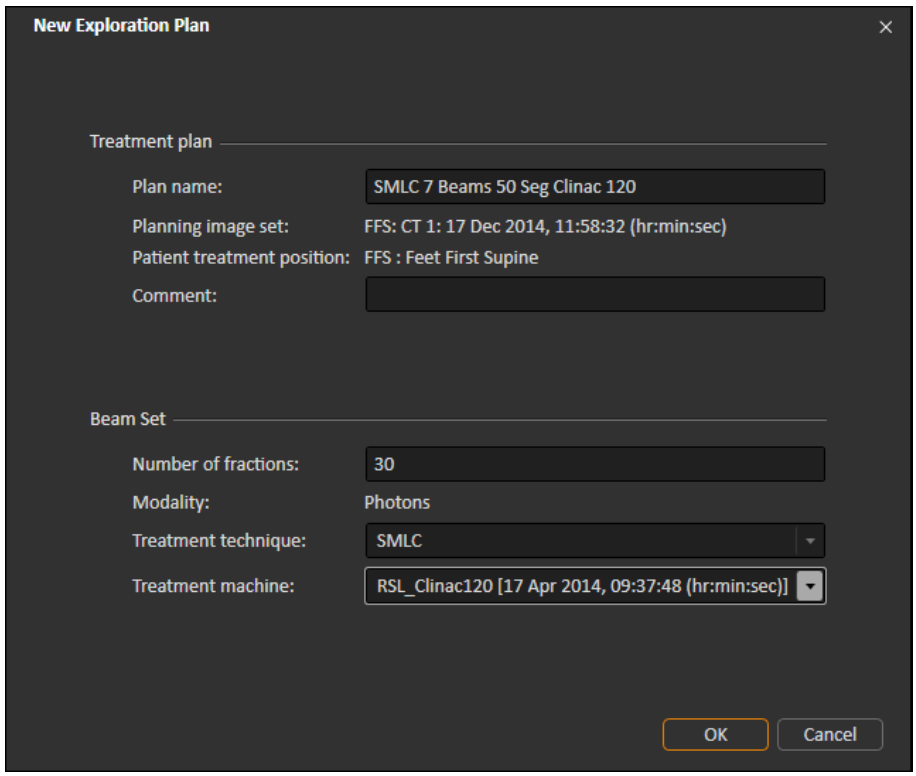


Figure 457. The **New Exploration Plan** dialog.

5. In the **New Exploration Plan** dialog, enter the **Plan name**, **Comment** (optional), **Number of fractions** and select **Treatment technique** and **Treatment machine** and click **OK**.

The **Edit Exploration Plan** dialog will open automatically once the **New Exploration Plan** dialog has closed.

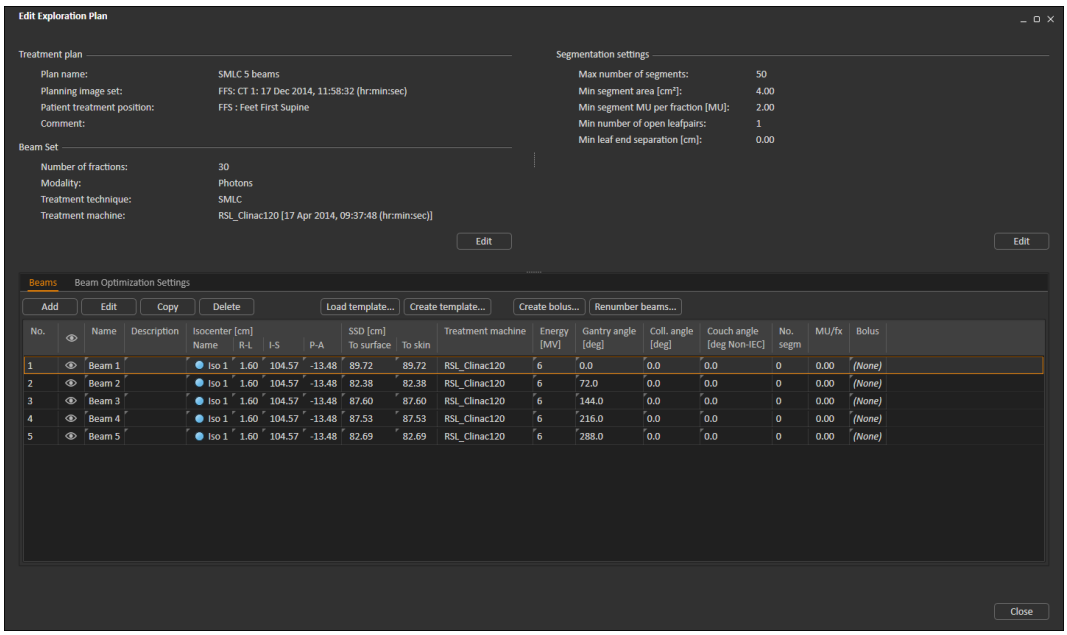

Edit Exploration Plan
Treatment plan
Plan name: SMLC 5 beams
Planning image set: FFS: CT 1: 17 Dec 2014, 11:58:32 (hr:min:sec)
Patient treatment position: FFS : Feet First Supine
Comment:
Beam Set
Number of fractions: 30
Modality: Photons
Treatment technique: SMLC
Treatment machine: RSL_Clinac120 [17 Apr 2014, 09:37:48 (hr:min:sec)]
Edit
Segmentation settings
Max number of segments: 50
Min segment area [cm²]: 4.00
Min segment MU per fraction [MU]: 2.00
Min number of open leafpairs: 1
Min leaf end separation [cm]: 0.00
Edit
Beams
Beam Optimization Settings
Add
Edit
Copy
Delete
Load template...
Create template...
Create bolus...
Renumber beams...
No.
Name
Description
Isocenter [cm]
Name
R-L
I-S
P-A
SSD [cm]
To surface
To skin
Treatment machine
Energy [MV]
Gantry angle [deg]
Coll. angle [deg]
Couch angle [deg Non-IEC]
No. segm
MU/fx
Bolus
1 Beam 1 Iso 1 1.60 104.57 -13.48 89.72 89.72 RSL_Clinac120 6 0.0 0.0 0.0 0 0.00 (None)
2 Beam 2 Iso 1 1.60 104.57 -13.48 82.38 82.38 RSL_Clinac120 6 72.0 0.0 0.0 0 0.00 (None)
3 Beam 3 Iso 1 1.60 104.57 -13.48 87.60 87.60 RSL_Clinac120 6 144.0 0.0 0.0 0 0.00 (None)
4 Beam 4 Iso 1 1.60 104.57 -13.48 87.53 87.53 RSL_Clinac120 6 216.0 0.0 0.0 0 0.00 (None)
5 Beam 5 Iso 1 1.60 104.57 -13.48 82.69 82.69 RSL_Clinac120 6 288.0 0.0 0.0 0 0.00 (None)
Close

Figure 458. The **Edit Exploration Plan** dialog.

6. In the **Edit Exploration Plan** dialog, it is possible to:

   a. add, edit or copy beams in the **Beams** tab in the same way as described in *section 6.1.6 Add, edit, copy or delete beams on page 316*. A Beam Dose Specification Point cannot be selected or created in the Plan Explorer module.

   b. create and load templates in the **Beams** tab in the same way as described in *section 6.1.7 Beam list templates on page 328*.

   c. edit the beam optimization settings in the **Beam Optimization Settings** tab in the same way as described in *section 7.1.9 Beam optimization settings on page 542*. All optimization variables will not be available in the Plan Explorer module.

   d. edit the settings for the treatment plan and beam set by clicking the corresponding **Edit** button.

   e. edit the segmentation settings by clicking the corresponding **Edit** button.

   Note: *Boluses are not stored in beam and Plan Exploration templates. Thus the use of boluses needs to be configured after a template has been applied.*

7. When the Exploration plan has been edited as desired, **Close** the **Edit Exploration Plan** dialog.
8. Create as many Exploration plans as desired (by repeating steps 4 to 7).

9. Click **Create template...** button to create a Plan Exploration template of all the plans in the Exploration.

10.2 THE AUTOMATED BREAST PLANNING MODULE

The Automated Breast Planning module provides tools for automated generation of tangential breast IMRT plans using heuristic optimization.

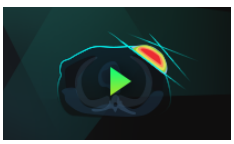
The module includes features such as:

- automatic detection of radio-opaque markers which helps the algorithm to identify the breast
- automatic contouring of all the relevant target and risk organs
- automatic setup of beams with skin flash and optimization of gantry and collimator angles
- automatic selection of SMLC optimization and segmentation settings
- dose statistics, DVH, clinical goal evaluation etc.

Note: *The Automated Breast Planning is implemented for machines with MLC in the x-direction and is not supported for machines with MLC in the y-direction.*

WARNING!

Automated Breast Planning. The patient has to be prepared with a precise setup of radio-opaque markers and wire before CT scanning. It is crucial that the placement of the markers and the shape of the External ROI are correct. These need to be carefully reviewed before continuing the automated plan generation process. Target ROIs and OAR ROIs are generated based on the markers. The resulting ROIs also depend on image quality and patient anatomy. Always verify the outcome of the automatic ROI generation. (117531, 117732)



Reference

T.G. Purdie et al., "Automated Planning of Tangential Breast Intensity-Modulated Radiotherapy Using Heuristic Optimization", Int. J. Radiation Oncology Biol.Phys. Vol. 81, No.2, pp. 575-583, 2011.

In this section

This section contains the following sub-sections:

10.2.1	Patient Setup Protocol	p. 831
10.2.2	The Automated Breast Planning user interface	p. 834
10.2.3	The Automated Breast Planning commands	p. 835
10.2.4	The Automated Breast Planning settings	p. 837

10.2.1 Patient Setup Protocol

In order to use the Automated Breast Planning module, the patient must be prepared with four radio-opaque markers (BB's) and a radio-opaque wire below the breast.

The ipsilateral arm (arm on the treated side) should be raised on the arm support to achieve an angle greater than 90° to the patient's body.

For one-arm raised setup: The arm on the contralateral side should rest at the patient's side (as shown below).

For two-arms raised setup: The arm on the contralateral side should be raised into same position as the ipsilateral arm.

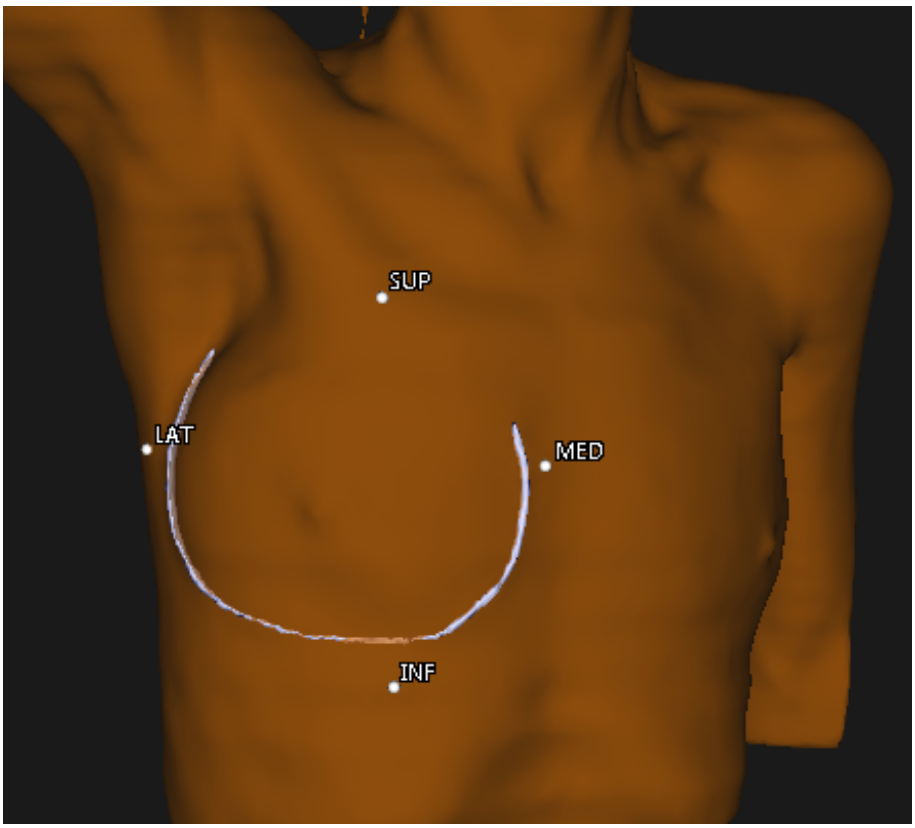


Figure 459. Example of marker and wire placement.

Wire placement

- Lumpectomy: The wire should be placed around the breast tissue.
- Mastectomy: The wire should be placed medially on the chest where the breast would have been (use the contra-lateral breast as a guide).

Note: *The wire must not be covered by breast tissue. If the breast is resting on the chest, the wire should be placed around the contour of the resting breast.*

Marker placement

Four BB's should be placed on the skin at the following locations:

- Superior marker: 1.5 cm superior to breast tissue or the level of suprasternal notch, whichever is more superior.
- Inferior marker: 1.5 cm below the inframammary crease or the lowest part of the breast (whichever is more inferior), in the same sagittal plane as the superior marker.
- Lateral marker (TTH): 1.5 cm posterior to the wire around the breast, in plane of the largest breast contour.
- Medial marker: 1.0 cm medial to breast wire and should not cross over to the midline, in the same transversal plane as the lateral marker.

Note: *If the scar crosses midline, the medial marker should be placed at midline.*

Special consideration for chest wall treatments

For patients that have had a mastectomy instead of a lumpectomy, ensure that the contralateral arm is raised into same position as the ipsilateral arm when placing BB's.

The laser and BB's should be placed as follows:

- Superior: Place laser on superior-most aspect of the contralateral breast. Place BB 1.5 cm superior to laser on ipsilateral side.
- Inferior: Place laser on inferior-most aspect of the contralateral breast. Place BB 1.5 cm inferior to laser on ipsilateral side.
- Medial: Place laser 1.0 cm medial of the contralateral breast. Measure the distance from midline. Place the BB at the same distance from medial measured on the ipsilateral side.
- Lateral: Place laser at posterior-most aspect of the contralateral breast. Place BB 1.5 cm posterior to laser on ipsilateral side.

Following the placement of the BB's, the patient can be returned to the final position for simulation scanning:

- For one-arm raised setup: the contralateral arm is moved back down.
- For two-arms raised setup: the contralateral arm remains raised.

Material requirements

The detection algorithms are not sensitive to the size of the markers or thickness of the breast wire. However, the algorithms have only been validated with 1.5 mm lead balls and 0.3 mm covered lead wire. If other sizes are used, special care should be taken to verify that the result of the detection is correct.

Note: *A recommendation is to use wire with diameter 0.3 mm. Thicker wires may produce artifacts that can cause the wire detection to fail.*

10.2.2 The Automated Breast Planning user interface

Workspace

The top left corner shows the dose for each visualized ROI in a dose volume histogram (DVH). Behind the DVH are tabs for dose statistics as well as for review of clinical goals.

There are three patient views which show image set data for the current plan in **2D**, **3D** or Beam's Eye View (**BEV**).

The bottom of the workspace shows the beam list. There are also tabs for the control point list and the objectives/constraints list.

Figure 460. The Automated Breast Planning module workspace.

10.2.3 The Automated Breast Planning commands

Preparation

Import new patient
Use the Import new patient dialog to create a new patient by importing CT data.

Note: *An optional structure set with a contoured operation scar (cavity) may also be imported. In order for the algorithm to recognize this ROI, it has to be named "cavity" (case insensitive). The cavity may also be manually contoured in the Patient Modeling module after import.*

New plan
Once the CT data is imported, a plan can be created. The new plan will use photon modality and SMLC treatment technique. It may only have one beam set. A prescription is set to the ROI "aCTV" according to the dose specified in the dialog. If this ROI does not exist, it will be created.

The plan may also be created in the Plan Design module or be imported. In this case, it still needs to be a photon SMLC plan with one single beam set, and the prescription must be set up manually as average dose to "aCTV".

Image set properties
If the imaging system has not been automatically detected during import, an imaging system must be selected before POI Detection and Plan Generation can be started.

Settings
Open the Settings dialog to adjust settings which affects structure set and plan generation. For a detailed description of each setting, see *section 10.2.4 The Automated Breast Planning settings on page 837*.

POI detection

Pressing the **Detect** button will auto-detect the Superior, Inferior, Medial and Lateral radio-opaque markers (see *Marker placement on page 832*) and create the POIs "SUP", "INF", "MED" and "LAT", respectively. It will also create an anterior point, "ANT". An external ROI will be created, and the algorithm will attempt to remove the CT couch from that ROI. The distance between the bottom part of the couch and the patient can be adjusted with the **Couch to immobilization distance** setting in the Settings dialog. Both the markers and the external ROI may be manually adjusted if needed, using the tools in the Patient Modeling module.

Plan generation

Pressing the **Start** button will start the automated plan generation process. This process consists of four steps. Each step will result in a separate undo item on the Undo list.

1. **Create structures from atlas**

   The lungs and the heart structures are created from the structure template atlas specified in the Settings dialog.

Note: *If the plan's examination set already has the ROIs "aLTLUNG", "aRTLUNG" and "aHEART" contoured, this step will be skipped. In order to re-run the step (for example if a new atlas has been chosen), these ROIs needs to be manually renamed or removed.*

2. **Generate plan**

   This steps creates a number of auxiliary ROIs including the target "aCTV", the breast wire "aWIRE" and other ROIs used internally by the algorithm. It then creates two beams, A1 and A2, with one initial segment each, and two empty beams, A1_OPT and A2_OPT. Finally, it adds optimization functions and clinical goals based on the prescription specified in the New plan dialog.

3. **Optimization**

   This step optimizes the MU of beams A1 and A2, as well as the segment shapes and MU of the beams A1_OPT and A2_OPT, using the optimization functions and segmentation settings created by the previous step.

4. **Merge beams**

   This step merges beam A1 with A1_OPT and A2 with A2_OPT, and calculates a final dose. If the beams have different energies, they will not be merged (see the **High Energy** setting in *section 10.2.4 The Automated Breast Planning settings on page 837*)

Note: *The final beams A1 and A2 will contain one generated segment and a number of optimized segments. To be able to continue the optimization in the Plan Optimization module, the Merge beams step has to be undone first. After having continued the optimization, the beams can be manually merged again.*

Pressing the **Start** button again will re-start the automated plan generation process and update the current patient and plan using the current settings. The **Create structures from atlas** step will be skipped if the ROIs "aLTLUNG", "aRTLUNG" and "aHEART" already exist. This allows for manual contouring adjustments to these ROIs after the atlas-based segmentation.

Approval

Use the **Approve button** to open the Approve plan workspace, see *section 8.1.15 Plan approval on page 748*.

Use the **Create Plan Report** button to open the Select Report Template dialog, see *section 4.3.8 Create a plan report on page 130*.

Use the **Export** button to open the DICOM Export dialog, see *section 4.4 Export patient data on page 132*.

10.2.4 The Automated Breast Planning settings

To edit the Automated Breast Planning settings, click the **Settings** button.

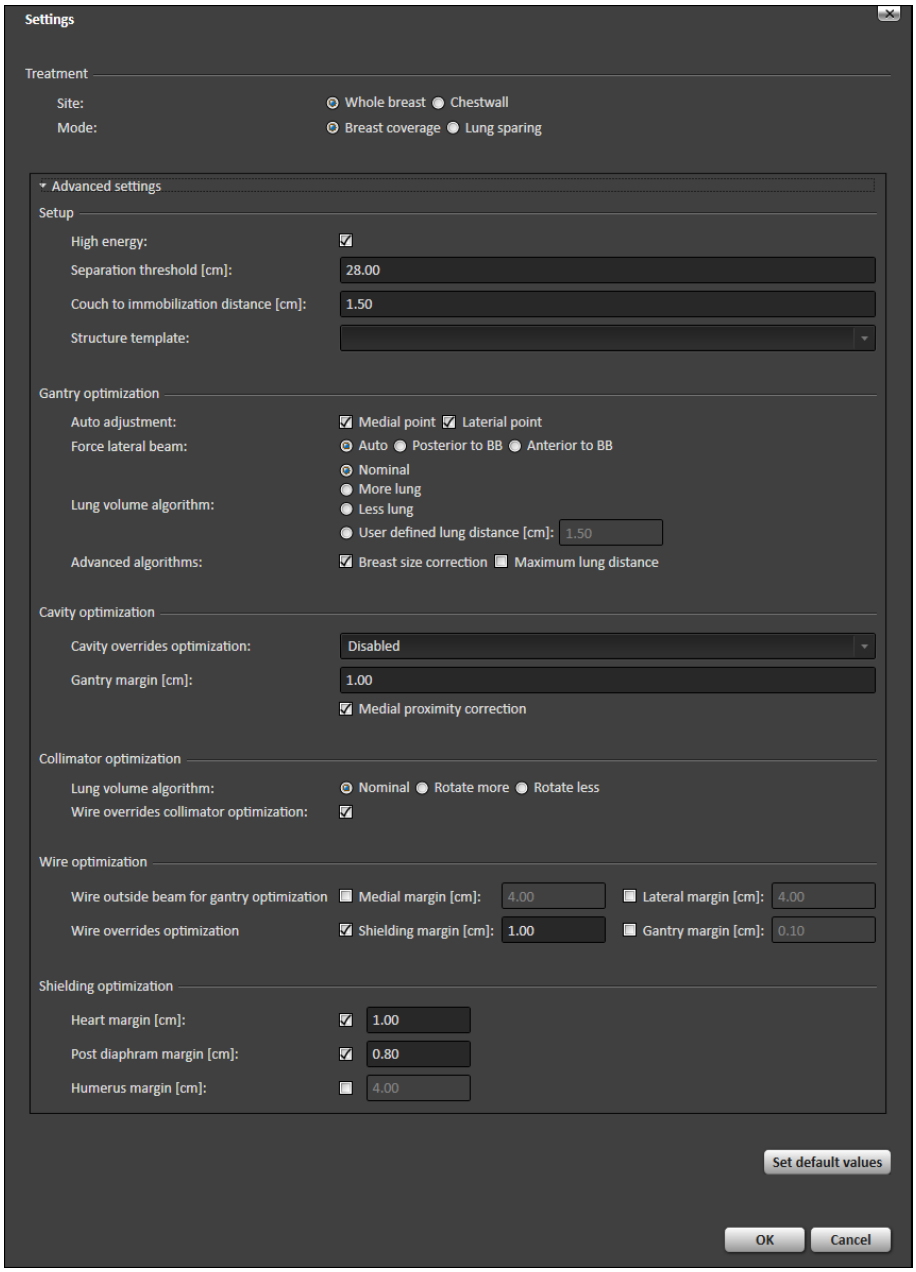


Figure 461. The Setting dialog for Automated Breast Planning.

Treatment settings

Parameter	Description
Site	Selecting the **Whole breast** or **Chestwall** option will enable a specific set of advanced default settings that are site specific.
Mode	Selecting either the **Breast coverage** or the **Lung sparing** option will enable a specific set of advanced default settings based on the treatment intent. The **Breast coverage** option will ensure the whole breast volume is in the treatment beams. The **Lung sparing** option will allow the breast coverage to be compromised (if necessary) in order to reduce the lung volume. ***Note:*** *The Cavity will still be covered by the specified margin unless explicitly de-selected.*

WARNING!

Treatment settings for Automated Breast Planning. Note that the advanced settings may be edited after selecting treatment settings Site and Mode. Hence, the advanced settings might not reflect the current status of the Site and Mode buttons. (117649)

Setup settings

Parameter	Description
High energy and **Separation threshold**	If **High energy** is enabled, and the longest diagonal of the breast volume in any slice is larger than the **Separation threshold**, and the selected treatment machine has more than one energy, the optimized segments will use the highest available energy. Otherwise, all segments will use the lowest available energy.
Couch to immobilization distance	During the POI detection step, the external ROI is created and the algorithm tries to remove the CT couch from it. This setting controls how far above the CT couch the external ROI will be cut.
Structure template	This setting allows the user to specify a custom structure template for generation of the lungs and the heart. If **Default** is selected, the template "ABPDefaultData – HeartAndLung" will be used. This template needs to be installed separately by importing it in the Patient Modeling workspace. A custom template must contain ROIs named "Lung (Left)", "Lung (Right)" and "Heart".

Gantry optimization settings

The Medial point ("MED" POI) and Lateral point ("LAT" POI) will be copied to the points "optMED" and "optLAT", defining the medial and lateral aspects of the beam respectively.

The gantry optimization will move these points until a certain amount of lung volume is inside the beams. These points determine the gantry angle, since the beams will be generated through the points. The following settings control this optimization:

Parameter	Description
Auto adjustment – **Medial point** and **Lateral point**	This setting specifies whether the Medial point and/or the Lateral point are adjusted by the algorithm or whether the points are fixed. **Example:** If the clinical intent is to ensure that the medial aspect of the breast is covered, the user can choose to force the beam to pass through the initial Medial point by de-selecting the **Auto adjustment** of the **Medial point**.
Force lateral beam	This setting controls whether the Lateral point is moved up or down by the algorithm. The **Auto** option determines the direction automatically based on the lung volume encompassed by the tangential beams that passes through the Medial and Lateral points. The **Posterior to BB** or **Anterior to BB** options can be used to force the algorithm to move the lateral part of the beam either posterior or anterior. **Example:** If there is very little lung in the field with the beams initially passing through the Medial and Lateral points, and the clinical intent is to minimize the amount of lung further, in Auto mode, the algorithm would attempt to increase the lung in the field by moving the Lateral point posterior to the BB. However, the user can select the **Anterior to BB** option to make sure that the algorithm do not increase the lung in the field and force the gantry optimization to only place the lateral aspect of the beam anterior to the Lateral point.

Parameter	Description
Lung volume algorithm and **Maximum lung distance**	The **Lung volume algorithm** controls the target lung volume of the gantry optimization algorithm. • The **Nominal** option aims to include a lung volume consistent with clinically acceptable values. • The **More lung** option sets the target lung volume to a higher value, that is, allow more lung in beam. • The **Less lung** option sets the target lung volume to a lower value, that is, allow less lung in beam. • The **User defined lung distance** option allows the user to enter a specific target lung distance. The user can specify the target lung volume based on the 1) maximum lung distance by also selecting the **Maximum lung distance** option in the **Advanced algorithms** or 2) mean lung distance by de-selecting the **Maximum lung distance** option. **Example**: If a patient has had previous treatment and the intent of treatment is to spare more lung than is typically accepted, the **Less lung** option can be selected. **Example**: If a patient with poor lung function cannot have more than 0.5 cm of lung in the beam, the user can select the **User defined lung distance** option with a value of 0.5 cm and also select the **Maximum lung distance** option.
Breast size correction	The **Breast size correction** option in the **Advanced algorithms** changes the target volume value the algorithm is striving to achieve based on the breast volume. This includes both a small volume and large volume correction.

Cavity optimization settings

Parameter	Description
Cavity overrides optimization and **Gantry margin**	If the **Cavity overrides optimization** setting is enabled, the gantry optimization algorithm will further optimize the gantry angle by ensuring that the minimum distance between the Cavity ROI specified and the beam edge is greater than the **Gantry margin** selected. A negative margin implies that the beam can go inside the Cavity ROI by the margin specified. ***Note:*** *Cavity delineation is optional. If no ROI named "cavity" (case insensitive) exists, the cavity optimization will be disabled regardless of the setting.*

Parameter	Description
Medial proximity correction	If this setting is enabled, and the cavity is more than 5 cm closer to the lateral than the medial point, the cavity optimization will only move the lateral point, not the medial point.

Collimator optimization settings

The goal of the collimator optimization is to minimize the amount of lung and normal tissue in the beam by rotating the collimator angle.

Parameter	Description
Lung volume algorithm	This setting makes the collimator **Rotate more** or **Rotate less** when the collimator angle determined by the **Nominal** algorithm is not desirable.
Wire overrides collimator optimization	Selecting this option ensures that the collimator angle determined by the optimization is selected so that the beam will still encompass the wire that was in the field following gantry optimization. De-selecting this option makes the collimator optimization only look at the lung volume in the field.

Wire optimization settings

The wire optimization will further optimize the gantry angle by ensuring that the minimum distance between the wire and the beam edge is greater than the margins selected. A negative margin would imply that the beam could go inside the wire by the margin specified.

Parameter	Description
Wire outside beam for gantry optimization	If **Medial margin** and/or **Lateral margin** is selected, the medial and/or lateral aspect of the beam may be placed so that parts of the wire are outside of the field in the isocenter slice, up to the specified margin.
Wire overrides optimization	If the **Shielding margin** option is selected, the wire will be unshielded in the first segment up to the specified margin. If the **Gantry margin** option is selected, the gantry angle will be chosen so that the minimum distance between the wire and the beam edge is greater than the specified margin.

Shielding optimization settings

The algorithm allows automated shielding of normal structures. The shielding margins in this section, **Heart margin**, **Post diaphragm margin** and **Humerus margin**, specify the amount of normal tissue allowed in the field. Therefore, if the user wants to completely shield a particular normal structure, the shielding margin should be set to 0.0 cm. The shielding specified here will be superseded by the **Shielding margin** specified in the **Wire overrides optimization** above.

Set default values

Pressing the **Set default values** button resets all the settings to their default values.

10.3 THE FALLBACK PLANNING WORKFLOW

Fallback planning is used to create backup plans for other machines to fall back on in case the treatment machine used for treating a patient becomes unavailable. This makes it possible to treat a patient on another machine, possibly with a different modality and/or treatment technique, without having to re-plan for the other machine at machine failure. If the original treatment machine becomes available again, it is also possible to convert back to the original plan.

It is recommended to create the fallback plans prior to the patient's treatment start so that they are available at any time in case of machine unavailability. To create fallback plans, fallback protocols must first be created. Fallback protocols define a treatment setup configuration that is suitable as a backup for a given treatment setup. The protocols contain information such as the modality, beams, machine and optimization settings for creating the fallback plan.

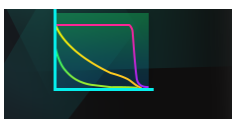
This section describes a suggested workflow for the entire fallback planning process, including how to create fallback protocols and fallback plans. Fallback planning can also be used for imported dose.

The Fallback Planning workflow is divided into six main parts:

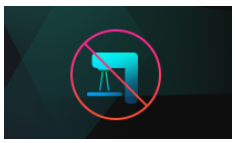
1. **Decide upon a fallback strategy** - preferably done in advance (before treatment planning)
2. **Create template plans for fallback** (Plan Setup module) - preferably done in advance (before treatment planning)

3. **Define fallback protocols** (Fallback Protocol Management module) - preferably done in advance (before treatment planning)

4. **Create fallback plans** (Plan Evaluation module) - preferably done every time a treatment plan is approved



5. **Select and approve fallback plan for delivery** (Fallback Planning module) - done when a treatment machine becomes unavailable



6. **If applicable, convert back to the original plan** (Fallback Planning module) - possible to do if the treatment machine becomes available again

Part 1. Decide upon a fallback strategy

Prior to creating the fallback protocols and the template plans, the user needs to reflect on a fallback strategy that determines what type of fallback plans should be available. The user can for example consider the following:

- the types of machines available in the clinic
- the treatment techniques that the machines can deliver
- the number of beams and their configuration where applicable

It might be preferable to use different fallback strategies for prostate and head and neck cases. In this case, name the plan types after the disease. Or, it might be preferable to use different fallback strategies for VMAT and PBS plans. In this case, name the plan types after the treatment technique.

Once it has been decided what kinds of fallback plans to create, the next step is to create template plans that match the fallback strategy.

Part 2. Create template plans for fallback (Plan Setup module)

In the Plan Setup module, create template plans for fallback that match the fallback strategy according to the instructions in *section 6.1.22 Create template plans for fallback planning on page 382*.

For example, the fallback plans for a PBS plan can be a VMAT plan and a 7-beam SMLC plan. Another example would be to use a similar treatment setup as the original plan but with an alternative treatment machine.

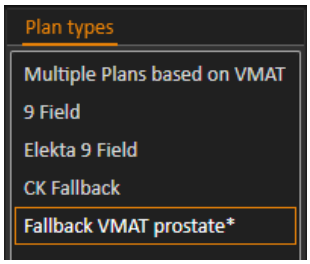
Part 3: Define fallback protocols (Fallback Protocol Management module)

It is recommended to define the fallback protocols in advance and before starting the treatment planning.

To define the fallback protocols in the Fallback Protocol Management module:

1. **Create the desired plan types** according to the instructions in *Step 1. Create a fallback plan type on page 858*.

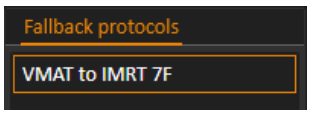
   A fallback plan type can be thought of as a group of similar protocols that can be applied to a patient for fallback planning.



2. **Select the plans to use for fallback protocol creation** according to the instructions in *Step 2. Select the plans to use for fallback protocol creation on page 859*.

3. **Perform dose mimicking optimization** according to the instructions in *Step 3. Perform dose mimicking optimization on page 859*.

4. **Create a fallback protocol.** Once the mimic dose operation is satisfactory, create a fallback protocol according to the instructions in *Step 4. Create a fallback protocol based on the template plan on page 861*.



5. **Edit the protocol steps (optional)** according to the instructions in *Step 5. Manually edit the protocol steps as desired (optional) on page 862*.

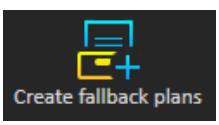
6. **Create as many fallback protocols as desired.** Repeat steps 3 to 5 to create as many fallback protocols as needed for the template plans in each plan type.

   Once the relevant plan types with protocols have been created, fallback planning can be used for patients.

Part 4: Create fallback plans (Plan Evaluation module)

Fallback plans can be created at any time after plan approval. It is recommended to create fallback plans directly after a treatment plan has been approved to be prepared if a treatment machine becomes unavailable.

Create a fallback plan in the Plan Evaluation module according to the instructions in *section 8.1.16 Create fallback plans on page 755*.



Note: *The original plan will in most cases not be the same as the one used as "Plan to mimic" when the protocol was created. It is recommended to set up the plan type and it's protocols once, and then reuse them for a lot of plans. The time consuming part of the Mimic dose operation is completely dependent on the original plan's dose, and hence needs to be recalculated for each original plan.*

Part 5: Select and approve fallback plan for delivery (Fallback Planning module)

If a treatment machine becomes unavailable, one of the created fallback plans can be selected for delivery of the remaining fractions.

To select and approve a fallback plan for delivery in the Fallback Planning module:

1. **Evaluate the created fallback plans and select the best fallback plan for delivery.** For more information, see *section 10.4.2 Evaluating fallback plans on page 851*.
2. **Enable editing and approval of the fallback plan.** To be able to edit and approve the fallback plan as well as to continue delivery from the fallback plan, it needs to be copied to the plan list. This is done according to the instructions in *section 10.4.3 Enable editing and approval of a fallback plan on page 852*.
3. **Final adjustments of the fallback plan.** Once the fallback plan is available in the plan list, it can be set to the active plan (current plan) in RayStation.

   Verify that the plan dose for the fallback plan is as intended. The plan dose will be the sum of the delivered fractions from the original plan (background dose) and the future fractions from the fallback plan (beam set dose).

   If necessary, the fallback plan can be further optimized in the Plan Optimization module prior to plan approval. The fallback dose mimic is automatically added as a Dose reference function.

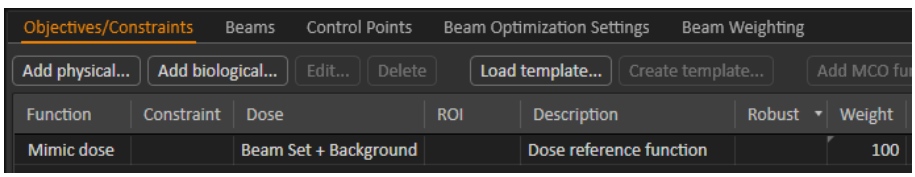
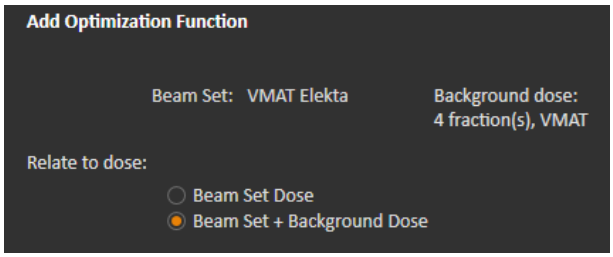


Figure 462. The fallback dose mimic is automatically added as a Dose reference function in the Plan Optimization module.

Add the desired optimization functions to the plan. The optimization functions will refer to either the beam set dose only or to the beam set + background dose, where the background dose will be the sum of the delivered fractions from the original plan.



The optimization problem for fallback planning is the same as when optimizing with multiple dependent beam sets and having a background dose dependency. For more information, see *section 7.1.19 Multiple beam set optimization on page 557*.

4. **Approve the fallback plan.** Before the fallback plan can be used for delivery, it needs to be approved. Plan approval is performed as usual in the Plan Evaluation module, see *section 8.1.15 Plan approval on page 748*.

   The usual methods of exporting and QA also applies for the fallback plan.

5. **Treat the patient for as many fractions as required with the fallback plan.**

6. **Repeat procedure if needed.** If the treatment machine of the fallback plan becomes unavailable, it is possible to repeat this part of the workflow and select a new fallback plan for delivery.

To see the total sum of the completed treatment plan, use **Sum doses** in Plan Evaluation. For more details, see *section 8.1.6 Dose summation on page 733*.

Part 6: If applicable, convert back to the original plan (Fallback Planning module)

If needed, it is possible to return to the original plan and select it for delivery of the remaining fractions. This may for example be the case if a broken treatment machine becomes available again.

To convert back to the original plan in the Fallback Planning module:

1. **Return to the original plan** according to the instructions in *section 10.4.5 Return to original plan on page 855*.

2. **Final adjustments of the "new" original plan.** Once the "new" original plan is available in the plan list, it can be set to the active plan (current plan) in RayStation. Verify that the plan dose for the "new" original plan is as intended or modify the plan until satisfied.

The plan dose will be a sum of delivered fractions from the original plan and the fallback plan, and future fractions from the original plan. The beam set dose will be equivalent to the one in the original plan.

3. **Approve the "new" original plan.** Before the "new" original plan can be used for delivery, it needs to be approved. Plan approval is performed as usual in the Plan Evaluation module. For more information, see *section 8.1.15 Plan approval on page 748*.

To see the total sum of the completed treatment plan, use **Sum doses** in Plan Evaluation. For more details, see *section 8.1.6 Dose summation on page 733*.

Repeat workflow if needed

The entire fallback planning workflow can be repeated several times if the treatment machine becomes unavailable again. Any of the available fallback plans can be selected each time this workflow is repeated.

10.4 THE FALLBACK PLANNING MODULE

Prior to entering the Fallback Planning module fallback plans have to be created in the Plan Evaluation module. For more information, see *section 8.1.16 Create fallback plans on page 755*.

The Fallback Planning module provides tools for evaluation of the automatically created fallback plans. The Fallback Planning module includes features such as:

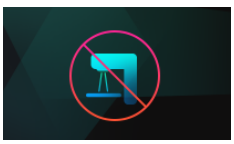
- side-by-side comparison of dose distributions from fallback plan alternatives and original plans
- dose statistics
- DVH
- clinical goal evaluation
- copying a fallback plan to the treatment plan list
- deletion of fallback plans
- having the option to return to the original plan

For a description of the entire fallback planning workflow, see *section 10.3 The Fallback Planning workflow on page 843*.

Note: *All fallback plans are deleted when the original plan is unapproved.*

Note: *All fallback plans not copied to the plan list are deleted when the original plan is deleted.*

Note: *A treatment plan cannot be deleted if a fallback plan in the plan list is referring to it.*



In this section

This section contains the following sub-sections:

10.4.1	The Fallback Planning module user interface	p. 850
10.4.2	Evaluating fallback plans	p. 851
10.4.3	Enable editing and approval of a fallback plan	p. 852
10.4.4	Delete fallback plan	p. 854
10.4.5	Return to original plan	p. 855

10.4.1 The Fallback Planning module user interface

Workspace

The top left corner shows the **Fallback plans** list that lists all fallback plans generated for the selected original plan as well as clinical goals information.

The left patient view shows the original plan selected in the **Plan** list in the top right corner of the workspace. The right patient view shows the fallback plan selected in the **Fallback plans** list.

The bottom of the workspace shows the **DVH**, **Dose statistics**, **Dose difference** and **Clinical goals** views.

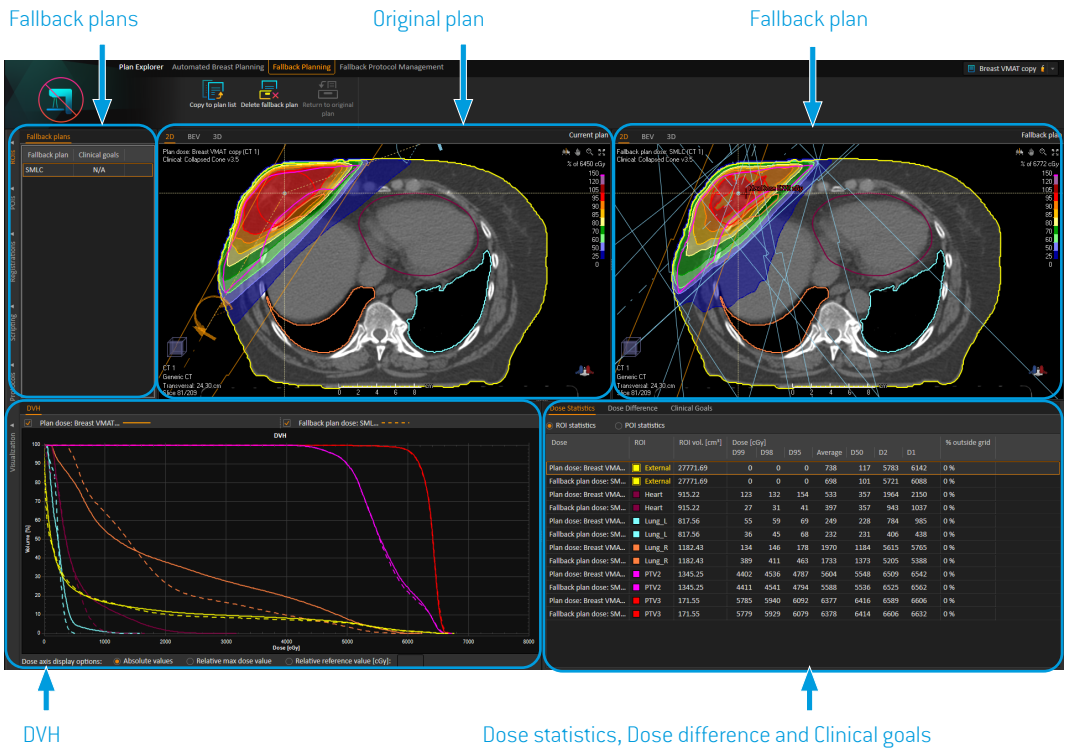


Figure 463. The Fallback Planning module workspace.

Graphical User Interface

For more information about the tools, operations and various view types in the Graphical User Interface, see *chapter 3 The Graphical User Interface*.

10.4.2 Evaluating fallback plans

Fallback plans can be evaluated using the evaluation tools described below. If the plans require further optimization, see *chapter 7 Plan Optimization*.

Dose Volume Histogram (DVH)

The DVH view presents the cumulative dose volume histograms of the ROIs selected in the ROI List. The dose can be displayed as **absolute** or **relative [%]**. It is also possible to manually set the reference value for the relative scale. For a further description of the DVH view, see *section 3.7.1 Dose Volume Histogram (DVH) on page 78*.

Dose statistics

The dose statistics view lists ROI dose information for the active plan and the selected fallback plan. For more information, see *section 3.7.2 Dose statistics table on page 79*.

Dose difference

The dose difference view displays the dose difference between the active plan and the selected fallback plan. See *The Dose difference view on page 75* for more information.

Clinical goals

The clinical goals functionality makes it possible to define evaluation criteria for specific ROIs and POIs. The result (pass/fail) is easy-to-read in a single column. For more information about the clinical goals functionality, see *section 3.7.3 Clinical goals on page 81*.

Clinical goals are displayed for the active plan and for all fallback alternatives. The clinical goals of the active plan are displayed and evaluated for all other plans.

A summary of the clinical goals is displayed in the **Fallback plans** list. The symbol in the Clinical goals column will indicate if the fallback plan is achieving the clinical goals or not (green = passed, red = failed, green/red = partially passed). If showing partial achievement as the example below, interpret this with discretion. If for example only one clinical goal is not achieved by a small value, it will be indicated as partially passed. Verify the detailed values in the clinical goals list.

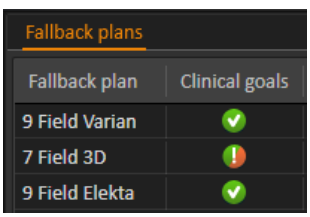
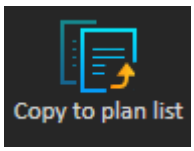


Figure 464. Clinical goals summary in the **Fallback plans** list.

10.4.3 Enable editing and approval of a fallback plan

In order to enable editing and approval of a fallback plan, the fallback plan has to be placed in the list of treatment plans. This is done by copying the fallback plan from the **Fallback plan** list to the **Plan** list.

1. Select a plan in the **Fallback plan** list.
2. Click the **Copy to plan list** button.



This opens the **Copy to plan list** dialog.

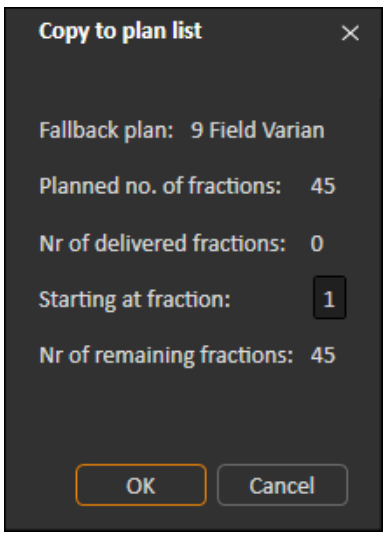
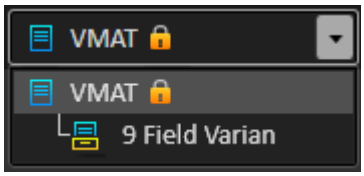


Figure 465. The Copy to plan list dialog.

3. Select **Starting at fraction**, that is, from which fraction the fallback plan should be used depending on how many fractions that already have been delivered from the original plan.

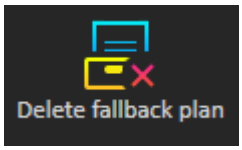
Note: *Ensure that the correct fraction is entered since this affects the dose at dose scaling etc. A treatment course will be created based on this information and it is assumed that the previous fractions were delivered with the original plan. Incorrect fraction information may cause erroneous delivery of the dose.*

4. Click **OK**. The fallback plan is moved to the **Plan** list and is attached to the original plan.



10.4.4 Delete fallback plan

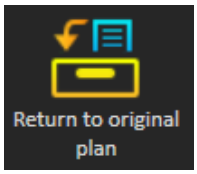
To delete a fallback plan, select it from the **Fallback plan** list and click the **Delete fallback plan** button.



10.4.5 Return to original plan

It is possible to deliver future fractions from the original plan instead of from the fallback plan. A copy of the original plan is then created with a treatment course displaying the delivered dose as background dose.

1. Click the **Return to original plan** button.



This opens the **Return to original plan** dialog.

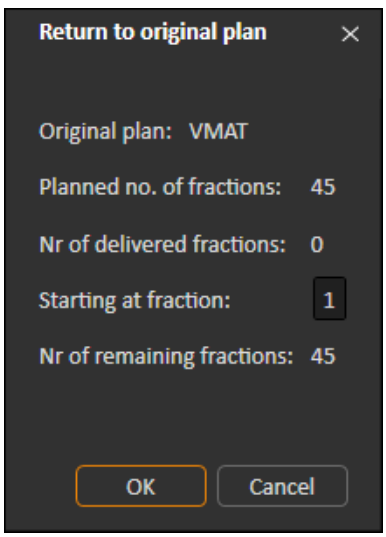
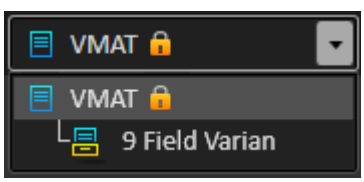


Figure 466. The **Return to original plan** dialog.

2. Select **Starting at fraction**.
3. Click **OK**.

A copy of the "new" original plan is created with a treatment course displaying the delivered dose as background dose. The new plan is displayed as an adaptive plan in the **Plan** list and will be a grandchild to the first original plan.



10.5 THE FALLBACK PROTOCOL MANAGEMENT MODULE

Fallback protocols define a treatment setup configuration that is suitable as a backup for a given treatment setup. The protocols contain information such as the modality, beams, machine and optimization settings for creating the fallback plan.

In the Fallback Protocol Management module the user can design plan types which are typical treatment plan categories, for example Proton Head and Neck. Each plan type can have a set of fallback protocols, for example protocols for different treatment techniques and/or treatment machines. The protocols are created based on a patient, but once created, they are general and not patient-specific. The protocols can then be applied to any patient to create fallback plans.

The fallback protocols are created in the Fallback Protocol Management module. The fallback protocols are automatically generated and each step can be modified as desired. By default, all the steps in the fallback protocol will reflect the values in the template plan from which the protocol was created, except for the dose mimicking step. The dose mimicking step will reflect the values specified when starting the dose mimic optimization.

It is possible to test if a template plan is suitable as fallback protocol for another plan by using the dose mimicking optimization. After the mimicking has finished, it is possible to compare doses, DVHs, dose statistics and clinical goals for the original plan and the fallback protocol template plan.

For a description of the entire fallback planning workflow, see *section 10.3 The Fallback Planning workflow on page 843*.

In this section

This section contains the following sub-sections:

10.5.1	The Fallback Protocol Management module user interface	p. 857
10.5.2	Define fallback protocols	p. 858

10.5.1 The Fallback Protocol Management module user interface

Workspace

The top left corner shows the **Plan types** list. The bottom left corner shows the **Fallback protocols** list where the fallback protocols from the selected plan type are displayed.

The window in the top middle shows the plan to mimic, and the window in the top right corner shows the current plan that will be used as a template for the fallback protocol.

The bottom shows the **DVH**, **Dose statistics**, **Dose difference** views.

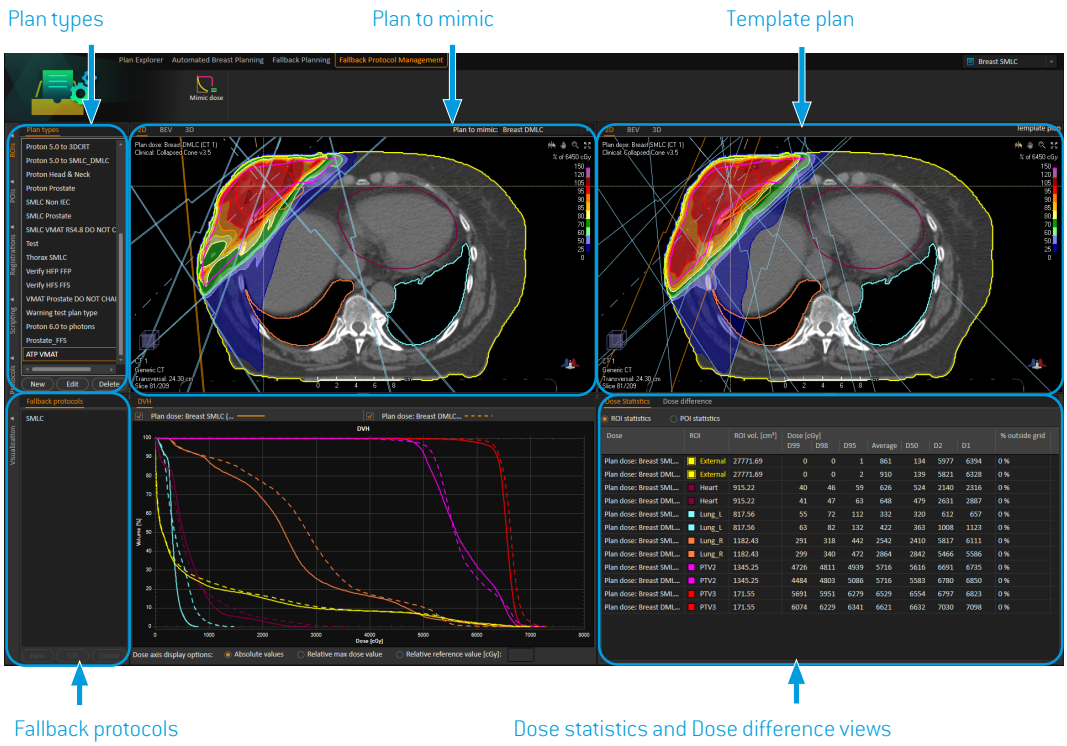


Figure 467. The Fallback Protocol Management workspace.

Graphical User Interface

For more information about the tools, operations and various view types in the Graphical User Interface, see *chapter 3 The Graphical User Interface*.

10.5.2 Define fallback protocols

The fallback protocols are defined in the Fallback Protocol Management module and this section describes a suggested workflow for defining the protocols. For a description of the entire fallback planning workflow, see *section 10.3 The Fallback Planning workflow on page 843*.

Step 1. Create a fallback plan type

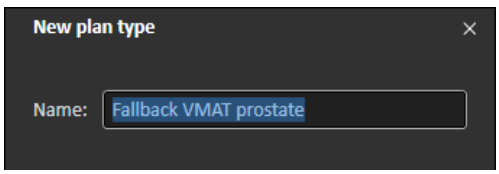
A fallback plan type can be thought of as a group of similar protocols that will be applied to a patient for fallback planning. The protocols can be grouped as desired e.g., by specific anatomy site, by technique or machine, by different values of the target vs OAR ratio settings. For example:

- A prostate VMAT plan could have a set of protocols in a plan type specified for all prostate VMAT patients of the clinic.
- Or a clinic may fall back on the only other available machine, delivering IMRT with different beam configurations.
- Or the protocols may be of the same technique and machine but with different target vs OAR ratio values.

To create a fallback plan type:

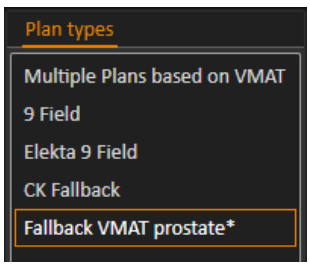
1. Click the **New** button in the **Plan types** list.

   This opens the **New plan type** dialog.



2. Enter a **Name** for the plan type, for example, "Fallback VMAT prostate".
3. Click **OK**.

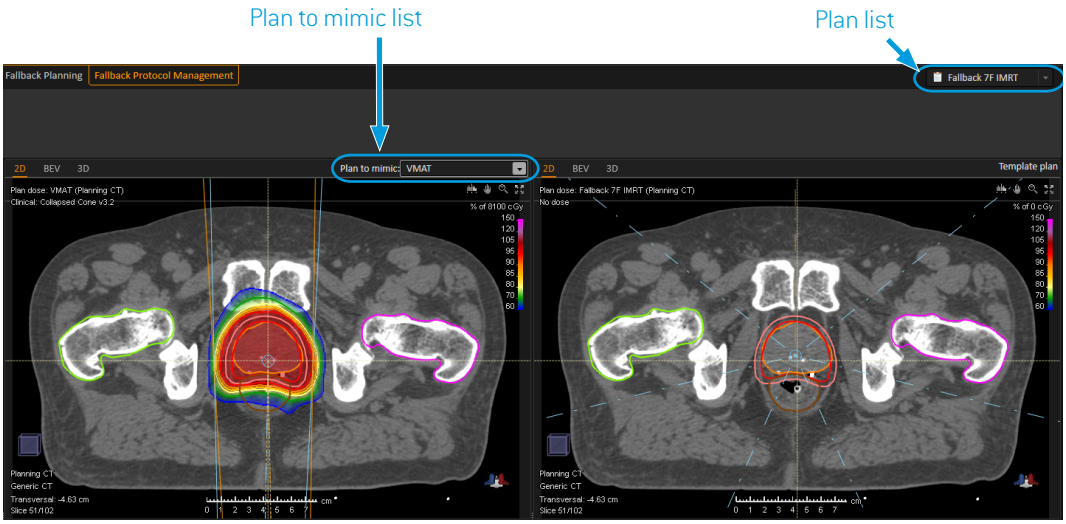
   The plan type will appear in the **Plan types** list with an asterisk, indicating that it is new.



To remove a plan type, click the **Delete** button. To rename a plan type, click the **Edit** button.

Step 2. Select the plans to use for fallback protocol creation

1. Select a template plan from the **Plan** list to use when creating the fallback protocol (**Template plan**). For example, if you want to use SMLC as fallback treatment technique for proton plans, choose a SMLC plan with enough beams to simulate a proton plan.



   For instructions on how to create a template plan, see *section 6.1.22 Create template plans for fallback planning on page 382*.

2. In the **Plan to mimic** list, select a plan that is representative for the plans you want to create fallback plans for, i.e., a plan that matches the current plan type.

3. Edit the current plan as desired using the common tools in RayStation 7.

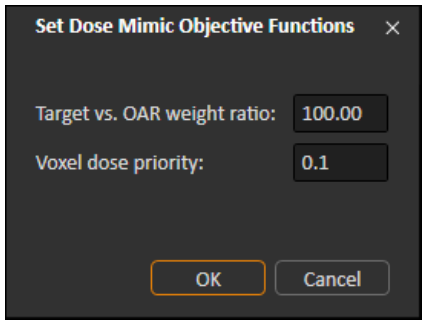
Step 3. Perform dose mimicking optimization

The purpose of dose mimicking optimization is to test how well the template plans mimic the original plan and to test and adjust the **Target vs. OAR weight ratio**.

To optimize the **Template plan** to mimic the dose in the **Plan to mimic**:

1. Click the **Mimic dose** button.

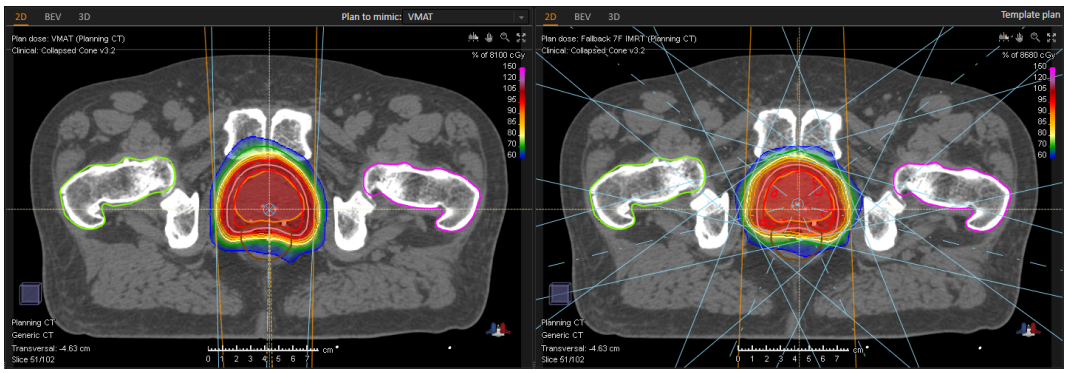
This opens the **Set Dose Mimic Objective Functions** dialog.



2. Enter **Target vs. OAR weight ratio** (0.1 – 100000). This parameter controls how much effort is spent on maintaining target uniformity versus reducing the dose in the risk organ(s).
3. Enter a **Voxel dose priority** (0-10). This parameter controls how much effort is spent on matching the dose per voxel of the dose distribution versus maintaining a good agreement in the DVHs in and around the target(s). The value 0 means that only DVHs are explicitly considered.
4. Click **OK**.

   Note: *The optimization problem in the template plan is replaced by a dose mimicking optimization problem.*

   Based on the plan setup of the template plan, RayStation will try to mimic the dose and DVHs of the selected plan in the **Plan to mimic** list. When the dose mimicking has completed clinical dose is available in the template plan.



5. Compare the doses using the evaluation view tools.

   The original dose and the mimicked dose are displayed in the patient views, the DVH view, the dose statistics view and the clinical goals view.

   Note: *The result of the Mimic dose operation is not supposed to be used for delivery. The template plan is not a fallback plan of the "Plan to mimic", it is just a temporary test plan used to set up the protocols.*

6. If the result of the mimic dose operation is not satisfactory, try another weight ratio or change the template plan (for example by adding more beams or editing the segmentation settings).

   If the target coverage needs improvement increase the **Target vs. OAR weight ratio**, or if OARs require better protection, decrease the **Target vs. OAR weight ratio**.

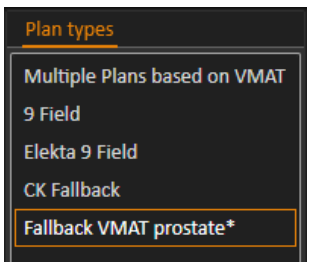
   If the match of the dose distribution per voxel needs improvement, increase the **Voxel dose priority**. This however may come at the cost of the DVH curve mimic.

Step 4. Create a fallback protocol based on the template plan

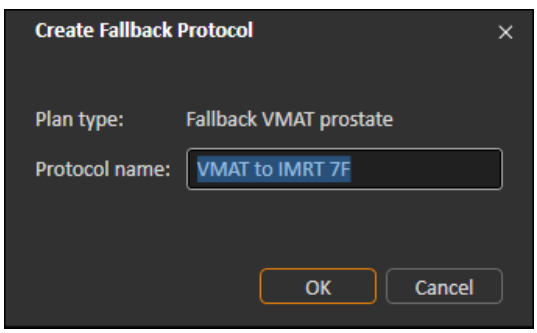
Fallback protocols are created based on the settings in a template plan. Supported treatment techniques are SMLC, DMLC, 3D-CRT, VMAT and TomoHelical.

To create a fallback protocol for the selected plan type based on the settings in the current plan (**Template plan**):

1. Make sure that you still have the correct plan type selected in the **Plan types** list as the protocol will be saved in the selected plan type.

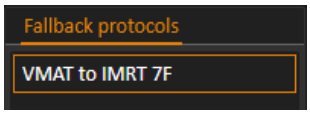


2. Click the **New** button in the **Fallback protocols** list. This opens the **Create Fallback Protocol** dialog.



3. Enter a **Protocol name** and click **OK**.

The fallback protocol is created and can be edited in the **Fallback protocols** list.



A fallback protocol will automatically include the following steps:

- Create plan
- Create beam set
- Add beams
- Beam optimization settings
- Segmentation settings
- Dose mimicking settings

Step 5. Manually edit the protocol steps as desired (optional)

1. Click the **Edit** button in the **Fallback protocols** list to open the **Edit protocol** dialog.

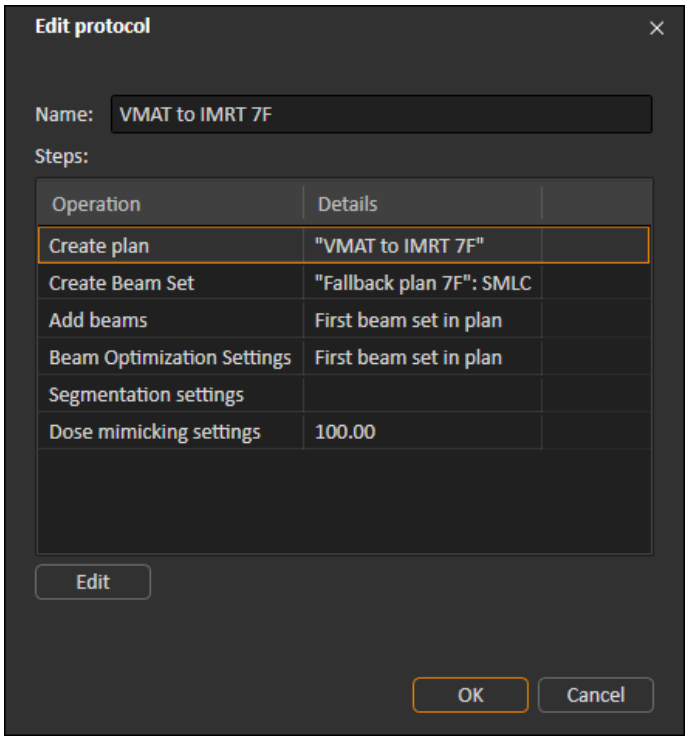
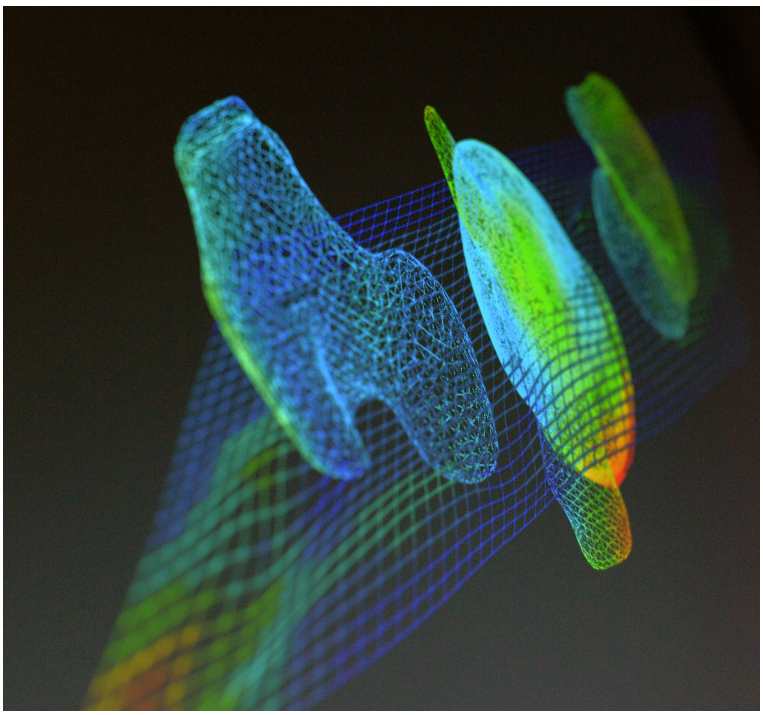


Figure 468. The **Edit protocol** dialog.

2. Select a protocol step in the list and click **Edit**. This opens a dialog where the protocol parameters for the selected protocol step can be edited.
3. Edit the protocol steps as desired.
4. Click **OK**.

11 TREATMENT ADAPTATION



The Treatment Adaptation planning activity tab contains the Dose Tracking module and the Adaptive Replanning module.

In the Dose Tracking module it is possible to evaluate the treatment delivery by computing dose on the images acquired during the treatment course using the beam setup from the approved treatment plan. Dose tracking can also be performed using an approved adapted plan.

In the Adaptive Replanning module, the user can create a new treatment plan that is adapted to the previous treatment plan, using the delivered accumulated dose from the treatment evaluation in the Dose Tracking module as a background dose when reoptimizing the plan on the new planning image set. Multiple adaptive plans can be created if desired.

In this chapter

This chapter contains the following sections:

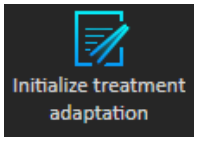
11.1	Initialize treatment adaptation	p. 867
11.2	Dose Tracking	p. 868
11.3	Adaptive Replanning	p. 885

11.1 INITIALIZE TREATMENT ADAPTATION

Treatment adaptation can be started from both the Patient Data Management module and the Dose Tracking module. The treatment plan must be approved before treatment adaptation can be initialized. Treatment adaptation can also be initialized for an adapted plan.

To initialize treatment adaptation:

1. Click the **Initialize treatment adaptation** button.



This opens the Initialize treatment adaptation dialog.

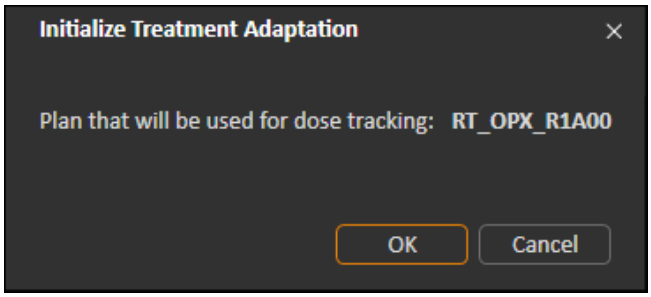


Figure 469. The Initialize treatment adaptation dialog.

2. Click **OK.** The treatment adaptation starts with the selected plan.

11.2 DOSE TRACKING

In the Dose tracking module it is possible to evaluate the treatment delivery by computing dose on the images acquired during the treatment course using the beam set up from the approved treatment plan. It is possible to compare:

- Planned fraction dose on the planning image set with delivered fraction dose on the fraction image set (See *Compute fraction dose on page 879*)
- Planned fraction dose on the planning image set with delivered fraction dose mapped to the planning image (See *Compute fraction dose on page 879*)
- Delivered fraction dose mapped to the planning image set with delivered dose on the fraction image set (See *Compare deformed dose on page 881*)
- Planned accumulated dose on the planning image set with the delivered accumulated dose on the planning image set (See *Compare accumulated dose on page 883*)
- Total dose beam set/plan (See *Compare total dose (beam set/plan) on page 883*)

Note: *For carbon ions, the dose tracking is always performed on the RBE dose. Physical dose cannot be viewed in this module.*

In this section

This section contains the following sub-sections:

11.2.1	Dose handling summary	p. 869
11.2.2	The Dose Tracking module user interface	p. 870
11.2.3	Dose tracking workflow	p. 872
11.2.4	Compute fraction dose	p. 874
11.2.5	Deform dose	p. 876
11.2.6	Estimate fraction dose	p. 877
11.2.7	Dose comparison	p. 879

11.2.1 Dose handling summary

Dose types	Description
Delivered doses	
Delivered fraction dose	The fraction image set needs to be (rigidly) registered with the planning image set. The beam set (beam configuration) which the selected fraction belongs to is used to compute dose on the fraction image set as given by the rigid registration.
Deformed delivered fraction dose	The delivered fraction dose mapped back to the planning image set using an approved deformable registration.
Accumulated delivered fraction dose	Summation of the deformed delivered fraction doses for the user selected consecutive fractions.
Estimated total dose (beam set / plan)	Summation of deformed delivered fraction doses up to total dose (beam set/plan), where missing fraction doses are estimated by an average of existing fraction doses. • If the user has computed fraction doses and deformed fraction doses for fractions in beam set 1, doses for non-evaluated fractions are estimated with an average of existing deformed fraction doses and total estimated beam set dose for beam set 1 is displayed • If the user has computed fraction doses and deformed fraction doses for beam set 1 and part of beam set 2, doses for non-evaluated fractions in beam set 2 are estimated with an average of deformed fraction doses in beam set 2 and total estimated plan dose is displayed. Note that consecutive deformed fraction doses starting from fraction 1 need to be available.
Dose scaling	
Actual	The actual dose is displayed.
Beam Set scaling	The dose will be scaled to a beam set. • If the user is displaying doses from the first beam set, the dose will be scaled to that beam set. • If the user is displaying doses from the second beam set, the dose will be scaled to the second beam set. • If the user is displaying doses from both beam sets, e.g. dose is accumulated from both beam sets, the fractions included to the first beam set will be scaled to the first beam set and the fractions included to the second beam set will be scaled to the second beam set.

11.2.2 The Dose Tracking module user interface

The Dose tracking workspace consists of a toolbar, six patient views (three for planned dose and three for delivered dose), a fraction schedule and two evaluation views.

Figure 470. The Dose Tracking workspace.

The fraction schedule

The **Fractions** tab in the tool panel to the left shows an overview of the planned treatment and the treatment delivery.

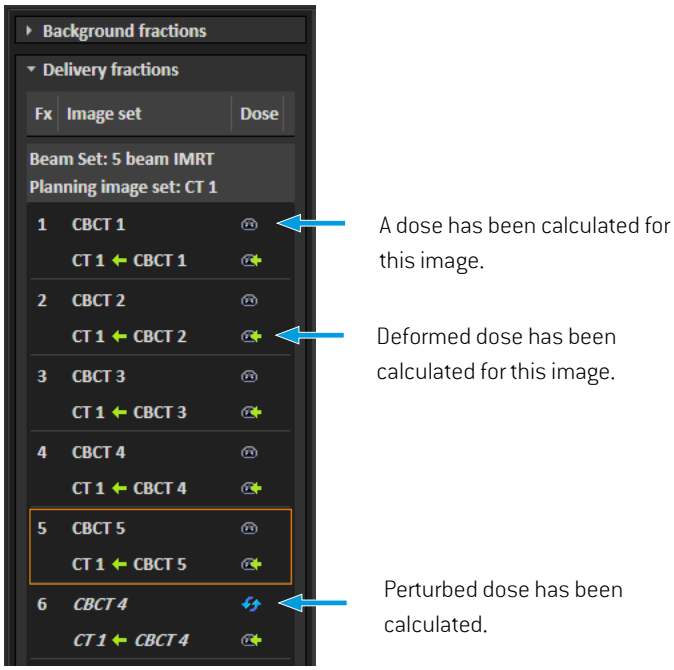

Background fractions
Delivery fractions
Fx
Image set
Dose
Beam Set: 5 beam IMRT
Planning image set: CT 1
1 CBCT 1
CT 1 ← CBCT 1
2 CBCT 2
CT 1 ← CBCT 2
3 CBCT 3
CT 1 ← CBCT 3
4 CBCT 4
CT 1 ← CBCT 4
5 CBCT 5
CT 1 ← CBCT 5
6 CBCT 4
CT 1 ← CBCT 4
A dose has been calculated for this image.
Deformed dose has been calculated for this image.
Perturbed dose has been calculated.

Figure 471. The **Fractions** tab shows the fraction schedule.

Evaluation views

Two evaluation views are located at the bottom of the workspace. They are identical and enable simultaneous comparison of for example **DVH** data and **Dose statistics**. The **Clinical goals** view can only display the result of a clinical goal if the accumulated dose is scaled to the plan dose.

The evaluation views are described in detail in *section 3.7 Common graphs, tables and tools on page 77*.

11.2.3 Dose tracking workflow

This is a suggested workflow for dose tracking in RayStation. Several steps need to be performed in other modules before dose tracking can be started in the Dose Tracking module. These steps are also described in this workflow.

1. **Initialize treatment adaptation.** See *section 11.1 Initialize treatment adaptation on page 867* for more information. This can be done in the Patient Data Management module and in the Dose Tracking module.
2. **Import one or several fraction images.** Import the CBCT image set(s) to the same patient case as the treatment plan. For more information, see *section 4.3.1 Import new patient data on page 112*.
3. **Set the CBCT image set properties**. For more information, see *section 4.7.2 Setting image set properties for CBCT image sets on page 151*. This is done in the Patient Data Management module.
4. **Align the CBCT image set and the planning CT image set via CBCT treatment position alignment.** This is done in the Patient Data Management module. For more information, see *section 4.7.4 Treatment position alignment on page 160*.
5. **Create a density table for the CBCT image set.** This is done in the Patient Data Management module. For more information, see *Density table for CBCT on page 152*.
6. **Create an External ROI on the CBCT image set.** This is done in the Structure Definition module. See *Create External ROI on page 206* for more information. If the image set has limited Field Of View (FOV), that is when parts of the body are outside the FOV, an ROI can be created for the FOV and can later be used for calculating the External ROI on the limited FOV data.
    a. Create an ROI for the FOV *Create Field-of-View ROI on page 219*. Creating the External ROI in this way is preferably done after creating the CBCT density table.
    b. Select to create an External ROI on limited FOV data. For more information, see *Generate external ROI on limited FOV data on page 219*.
7. **Add a rigid transformation.** Although the image sets are treatment position aligned for computation of dose on the CBCT image set, it may not be an ideal rigid registration. Adding a rigid transformation can create a better starting point for the deformable registration. This is done in the Image Registration module. For more information, see *Other registration options on page 180*.
8. **Perform a hybrid intensity and structure based deformable registration.** This is done in the Deformable Registration module. For more information, see *section 5.4.4 Hybrid deformable registration on page 261*.
9. **Map ROIs to the CBCT image set.** Map structures to segment the CBCT image set. Use controlling ROIs and Focus ROIs as necessary to improve the deformable registration. This is done in the Deformable Registration module. For more information, see *section 5.4.12 Map structures on page 283* for more information.

10. **Approve the deformable registration.** An approved deformable registration is required for dose tracking. This is done in the Deformable Registration module. For more information, see *section 5.4.13 Approval of a deformable registration on page 287*.

11. **Begin dose tracking.** This is done in the Dose Tracking module.

    a. Compute dose on the images acquired during the treatment using the beam setup from the approved treatment plan.

       - **Compute fraction dose.** (For more information, see *Compute fraction dose on page 879*).
       - **Deform dose**. (For more information, see *Compare deformed dose on page 881*).
       - **Estimate fraction dose.** (For more information, see *section 11.2.6 Estimate fraction dose on page 877*).

    b. Evaluate the treatment delivery by using the dose comparison tools. For more information, see *section 11.2.7 Dose comparison on page 879*.

11.2.4 Compute fraction dose

In the Dose tracking module it is possible to calculate the dose that was delivered to the patient during the treatment. More specifically, it is possible to use the settings for the estimated fraction dose in the treatment plan to compute the dose on the image set that gives the best presentation of the patient's current appearance (typically the CBCT image acquired at the time of patient positioning in the treatment room). Several image sets can be assigned to a specific fraction. The same image set can also be used for several fractions. To compute fraction dose:

1. Click the **Compute fraction dose** button in order to open the Compute fraction dose dialog.

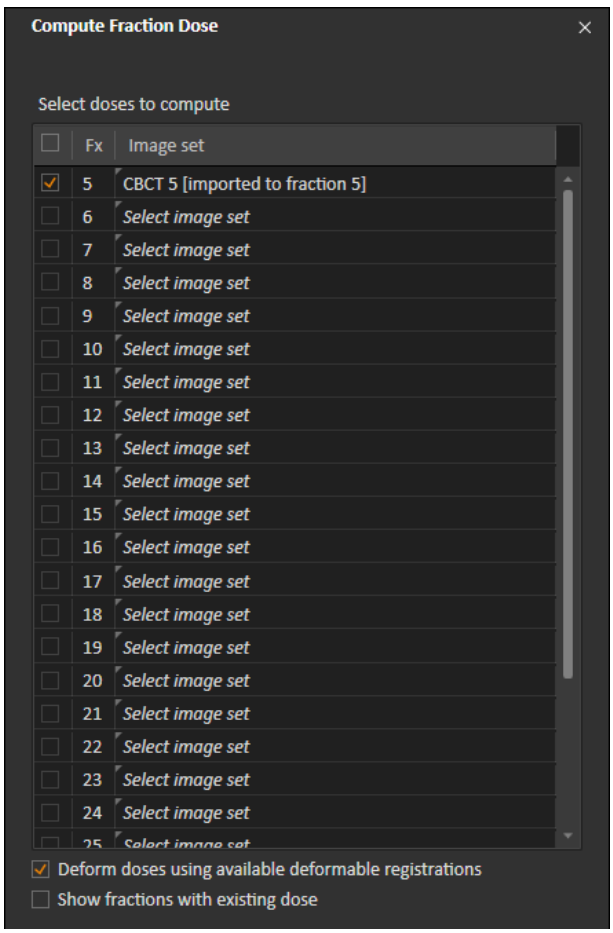

Compute Fraction Dose
Select doses to compute
Fx
Image set
5 CBCT 5 [imported to fraction 5]
6 Select image set
7 Select image set
8 Select image set
9 Select image set
10 Select image set
11 Select image set
12 Select image set
13 Select image set
14 Select image set
15 Select image set
16 Select image set
17 Select image set
18 Select image set
19 Select image set
20 Select image set
21 Select image set
22 Select image set
23 Select image set
24 Select image set
Deform doses using available deformable registrations
Show fractions with existing dose

Figure 472. The **Compute Fraction Dose** dialog.

2. Select an **Image set** for each selected fraction. (The fraction image imported for the selected fraction is set as default).
3. Select the fraction(s) that the dose will be calculated for.
4. If desirable, select to **Deform doses using available deformable registrations** by checking the corresponding checkbox. This checkbox is checked by default. This will map the dose to the planning image set.

   Note: *A deformed dose can only be calculated if a deformable registration that is approved for dose accumulation already exists, where the planning image set is the reference image set and the fraction image set is the target image set. If no approved deformable registration exists for the fraction CBCT, doses will only be computed on the CBCT and will not be deformed. To complete the deform dose action, create and/or approve the deformable registration and use the Deform dose function from the toolbar.*

   Note: *Deform doses using available deformable registrations in this dialog performs the same function as the Deform dose button in the toolbar.*
5. Select to **Show fractions with existing dose** by checking the corresponding checkbox.
6. Click **OK**. The fraction dose will now be visible in the **Fractions** tab in the tool panel and can then be selected for dose comparison, see *section 11.2.7 Dose comparison on page 879* for more information.

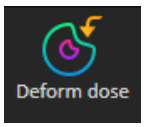
11.2.5 Deform dose

Dose deformation in RayStation is always performed in the direction from the target image set to the reference image set. Therefore, in order to deform dose computed on image set B to image set A, a deformable registration with A as reference image set and B as target image set must have been created. The dose deformation is performed through an interpolation procedure. Given a point in the reference image set, the displacement field and the rigid registration is applied in order to find the corresponding point in the target image set. The dose on the target image set is then tri-linearly interpolated and mapped back to the reference image set. If any of the doses selected for deformation is not fully covered by the deformation grid, the grid will be automatically expanded. The expansion will be smoothly extended from the boundary and finally padded by zero deformation vectors to cover the dose.

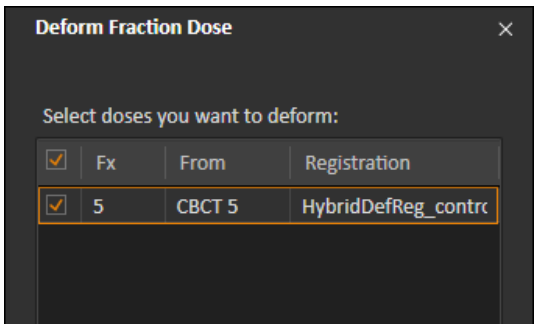
The deformed dose can be calculated from the compute fraction dose dialog (See *section 11.2.4 Compute fraction dose on page 874*). If no deformable registrations were created at the time of the fraction dose computation, the Deform dose option can be used. Only fraction doses, which are not yet deformed, with corresponding deformable registrations that are set to 'approved for dose accumulation' can be used for deformed dose calculations. For information on how to approve the deformable registration for dose accumulation, see *section 5.4.13 Approval of a deformable registration on page 287*.

To calculate the deformed dose:

1. Click the **Deform dose** button.

   This opens the Deform fraction dose dialog.

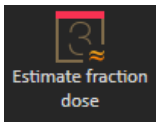
2. Select which dose to deform by checking the corresponding checkbox.
3. Click **OK**. The deformed dose can then be selected for dose comparisons, see *section 11.2.7 Dose comparison on page 879*.

11.2.6 Estimate fraction dose

An estimated dose can be calculated for fractions with missing fraction image sets. The dose can be based on an existing fraction dose or perturbation can be added.

To estimate fraction dose:

1. Click the **Estimate fraction dose** button in order to open the Estimate Fraction Dose dialog.



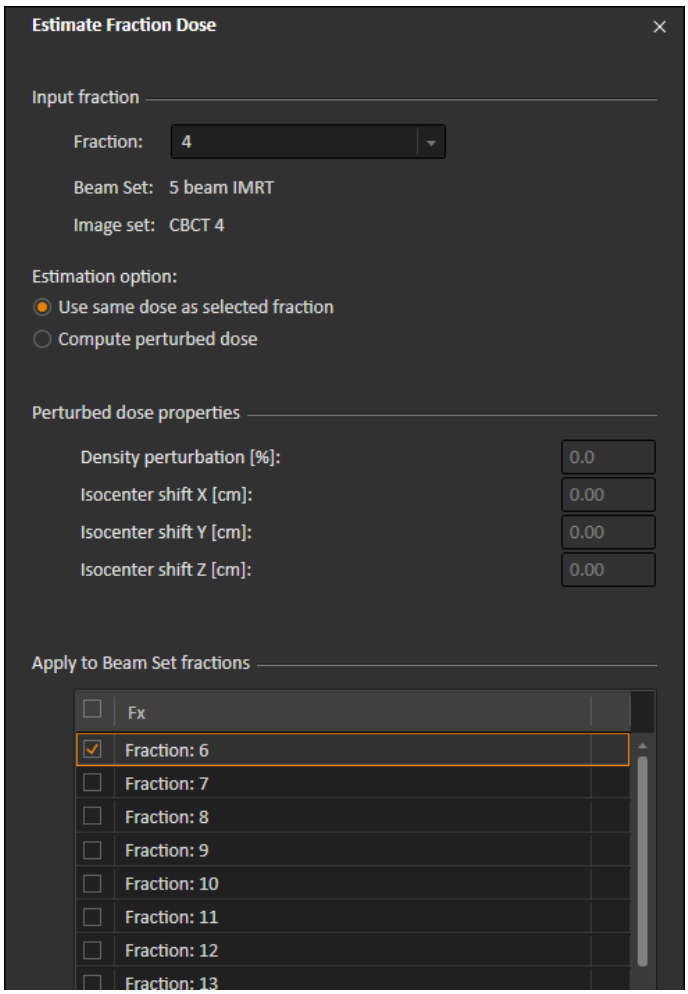


Figure 473. The Estimate Fraction Dose dialog.

2. Select **Input fraction**.
3. Select **Estimation option.** The alternatives are **Use the same dose as selected fraction** and **Compute perturbed dose**.

   For evaluation of robustness, doses can be computed including a perturbation of the dataset. Perturbations are specified as a scaling of densities (in %) and/or a shift of the isocenter in x, y and/or z (IEC, cm) direction.
4. Select the fractions to estimate dose for in the **Apply to Beam Set fractions** list.

   If an image set is already imported to a fraction, this will be marked *. In case of multiple beam sets, only the fractions included in the input fraction beam set will be displayed.
5. Click **OK**.

11.2.7 Dose comparison

The dose comparison tools can be used to display fraction doses, deformed doses or accumulated doses for a specific fraction or total dose. The dose can be scaled to a plan or the beam set scaling can be shown.

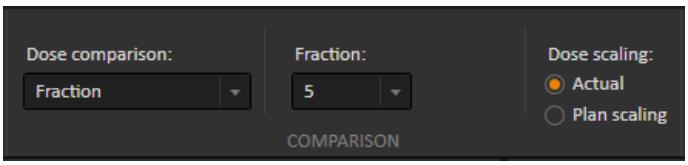


Figure 474. The dose comparison tool. In this example, the actual fraction dose for fraction number 5 is selected.

Note: *Due to discrete window coordinates (pixels) the accuracy of the positioning of the haircross, when doing dose comparison, is dependent of the zoom level of the window. This may cause a small discrepancy in positioning, resulting in slightly unsynchronized views. Both positions and dose difference may differ slightly. The actual position and dose reported in each view will be consistent within each view.*

Note: *When comparing two image sets or plans, the secondary image set might need a slight rotation in order to match the primary image set. The primary image set always will be fixed. If there is an image registration with a rotation this will be indicated in the view by an asterisk in conjunction to the patient plane direction. "* Transversal" will for example denote that this is a rotated view based on a transversal patient view, i.e., the reference view is transversal but the image registration between the reference image set and the shown image set may rotate the image data in the view so that it is not transversal. The same applies to the coronal and the sagittal patient views.*

Compute fraction dose

In this example, the planned fraction dose on the planning image set is compared to the delivered fraction dose on the fraction image set. (Settings: **Dose comparison: Fraction, Dose scaling: Actual**). Select which fraction to view from the **Fraction** drop-down list in the **Comparison** toolbar, or by clicking a fraction in the fraction schedule.

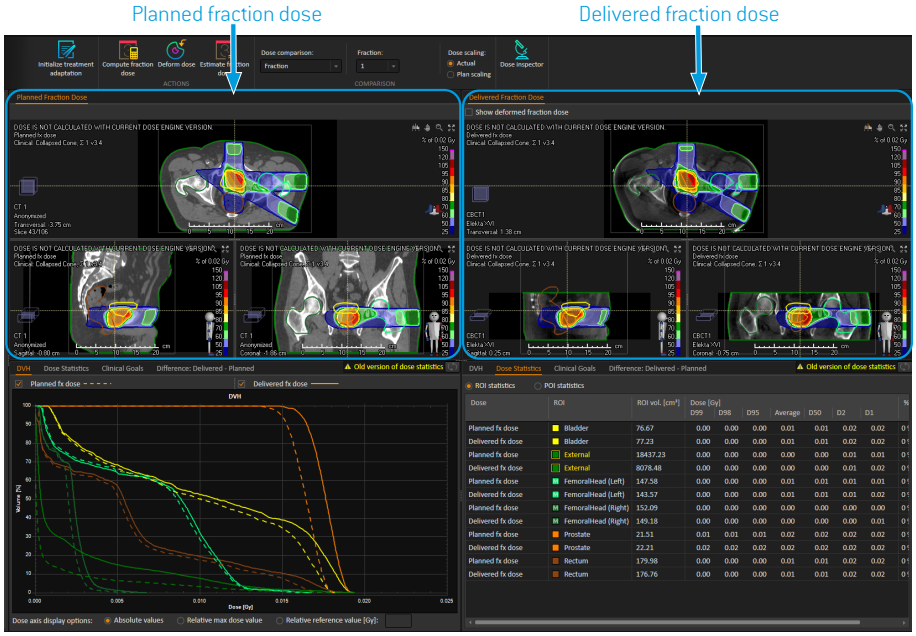


Figure 475. The planned fraction dose is compared to the delivered fraction dose.

If the checkbox **Deform fraction dose** is checked, the planned fraction dose on the planning image set will be compared to the delivered fraction dose mapped to the planning image set.

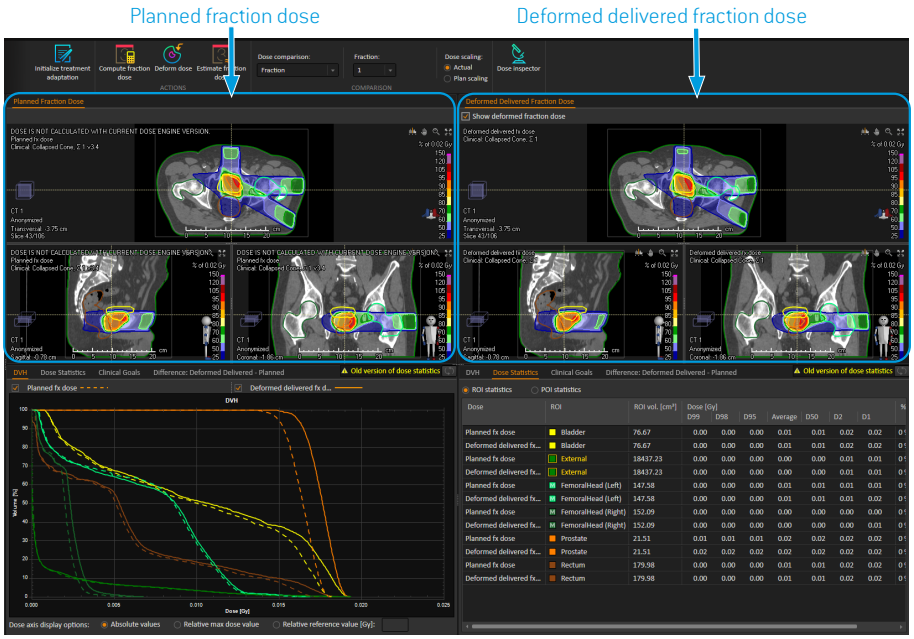


Figure 476. The planned fraction dose is compared to the deformed delivered fraction dose.

Compare deformed dose

In this example, the delivered fraction dose is mapped to the planning image set and compared to the delivered fraction dose displayed on the fraction image set. (Settings: **Dose comparison: Deformation, Dose scaling: Actual**).

Select which fraction to view from the **Fraction** drop-down list in the **Comparison** toolbar, or by clicking a fraction in the fraction schedule.

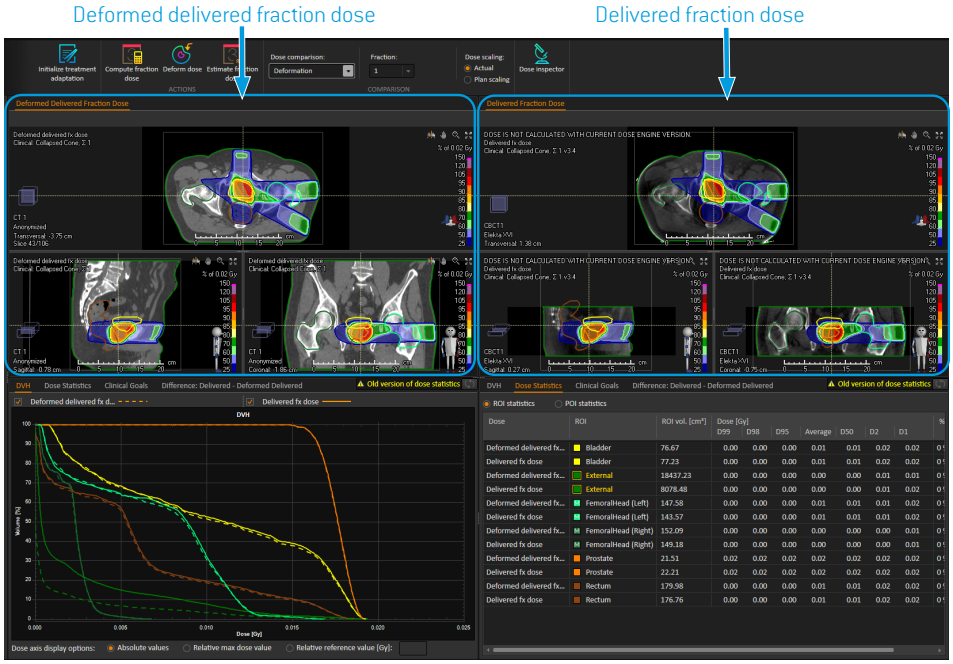


Figure 477. The dose tracking view. In this example, the deformed delivered fraction dose is compared to the delivered fraction dose.

Compare accumulated dose

In this example, the planned accumulated dose is displayed on the planning image set and compared to the accumulated delivered fraction dose displayed on the planning image set. (Settings: **Dose comparison: Accumulation, Dose scaling: Actual**).

Figure 478. The dose tracking view. In this example, the accumulated planned dose is compared to the accumulated delivered fraction dose.

Select which fractions to display dose for from the **From fraction** and **To fraction** drop-down lists in the **Comparison** toolbar.

Figure 479. The Comparison toolbar. Select the fractions to include in the dose accumulation.

Compare total dose (beam set/plan)

The compare total dose option requires that fraction dose and deformed dose have been calculated for all fractions.

Total delivered dose is estimated by summing existing fraction doses deformed to the planning image set with an average of existing fraction doses for missing fractions. See *section 11.2.1 Dose handling summary on page 869* for more information.

Total beam set dose is estimated if the plan has multiple beam sets but only fractions evaluated for the first beam set.

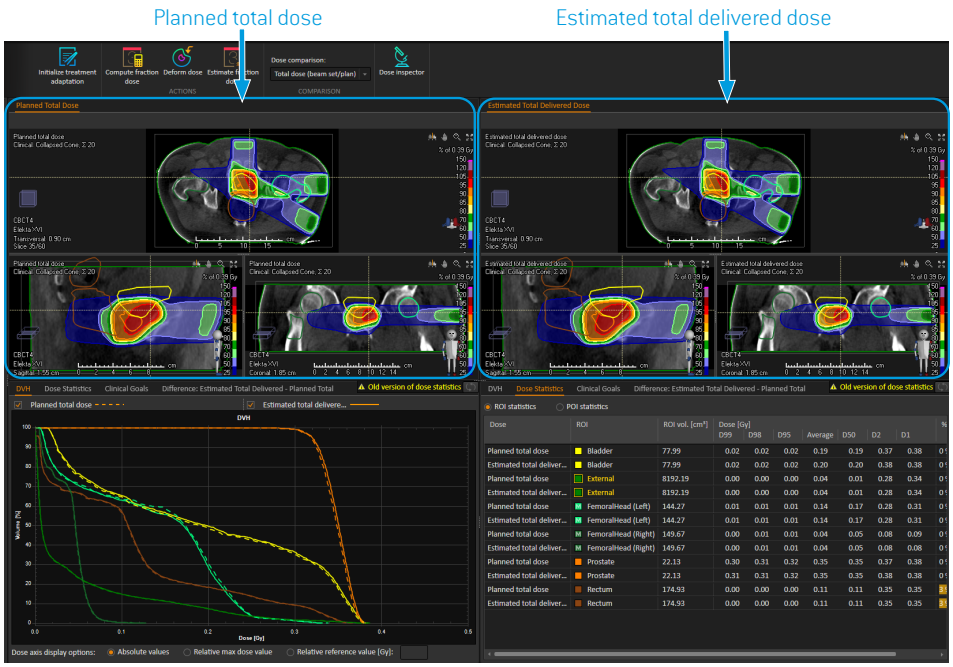


Figure 480. The dose tracking view. In this example, the total planned dose is compared to the total delivered fraction dose.

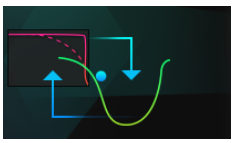
11.3 ADAPTIVE REPLANNING

Prior to entering the Adaptive Replanning module, a plan has been approved, treatment delivery has started and a number of delivered fractions, 1 ... n fractions, have been computed and evaluated in the Dose Tracking module. Based on the evaluation, the user has taken the decision that replanning is required.

In the Adaptive Replanning module, the user can create an adapted treatment plan based on a new planning image set, which is optimized using the delivered accumulated dose from the treatment evaluation in the Dose Tracking module as a background dose.

Note: *For carbon ions, background dose always refers to RBE dose.*

Before an adapted treatment plan can be created, there must exist an approved deformable registration with the new planning image set as reference image and original planning image set as target image.



In this section

This section contains the following sub-sections:

11.3.1	The Adaptive Replanning module user interface	p. 886
11.3.2	Adaptive Replanning workflow	p. 888
11.3.3	Plan creation	p. 889
11.3.4	Optimization of an adaptive plan	p. 895
11.3.5	Scale dose	p. 896
11.3.6	Approval	p. 898

11.3.1 The Adaptive Replanning module user interface

The Adaptive Replanning workspace consists of two dose lists, one for delivered fraction doses and one for adapted fraction doses, evaluation views, 2D and 3D patient views, BEV, DRRs, objectives/constraints lists and an optimization progress graph.

For TomoHelical plans there is a **Leaf Open Times** view that displays a histogram for the leaf open time of all leaves and of all projections.

Figure 481. The Adaptive Replanning workspace.

The delivered fraction doses and the corresponding symbols are described in detail in *The fraction schedule on page 871*.

Dose selection buttons

The buttons in the Plan and dose selection bar are specific for the Adaptive Replanning workspace. See *The plan and dose selection toolbar on page 51* for more information.

The **Plan dose** button displays the total dose, i.e. the dose from all the contributing beam sets in the plan.

The **Beam Set dose** button displays the total dose in the selected beam set.

The **Beam dose** button displays the dose for the selected beam.

The **Delivered dose** button displays the dose for the already delivered fractions.

The **Background dose** button displays the dose from the beam set that is set as background dose.

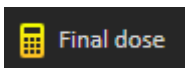
The **Beam Set + Background dose** button displays the dose for the selected beam set and the beam set that is set as background dose.

For carbon ions, there are also buttons to switch between display of physical or RBE dose. The physical dose is only avaiable for the current beam seat and not for the background dose.

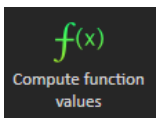
11.3.2 Adaptive Replanning workflow

Prior to entering the Adaptive Replanning module, a plan has been approved, treatment delivery has started and a number of delivered fractions, 1 ... n fractions, have been computed and evaluated in the Dose Tracking module. Based on the evaluation, the user has taken the decision that replanning is required. This section describes a suggested workflow for Adaptive Replanning.

1. **Perform dose tracking**. Perform dose tracking according to the workflow in *section 11.2.3 Dose tracking workflow on page 872*.
2. **Create a new adapted plan.** See *Create new adapted plan on page 889* for more information.
3. **Define or modify prescription.** For instructions on how to define or modify a dose prescription, see *section 6.1.12 Define or modify prescription on page 343*.
4. **Optimize the adapted plan.** See *section 11.3.4 Optimization of an adaptive plan on page 895* for more information.
5. **Compute dose.** Compute dose according to the instructions in *section 6.1.14 Compute dose on page 354*.

6. **Scale dose.** See *section 11.3.5 Scale dose on page 896* for more information.
7. **Compute function values.** If an optimization function is altered after an optimization has been completed the value for the changed function can be updated by clicking the **Compute function values** button in the toolbar.

8. **Approve the adapted plan.** See *section 11.3.6 Approval on page 898* for more information. An approved adapted plan can be used for dose tracking purposes in the Dose Tracking module.

11.3.3 Plan creation

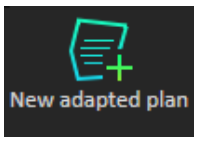
The **Plan creation** tab contains buttons for creating and editing a new adapted plan, editing the dose grid and showing the deformable registration properties.

Create new adapted plan

Before an adapted treatment plan can be created, there must exist an approved deformable registration between the original planning image set and the new planning image set, where the new planning image set is set as the reference image set and the original image set is set as the target image set.

To create a new adapted plan:

1. Click the **New adapted plan** button.

   This opens the New adapted plan dialog.

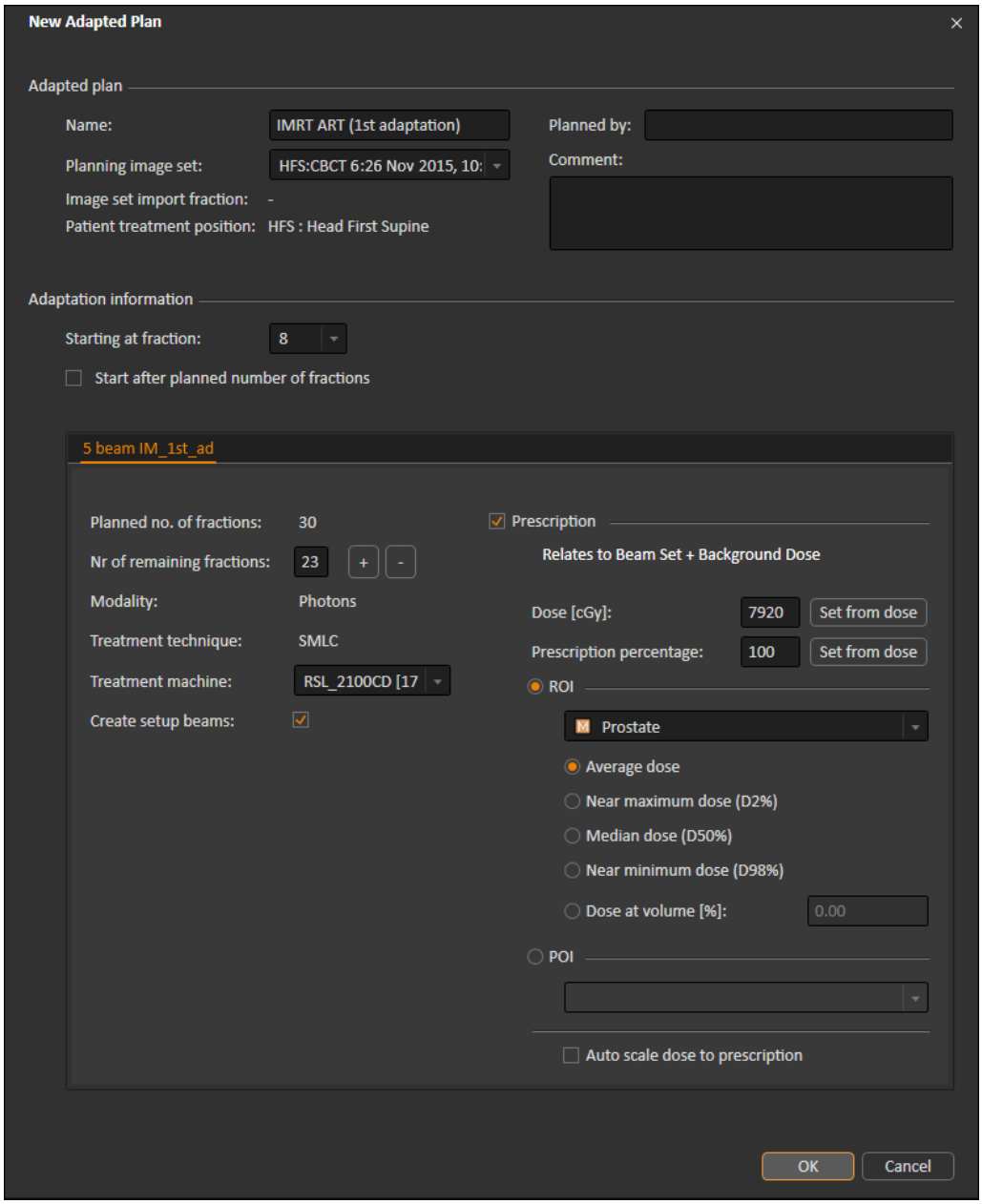


Figure 482. The New adapted plan dialog.

2. Enter a plan **Name**.
3. Select **Planning image set**.

4. Enter information in the **Planned by** field (optional).
5. Enter a **Comment** in free text (optional).
6. Select starting fraction for the adaptation in the **Starting at fraction list** or check the **Start after planned number of fractions** checkbox.

   Note: *If the selected starting fraction number for the adapted plan is higher than the number of evaluated fractions, the missing fraction doses (planned fraction doses) will be estimated with an average of the existing fraction doses.*
7. If desirable, the number of remaining fractions can be changed using the **+** and **-** buttons.
8. Select **Treatment machine**. The treatment machine selected for the original plan will be the default choice.
9. If desirable, select to **Create setup beams**.
10. Select to define a **Prescription**.
11. Click **OK**.

A new plan will be created with the same number of beam sets as the original treatment plan. In order to create a beam set in the adapted plan, the number of remaining fractions must be larger than zero. Otherwise, the beam set will not be created.

The RayStation 7 system automatically:

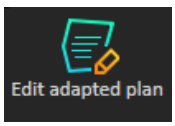
- sets the treatment position to the same as in the original plan.
- populates the dose list with the delivered fraction dose history.
- updates the beam list with beam geometry from the original plan moved to the new planning image set geometry. Isocenter for each beam is set to the isocenter for the original planning image set deformed to the new planning image set.
- updates the setup beams to the new beam geometry if the checkbox Create setup beams was checked in the New adapted plan dialog.
- sets a default dose grid which allows for dose computation on the new planning image set.
- sets the treatment machine for each beam set to the one selected in the New adapted plan dialog.
- sets the treatment delivery technique for each beam set to the same as for the respective beam set in the original plan.
- adds beam dose specification point (BDSP) corresponding to the BDSP for the original planning image set deformed to the new planning image set.
- sets the prescription for each beam set so that it relates to the beam set + background dose.

- sets the optimization goals for each beam set to the same as for the respective beam set in the original plan. The optimization goals for a beam set in an adapted plan relate to the beam set dose plus the background dose.
- sets the same optimization and segmentation settings as for the original plan.
- sets the same RBE model as for the original plan.

Note: *Always review the automatically generated adapted treatment plan data before proceeding with plan optimization and dose computation.*

Edit adapted plan

To edit the plan information, click the **Edit adapted plan** button.



This opens the Edit adapted plan dialog.

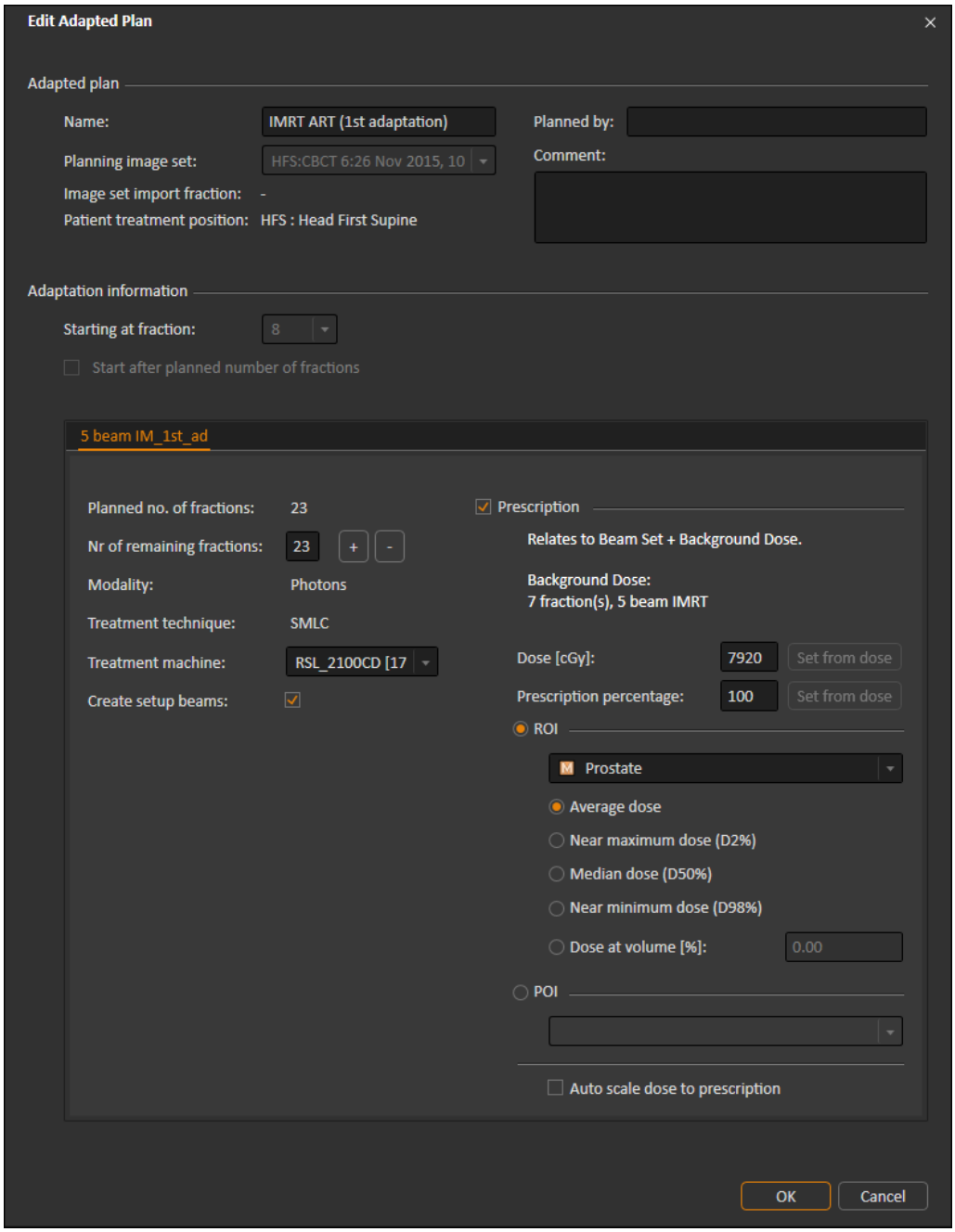
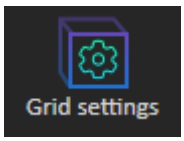


Figure 483. The Edit adapted plan dialog.

The editable parameters are **Name**, **Planned by**, **Number of remaining fractions**, **Treatment machine**, **Prescription** and if the option **Create setup beams** should be selected.

Edit the dose grid

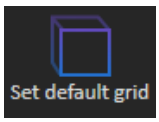
A dose grid will be created automatically when a new adapted plan is created. To edit the dose grid, click the **Edit grid** button.



This opens the Edit dose grid dialog. For more information, see *section 6.1.4 Define and edit the dose grid on page 312*.

Set the default dose grid

To set a dose grid that covers the external ROI, bolus included in the plan, Support and Fixture ROIs, click the **Set default grid** button.



View the deformable registration properties

To view the properties of the deformable registration, click the **Registration info** button.

11.3.4 Optimization of an adaptive plan

The new adapted plan can be optimized using the optimization settings from the previous treatment plan. Since the beams in the adapted plan already have segments, the only available option is to start the optimization from the current state. The optimization workspace is further described in *section 7.1 The Plan Optimization module - photons on page 518*.

Note: *Always review the automatically generated adapted treatment plan data before proceeding with plan optimization and dose computation.*

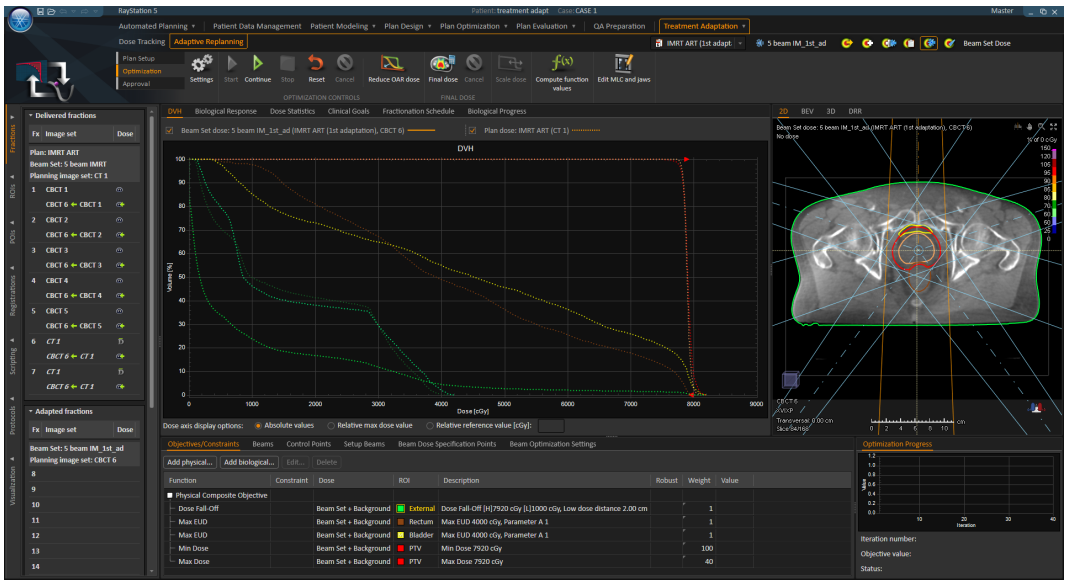


Figure 484. The optimization workspace in the Adaptive Replanning module.

11.3.5 Scale dose

The dose can be scaled to fulfill the prescription or to fulfill an arbitrary dose-volume relation for some ROI or POI. A prescription for a beam set in an adapted plan relates to the beam set dose and the background dose. The beam set dose will be scaled to achieve a plan dose of the desired dose level, which is the combined background dose and the beam set dose. This is done in the same way as for multiple beam sets. See *Use combined dose or separate beam set dose as objective/prescription for additional beam sets on page 375*.

To scale the dose:

1. Click the **Scale dose** button.

This opens the Scale dose dialog.

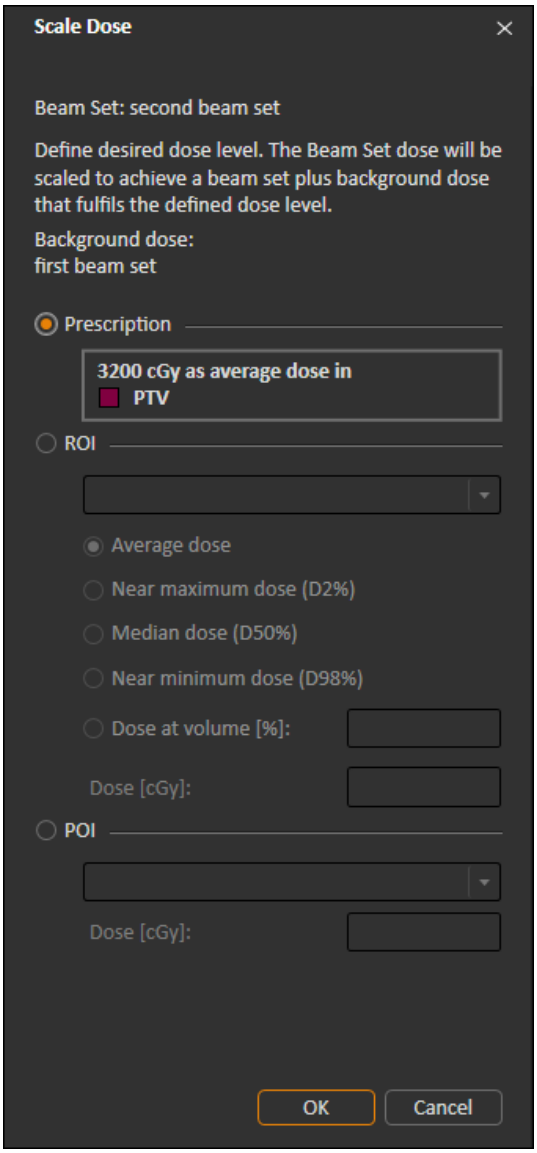


Figure 485. The **Scale Dose** dialog.

11.3.6 Approval

The **Approval** tab in the Adaptive Replanning workspace contains buttons for plan approval and for computing dose. The plan approval procedure is described in *section 8.1.15 Plan approval on page 748*.

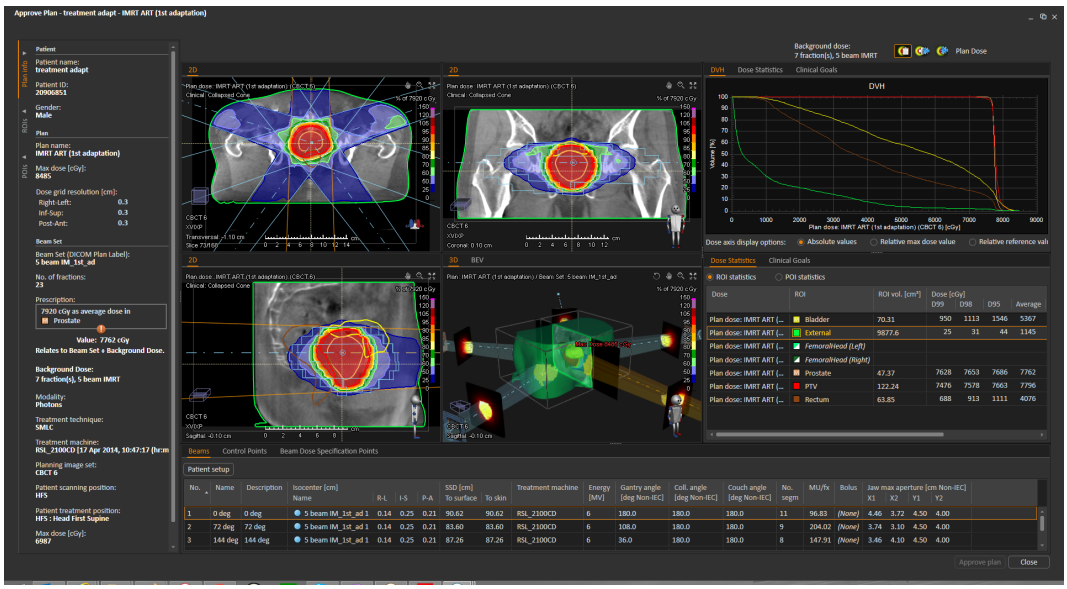


Figure 486. The Approve plan workspace in the Adaptive replanning module.

Before the adaptive plan can be approved, both the **Plan dose** and **Beam Set dose** must be reviewed. These buttons are located in the top right corner of the **Approve plan** window.

An approved adapted plan can be used for dose tracking purposes in the Dose tracking module. See *section 11.2 Dose Tracking on page 868* for more information.

A DEFINITIONS

Term	Meaning
BEV	Beam's Eye View
CBCT	Cone Beam Computed Tomography
CT	Computed Tomography
DCR	Digitally Composited Radiograph
DVH	Dose Volume Histogram
deg	When the term deg is seen in RayStation 7 this refers to degrees
DMLC	Dynamic Multi-Leaf Collimator
DRR	Digitally Reconstructed Radiograph
External ROI	The ROI used to define patient outline. Defines the region used for dose computation, together with BOLUS for beam, SUPPORT and FIXATION ROIs.
GUI	Graphical User Interface
IMRT	Intensity Modulated Radiation Therapy
LINAC	Linear accelerator, conventional radiation therapy treatment unit.
LS	Line Scanning
MBS	Model-Based Segmentation
MCO	Multi-Criteria Optimization
MU	Monitor Units
NP	Number of Particles. For protons the MU fields are replaced with Number of particles (NP) if the machine has Primary Dosimetry Unit set to Number of Particles.
NTCP	Normal tissue complication probability
OAR	Organ at risk
P+ or PPLUS	Probability of complication free tumor control
PBS	Pencil Beam Scanning

Term	Meaning
PHY	Physical ion dose (used in carbon ion planning)
POI	Point of Interest
RBE	Relative Biological Effectiveness (used in carbon ion planning)
RBE dose	RBE weighted dose is in RayStation and this manual referred to as RBE dose.
ROI	Region of Interest
ROI Geometry	The image set-specific geometric representation of an ROI
SMLC	Segmental Multi-Leaf Collimator
SOBP	Spread Out Bragg Peak
SSD	Source to Skin Distance
SUV	Standardized Uptake Value
TCP	Tumor control probability
UI	User Interface
VMAT	Volumetric Modulated Arc Therapy

B SHORTCUTS

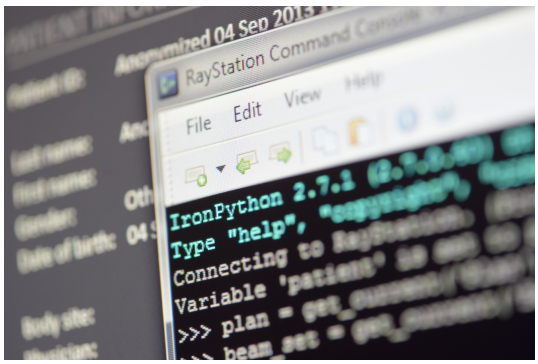
Several shortcuts can be used in RayStation 7. To access the **Shortcuts** dialog, select **Help: View shortcuts** from the RayStation menu.

The following table lists the shortcuts in RayStation 7.

Shortcut	Command
F1	Opens the RayStation help
Ctrl + Z	Undo
Ctrl + Y	Redo
Ctrl + O	Open patient case dialog
Ctrl + S	Save
Ctrl + P	Create plan report
Ctrl + D	Compute final dose
T, A	Set the current window to Transversal (aka Axial)
C	Set the current window to Coronal
S	Set the current window to Sagittal
L	Set the current window to Slice Aligned (Used to allow for contouring in a tilted image set.)
I	Zoom in, current window (factor 1.10)
O	Zoom out, current window (factor 1.10)
R	Reset zoom for current window
P, PageUp	Scroll to previous slice
N, PageDown	Scroll to next slice
Shift + P	Move to previous 4DCT or 4DMR phase
Shift + N	Move to next 4DCT or 4DMR phase
Arrow up	Move to previous beam
Arrow down	Move to next beam

Shortcut	Command
Arrow left	Move to previous segment (BEV, 3D view)
Arrow right	Move to next segment (BEV, 3D view)
Ctrl + mouse button	By holding down the Ctrl key the mouse can be used to zoom any patient view at any time
Shift + mouse button	By holding down the Shift key the mouse can be used to pan any patient view at any time
Middle mouse button/ mouse wheel	By holding down the middle mouse button the mouse can be used to rotate the 3D view
Middle mouse button/ mouse wheel	Align concurrent patient views. Press the middle mouse button somewhere in the patient view, all views will scroll to display the slice containing that point. By pressing and holding down the middle mouse button and moving the mouse, it is possible to easily scroll through the image data of the other patient planes.
Alt + mouse wheel, +/-	Change Brush/Nudge tool size
X	Temporarily disable edge detection for smart brush and smart contour
Alt	Force draw mode when using brush and smart brush
Z	Force erase mode when using brush and smart brush
Enter	Accept current interpolated contour
Alt + mouse button	Move fusion pattern (checkers, blinds)

C SCRIPTING



Common processes and use cases in RayStation 7 can be automated using scripting. The scripts can be run from a database or from a file. The database scripts are available for all users and can be categorized as general scripts or as module specific scripts.

- General scripts can be run from all modules.
- Module specific scripts can only be run from a specific module.

For more detailed information about scripting, refer to *RSL-D-RS-7.0-SG, RayStation 7 Scripting Guideline*.

In this chapter

This chapter contains the following sections:

C.1	The Scripting tab	p. 906
C.2	Search for a script in the database	p. 907
C.3	Run a script from the database	p. 908
C.4	Script management	p. 909
C.5	Create a new script	p. 911

Precautions

WARNING!

Validate all scripts for their intended use. Carefully validate all scripts before they are used clinically. Be aware that not all actions are scriptable/recordable. A recorded script may not be equivalent to the GUI steps performed in RayStation when recording. (54133)

WARNING!

Coordinate systems in Scripting. In scripting, coordinates are always interpreted according to the DICOM coordinate system specification. For machine coordinate systems, the IEC standard and the DICOM standard are equivalent. Machine scales are not taken into account. (54108)

WARNING!

Units in Scripting. In scripting, dose is always measured in cGy. Clinic settings for Gy/cGy are not taken into account. (54127)

WARNING!

Dosimetry unit in scripting. In scripting, the primary dosimetry unit is always MU. Configuration of other primary dosimetry units is not taken into account. All parameters related to beam meterset are named MU and contains values in MU. However, there exist script methods GetBeamNP() and SetBeamNP() on ion beams with primary dosimeter unit NP. (126108)

WARNING!

Use exception handling with care. When executing a script, exceptions not caught in the script will be handled by the script framework automatically, causing the script execution to stop and an error message to be displayed.

If exceptions are manually caught in the script (by adding exception handling to the script), it may override the script framework exception handling and as a consequence, the error message will not be displayed.

If exception handling is added to the script, ensure that all important error messages are displayed. (54100)

WARNING!

Line Scanning: Recompute dose after changing number of paintings using scripting. If the number of paintings for each segment is changed using scripting for a Line Scanning plan, there might be a slight mismatch between the planned and delivered dose. The reason for this is that the dose is not invalidated when changing the number of paintings. However, it will affect the MU rounding in the Sumitomo treatment Control system. To correctly account for this, the dose should be invalidated by the user (e.g., by changing the dose grid to a new value and then changing it back to the previous value) and then recomputed. (150000)

C.1 THE SCRIPTING TAB

The Scripting tab has three main sections:

- **General scripts.** Contains a list of the general scripts in the database. Non-validated scripts are indicated with an exclamation mark.
- **Module specific scripts.** Contains a list of the module specific scripts in the database.
- **Script execution.** Contains the script execution status and details. The script execution can be stopped by clicking the stop button.

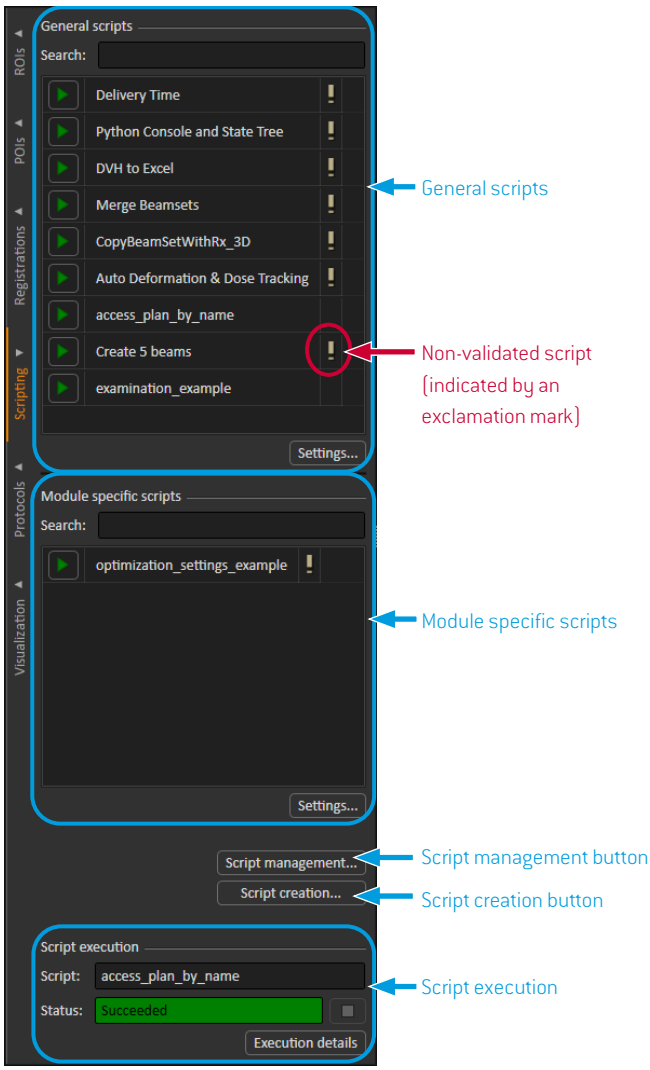


Figure 487. The **Scripting** tab.

C.2 SEARCH FOR A SCRIPT IN THE DATABASE

To search for a script in the database:

1. Click the **Settings** button in either the **General scripts** section or the **Module specific scripts** section to open the **Script list settings** dialog.

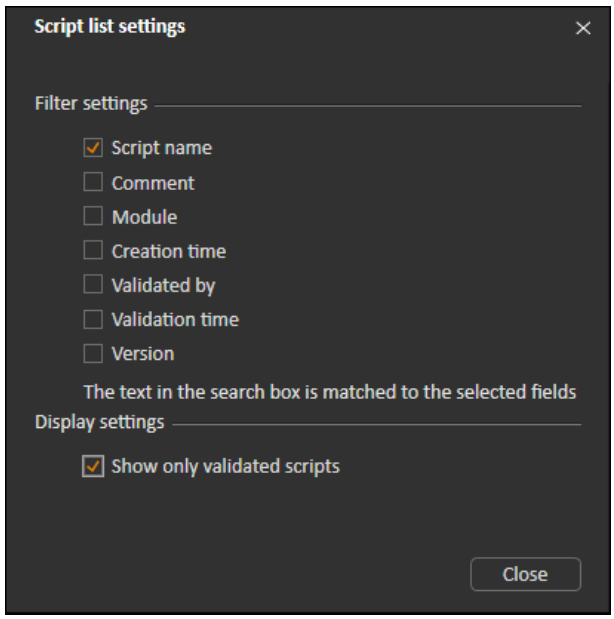
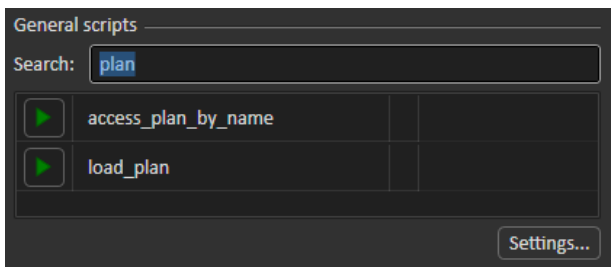


Figure 488. The **Script list settings** dialog.

2. Select the desired **Filter settings**. The filter settings control what is possible to search for in the **Search** field.
3. If desired, select to only show validated scripts in the **Display settings**.
4. Click **Close**.
5. Enter the search text in the **Search** field in the applicable section.

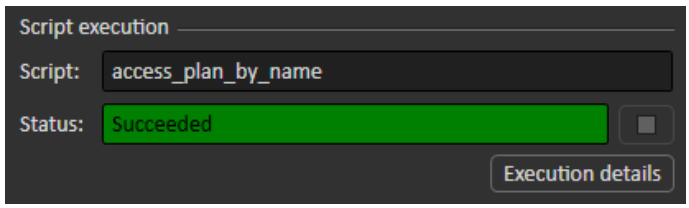


C.3 RUN A SCRIPT FROM THE DATABASE

To run a script from the database:

1. Select a script from one of the lists in the **Scripting** tab.
2. Click the play button.

The script will be executed and the script execution status and name are displayed at the bottom of the **Scripting** tab.



3. Click the **Execution details** button. This opens the Execution details dialog which consists of two tabs where the **Execution details** tab displays all the state changes that occurred during the run and the **Execution summary** tab which lists all modified patients.
4. If desired, the script execution can be stopped by clicking the stop button.

C.4 SCRIPT MANAGEMENT

Click the **Script management...** button. This opens the Script management dialog.

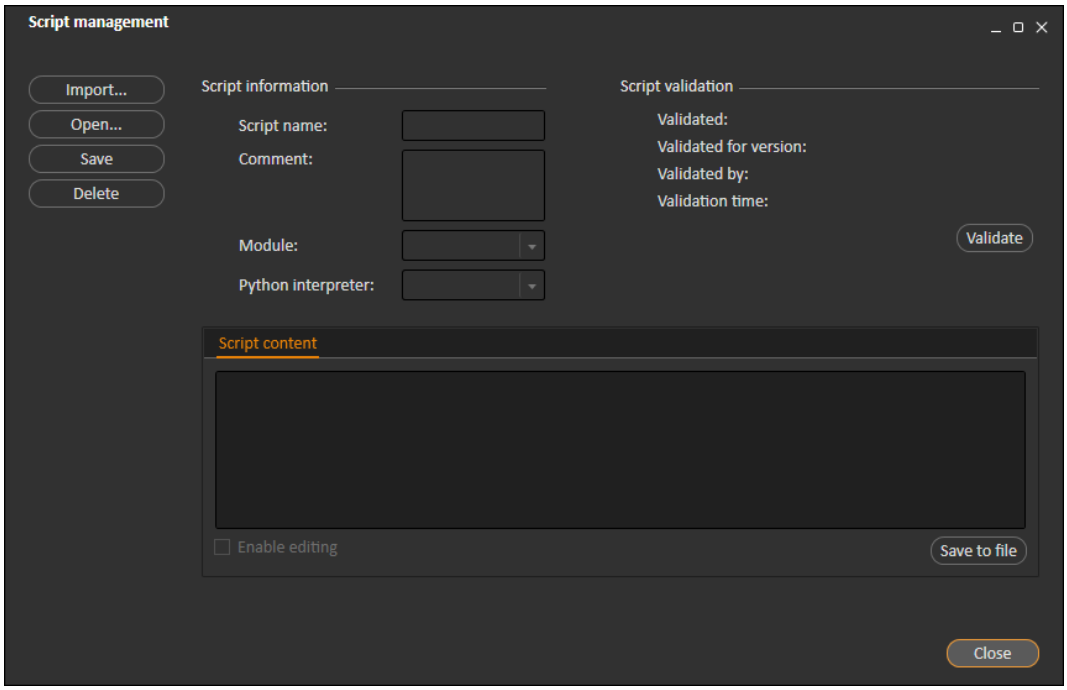


Figure 489. The **Script management** dialog.

The Script management dialog provides Script information and Script validation information.

- The **Script information** area lists the script name, a comment (if a comment was entered at script creation), the module where the script can be used and which Python interpreter the script should be executed with.
- The **Script validation** area states if the script is validated, the RayStation version that the script is validated for, the user name of the user who validated the script and the date and time of validation.

From the Script management dialog it is possible to:

- **Import** a script from file and add it to the database.
- **Open** a script in the database.
- Edit the script content. (Check the **Enable editing** checkbox).
- **Save** the script to the database or save the script content to a file. (The command Ctrl + S can be used to save the script content to the database)

- **Delete** a script from the database. Only members of the RayStation-Administration group are allowed to delete validated scripts.
- **Validate** a script. A script can be validated and will then be protected from editing. The validation is associated with specific versions of RayStation and IronPython or CPython. For scripts executed in CPython, the validation is also associated with specific versions of the CPython packages pythonnet and numpy. If one or more software versions associated with the validated script are changed, the validation is voided and needs to be performed again. Only members of the RayStation-Administration group are allowed to validate scripts. A script that is validated must be invalidated before it can be edited.

Note: *Always use script validation before clinical use of the script. If a non-validated script is executed, a warning will be displayed, but the script can continue running if this warning is disregarded.*

C.5 CREATE A NEW SCRIPT

A script (file) can be created in two ways;

- By recording a set of actions executed in RayStation.
- By directly entering code in the **Script content** tab.

Record a script

To record a script:

1. Click the **Script creation…** button. This opens the **Script creation** dialog.

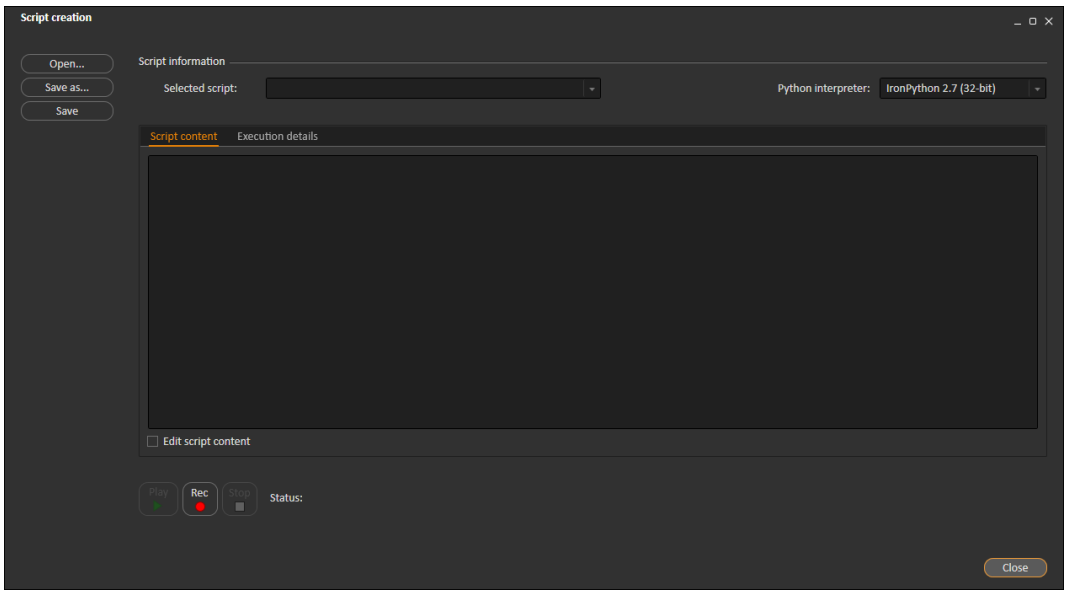


Figure 490. The **Script creation** dialog.

2. Click the **Rec** button (the **Script creation** dialog is automatically closed).

3. Perform a set of actions.
4. Stop the recording by clicking the **Stop** button in the **Script creation** dialog or in the **Scripting** tab.
5. After recording, view the **Script content** and the **Execution details**.

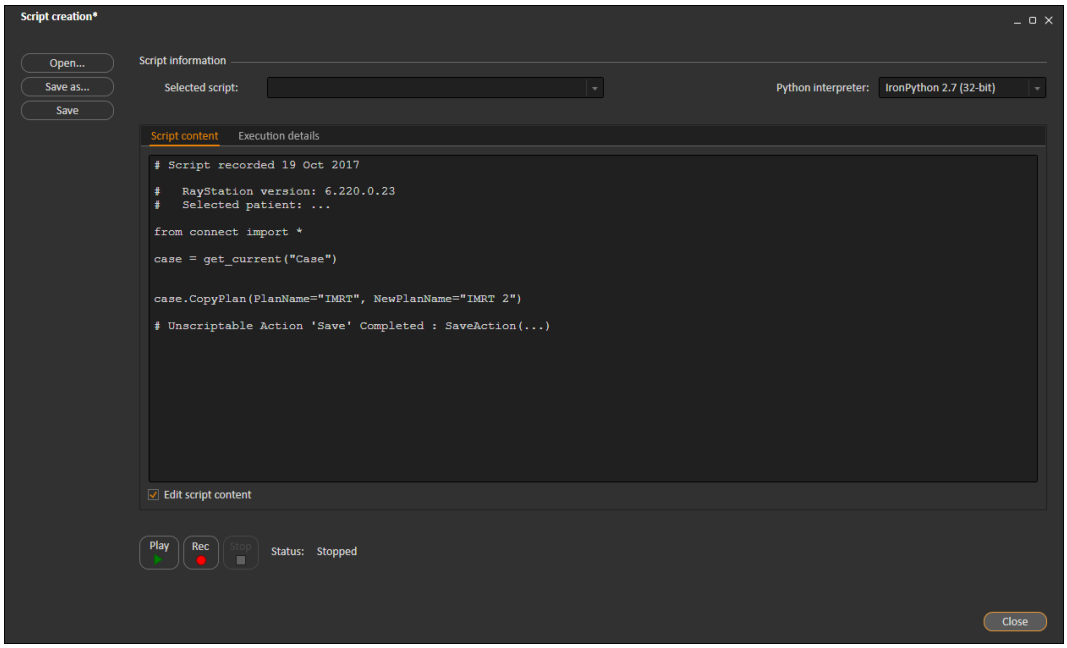
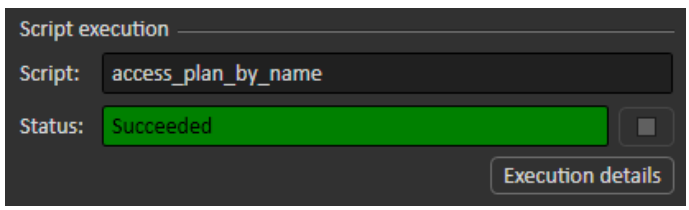


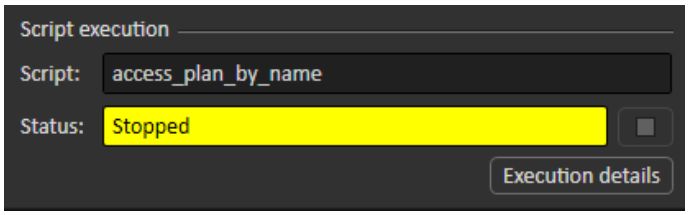
Figure 491. The **Script creation** dialog, after a script has been recorded.

6. If desired, check the **Edit script content** checkbox and edit the script content.
7. Save the script as a file by clicking the **Save** or **Save as...** button. Ctrl + S can also be used.
8. Use the **Python interpreter** drop-down list to select which Python interpreter the script should be executed with.
9. To run the recorded script, click the **Play** button.

The script will be executed and the script execution status and name are displayed in the status field at the bottom of the **Scripting** tab.



10. Click the **Execution details** button. This opens the **Execution details** dialog which consists of two tabs where the **Execution details** tab displays state changes that occurred during the run and the **Execution summary** tab which lists all modified patients.



To stop a script during run, click the **Stop** button. The script execution status field will indicate that the script was stopped.

Note: *In the execution details, sub modifications may be listed that are part of an overall modification of the patient. The completion of the sequence of modifications are indicated at the end of the last sub modification.*

Create or edit a script from file

To open a script file:

1. Click the **Script creation ...** button. This opens the **Script creation** dialog.

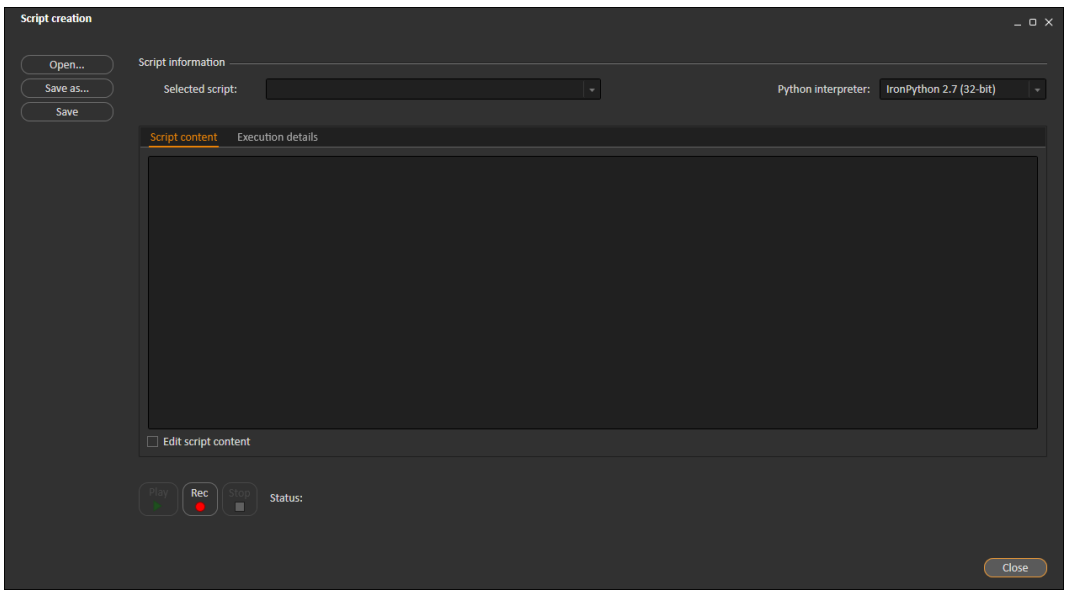


Figure 492. The **Script creation** dialog.

2. Click the **Open...** button, select a script file and click **Open** or select a script from the **Selected script** drop-down list (The last five scripts are selectable in the list.) This opens the script content in the **Script content** tab. The selected script field shows which script is open.

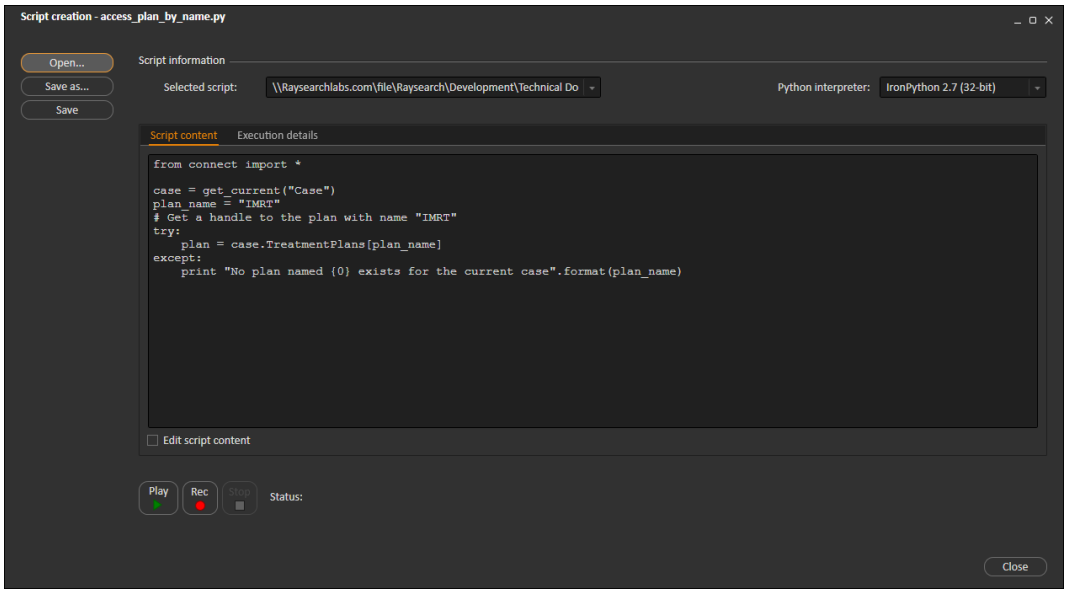
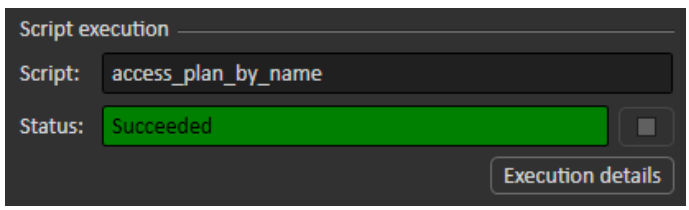


Figure 493. The **Script creation** dialog, displaying the content in the script file.

3. If desired, check the **Edit script content** checkbox to enable editing of the script.
4. Use the **Python interpreter** drop-down list to select which Python interpreter the script should be executed with.
5. To run the script, click the **Play** button.

The script will be executed and the script execution status and name are displayed at the bottom of the **Scripting** tab.



6. Click the **Execution details** button. This opens the **Execution details** dialog which consists of two tabs where the **Execution details** tab displays all the state changes that occurred during the run and the **Execution summary** tab which lists all modified patients.

D SYSTEM ADMINISTRATION

This section describes the various tools and procedures associated with system administration such as database administration, the Clinic Settings application and how to update the graphic card drivers.

In this chapter

This chapter contains the following sections:

D.1	Database administration	p. 918
D.2	The Clinic Settings application	p. 920
D.3	The RayStation Storage Tool application	p. 940
D.4	GPU settings	p. 961
D.5	Graphics card update	p. 966

D.1 DATABASE ADMINISTRATION

It is recommended that all RayStation databases (the patient database, the machine database, the clinic database and the resource database) are set to recovery model full. This option makes it possible to run frequent backups and minimizes the risk of losing data in a database crash.

Database Backups

- Regular backups of all RayStation databases should be scheduled and the success of these backups verified on a regular basis. We recommend that Full backups are performed as often as time, space and system usage allows and/or differential backups. Transaction Log Backups are also recommended on an hourly basis – but the frequency can be increased or decreased based on the specific clinic needs. Backups of the databases should also be stored in an alternative location e.g., offsite. RayStation alerts on the start screen if no valid backups can be found.
- SQL Server OS maintenance. We recommend that the fragmentation on drives hosting the SQL data files be checked for defragmentation. Where defragmentation is required this should be performed during maintenance windows.
- SQL Indexing. It is highly recommended that re-indexing of the RayStation Databases occurs on a regular basis, e.g., following every full database backup. Fragmented indexes affect the performance of RayStation and might even cause crashes.

Firewall

The firewall can be turned on for the SQL server but must have accessibility on the default SQL port (1433) if using static port addressing and all UDP ports. If using dynamic ports for SQL it is recommended that all TCP and UDP ports for the IP ranges that the RayStation clients will use should be allowed access through the Firewall on the SQL server. The firewall also needs to be configured to allow FileStream data access. Allow inbound traffic on ports 139 and 445.

Firewall software should also be considered when setting up access to DICOM data within RayStation or by RayStation on external systems. Firewall software on client machines running RayStation will need to be configured based on the access solution being provided but will at minimum need TCP and UDP access to the SQL Server.

User groups

RayStation uses Windows active directory group membership to assign roles to users. To be able to delete patients, change system settings, approve plans etc., the user has to be a member of one of the user groups described in the table below.

User group	Description
RayStation-Administration	Users belonging to this group are authorized to delete patients, approve templates, delete approved templates and change settings in Clinic Settings.
RayStation-PlanApproval	Users belonging to this group are authorized to approve structure sets and plans.
RayStation-BeamCommissioning	Users belonging to this group are authorized to commission imaging systems and treatment machines.

Where a clinic has specific naming conventions for Active Directory Groups the Group mapping section on the **Preferences** tab of Clinic Settings can be used to provide a group mapping.

Resource database

All settings and database systems visible in the RayStation Storage Tool are stored in the resource database. The resource database is not part of any database system. There can be several different resource databases.

D.2 THE CLINIC SETTINGS APPLICATION

In the Clinic Settings application it is possible to edit clinical settings such as Dose settings, Report settings and DICOM Storage SCP. Modifying parameters in Clinic Settings will affect all RayStation 7 clients. RayStation 7 clients need to be restarted in order for new clinic settings to take effect. Access to the Clinic Settings application requires membership of the RayStation-Administration group or mapped equivalent.

Note: *Ensure that only one instance of the Clinic Settings application is run at a time. Close the application when done.*

Note: *Ensure that all RayStation 7 users are informed about changes made in the Clinic Settings application.*

In this section

This section contains the following sub-sections:

D.2.1	Recommended workflow	p. 921
D.2.2	The Preferences tab	p. 922
D.2.3	The Ion Settings tab	p. 927
D.2.4	The DICOM tab	p. 929
D.2.5	Report Templates	p. 933
D.2.6	License	p. 935
D.2.7	HPC	p. 937

D.2.1 Recommended workflow

1. Close all RayStation 7 clients.
2. Launch the Clinic Settings application from RayStation Launcher.
    a. Edit the settings.
    b. Save the new settings.
3. Close the Clinic Settings application.
4. Start one RayStation 7 client and verify that the new settings have been implemented.
5. Start all RayStation 7 clients.

D.2.2 The Preferences tab

To run the application:

1. On a machine where the Clinic Settings option has been selected during installation, the Clinic Settings application can be launched from the RayStation Launcher.

   This starts the application and opens the **Preferences** tab in the **Clinic Settings** dialog.

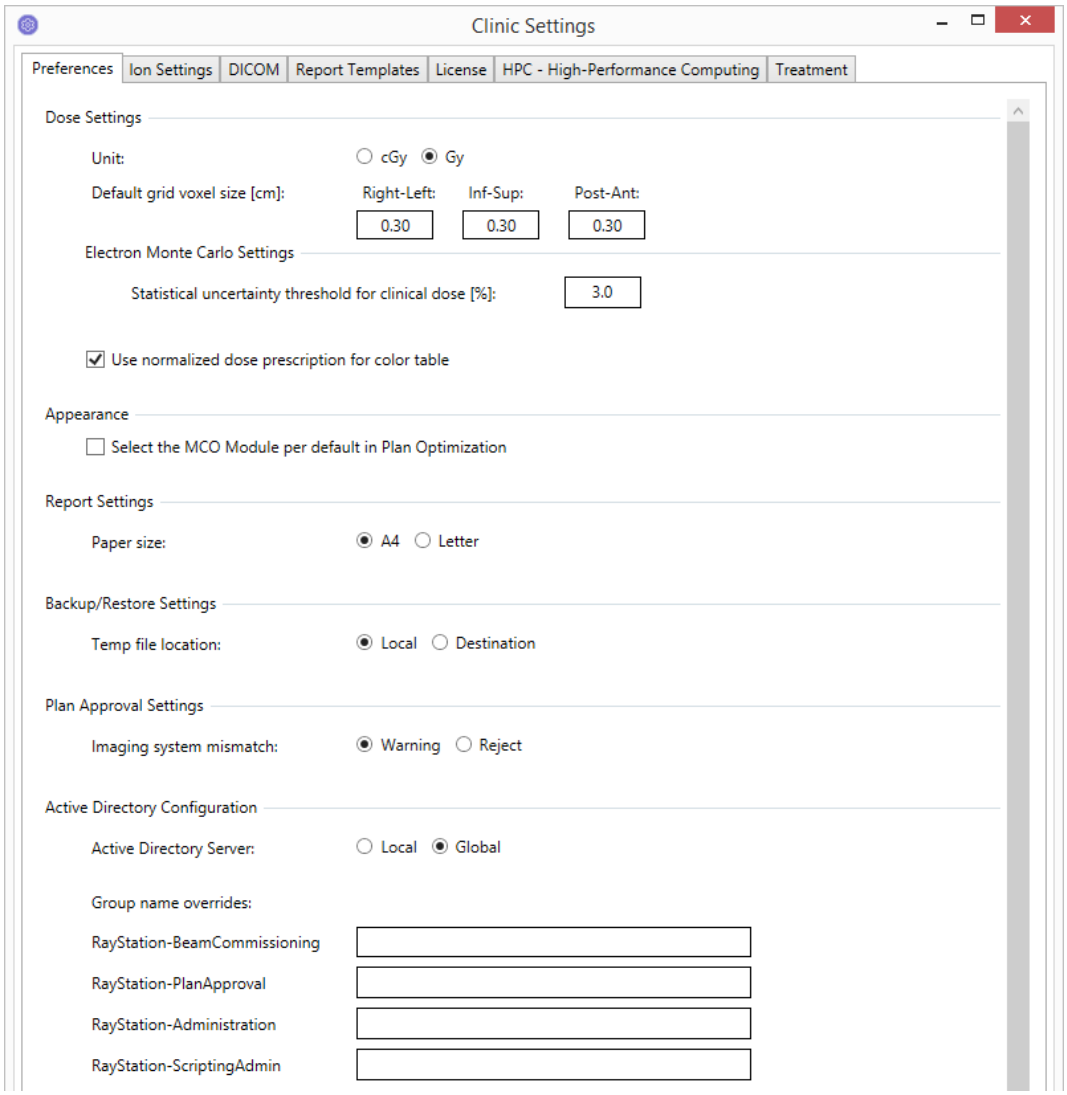


Figure 494. The **Preferences** tab in the Clinic Settings application.

2. The dose unit can be set to **cGy** or **Gy** and the **Default grid voxel size** can be entered (in cm).

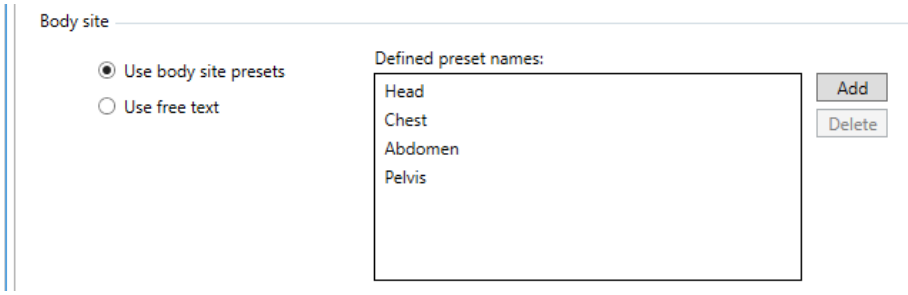
3. If electrons are used, edit **Electron Monte Carlo Settings**. Enter **Statistical uncertainty threshold for clinical dose [%]**. The number specifies the maximum allowed statistical uncertainty per beam for an electron dose to be classified as 'clinical'. The statistical uncertainty is defined as the average statistical uncertainty (1 std. dev.) for all voxels with dose larger than 50% of the max dose. The statistical uncertainty is specified relative to the max dose per beam.
4. Check or uncheck the **Use normalized dose prescription for color table** checkbox do determine if the 100% level of the dose color table should be dependent on prescription percentage or not:
   - If this option **is** checked, the 100% level of the dose color table will be *Prescription dose value / Prescription percentage*.
   - If this option **is not** checked, the 100% level of the dose color table will be *Prescription dose*.

   For more information about prescription percentage, see to *section 6.1.12 Define or modify prescription on page 343*.
5. Select to open the MCO module per default in Plan Optimization.
6. Edit **Report** settings. The Paper size can be set to A4 or Letter.
7. Edit **Backup/Restore** settings. When an RSBAK file is created, temporary files are created. The location of these files might influence performance, depending on the system configuration. The location of temporary files can be set to either **Local** (local directory for temporary files) or **Destination** (the same directory as the destination file).
8. Edit **Plan Approval** settings. Select if an imaging system mismatch between imported DICOM data and selected imaging system should trigger a warning (**Warning**), or prevent the user from proceeding with plan approval (**Reject**).
9. The **Active Directory Configuration** is performed during installation but can be edited using the Clinic Settings application.

   Note: *Changing the RayStation - Administration group to an invalid group will prevent the Clinic Settings application from launching and lock the system.*

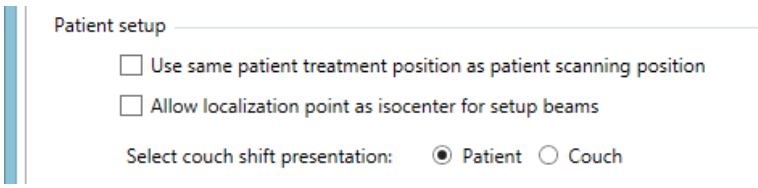
   Edit the **Active Directory Configuration** to override the default AD group names used for RayStation security.

10. Edit **Body site** settings. The body site of a case can be set in the **Edit case data** dialog in RayStation (see *section 4.3.5 Edit case data on page 125*).



- Select **Use body site presets** to show a list of predefined body sites in the **Edit case data** dialog. The list of predefined body sites is managed in the **Defined preset names** area in Clinic Settings. Use the **Add** and **Delete** buttons to add or delete body sites in the list.
- Select **Use free text** to allow the user to enter any body site in free text the **Edit case data** dialog.

11. Edit **Patient setup** settings (optional):


Patient setup
Use same patient treatment position as patient scanning position
Allow localization point as isocenter for setup beams
Select couch shift presentation:
Patient
Couch

- Select to **Use same patient treatment position as patient scanning position** as default by checking the corresponding checkbox.

  If this option **is** checked, the patient treatment position defaults to the patient scanning position in the planning image set when creating new plans. The patient treatment position cannot be edited.

  If this option **is** checked and a plan is opened where the patient treatment position is not the same as the patient scanning position, final dose cannot be computed for that plan.

- Select to **Allow localization point as isocenter for the setup beams** by checking the corresponding checkbox.

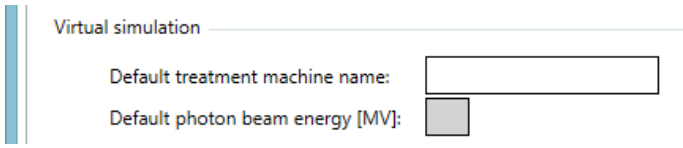
  If this option **is not** checked, setup beams are always created using isocenters from treatment beams. Only check this option if there is a need for setup beams using the localization point as isocenter.

- Select coordinate system for the couch shift:

  - the **Patient** coordinate system

- the **Couch** coordinate system

12. For Virtual Simulation:



- Enter a **Default treatment machine name**.

  The entered treatment machine will be used as default when creating a default plan in the Virtual Simulation module.

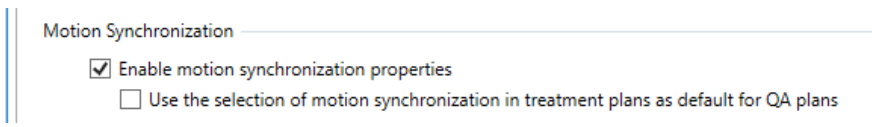
  If the entered name does not exist or if no name is entered, the system will select the first available treatment machine in alphabetical order.

- Enter **Default photon beam energy [MV]**.

  The entered energy will be used as default when creating a default plan in the Virtual Simulation module.

  If the entered energy does not exist or if no value is entered, the system will select the lowest available energy.

13. For Motion Synchronization (optional):


Motion Synchronization
Enable motion synchronization properties
Use the selection of motion synchronization in treatment plans as default for QA plans

Check the **Enable motion synchronization properties** checkbox to enable export of motion synchronization parameters for beam sets.

Check the **Use the selection of motion synchronization in treatment plans as default for QA plans** checbox if QA plans should inherit parameters from the verified treatment plan. Motion Synchronization will be disabled by default for QA plans.

14. For Online help (optional):

Enter a **Url** for the RayStation help files.

For more information about the RayStation help configuration, refer to the *RSL-D-RS-7.0-SEG, RayStation 7 System Environment Guidelines*.

15. Disable auto recovery (optional). Uncheck the **Enable auto recovery** checkbox to disable auto recovery.
16. Disable warnings when uploading an unapproved template (optional). Uncheck the **Show warning if loading an unapproved template** checkbox to disable these warnings.
17. Click **Save**.

D.2.3 The Ion Settings tab

The **Ion Settings** tab contains default settings for plans made on ion machines.

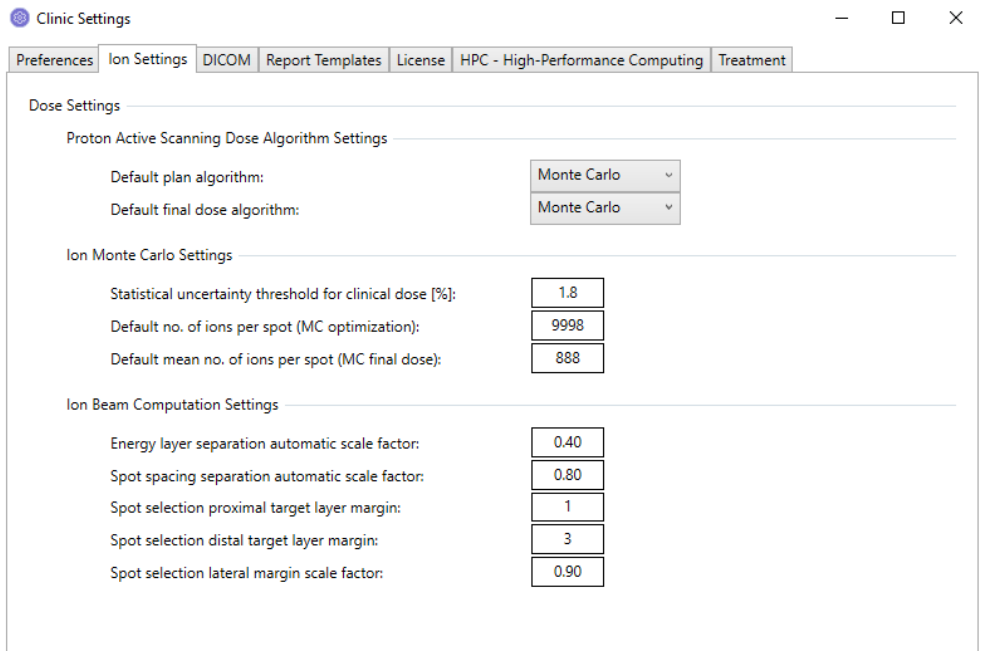


Figure 495. The **Ion Settings** tab in the Clinic Settings application.

1. Edit **Proton active scanning dose algorithm settings**.
   - Enter the **Default proton active scanning plan algorithm** to set the default algorithm for proton planning dose calculation. This dose algorithm will be the default for optimization, including MCO Pareto plan generation and deliverable plan generation.
   - Enter the **Default proton active scanning final dose algorithm** for proton final dose calculation.

2. If protons are used, edit **Ion Monte Carlo Settings**.
   - Enter **Statistical uncertainty threshold for clinical dose [%]**. The number specifies the maximum allowed statistical uncertainty per beam for proton dose to be classified as 'clinical'. The statistical uncertainty is defined as the average statistical uncertainty (1 std. dev.) for all voxels with dose larger than 50% of the max dose. The statistical uncertainty is specified relative to the max dose per beam.
   - Enter **Default no. of ions per spot (MC optimization)**. The value specifies the default number of ions per spot during Monte Carlo optimization.

- Enter **Default mean no. of ions per spot (MC final dose)**. The value specifies the default number of ions per spot when computing final dose using the Monte Carlo dose engine.

WARNING!

Maximum allowed statistical uncertainty does not affect already computed clinical Monte Carlo dose for protons. When changing the Maximum allowed statistical uncertainty for clinical Monte Carlo proton dose, be aware that already computed doses are not affected. Doses computed prior to the change may therefore be marked as clinical although they have a statistical uncertainty that should not result in clinical dose if they were recomputed. (369534)

3. Edit **Default ion beam computation settings**. The following settings affect both proton and carbon ion plans.
   - Enter **Energy layer separation automatic scale factor**. The value specifies the default scaling factor used when energy layers are determined based on Bragg peak width in water.
   - Enter **Spot spacing automatic scale factor**. The value specifies the default scaling factor used when spot spacing for each layer is determined based on spot size at bragg peak maximum in water.
   - Enter **Spot selection proximal target layer margin**. The value specifies the default proximal target margin defined in number of additional energy layers in front of the target.
   - Enter **Spot selection distal target layer margin**. The value specifies the default distal target margin defined in number of additional energy layers behind the target.
   - Enter **Spot selection lateral margin scale factor**. The value specifies the default scale factor for the automatically determined lateral margin, when using automatic scale factor.

D.2.4 The DICOM tab

The **DICOM** tab contains the DICOM Application Entities and the DICOM Settings.

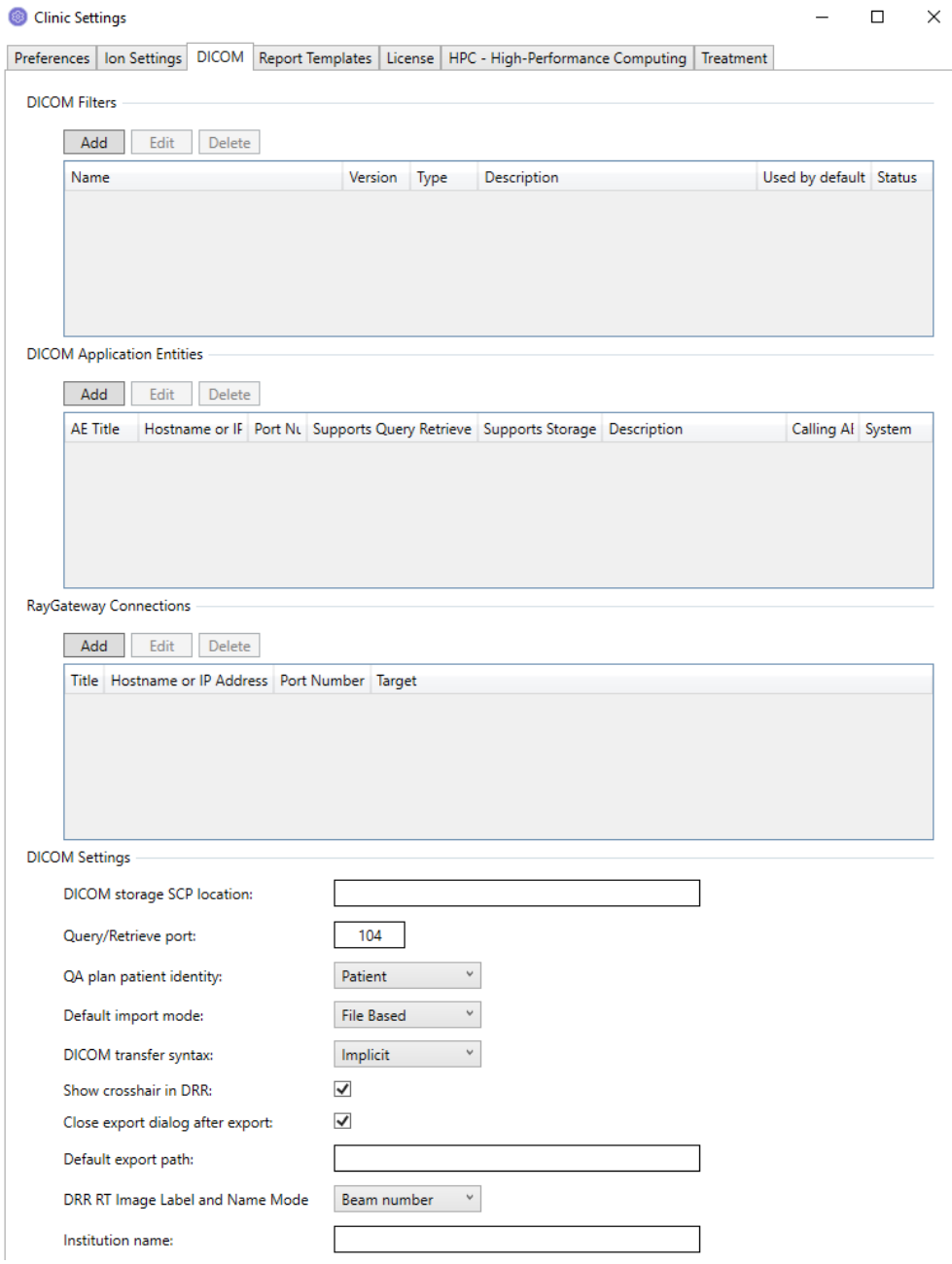


Figure 496. The **DICOM** tab in the Clinic Settings application.

DICOM Application Entities

A DICOM device on a network is referred to as an Application Entity Title (AE Title). An AE Title can take on many different forms, for example Service Class User (SCU), Service Class Provider (SCP), Storage SCP and Picture Archiving and Communication System (PACS). These terms are explained with the following example; a CT scanner sending images to a Storage SCP. In this case, the CT scanner requests to send data to the Storage SCP, making the CT scanner the SCU. Each AE is often associated with a certain service, for example storing images. The combination of the data that is processed (the IOD's) and the service provided is called Service-Object-Pair (SOP). In the example above, storing a CT image from a CT machine to a Storage SCP corresponds to the CT Storage SOP. A PACS can be seen as development of the Storage SCP. A PACS not only supports the Storage SCP but also allows other AE's to query and retrieve data from it by requesting data to be sent from it (using the C-MOVE request).

To add DICOM Application Entities:

1. Click the **DICOM** tab in the Clinic Settings application.
2. Click **Add** in the **DICOM Application Entities** section. This opens the **Add AE Title** dialog.

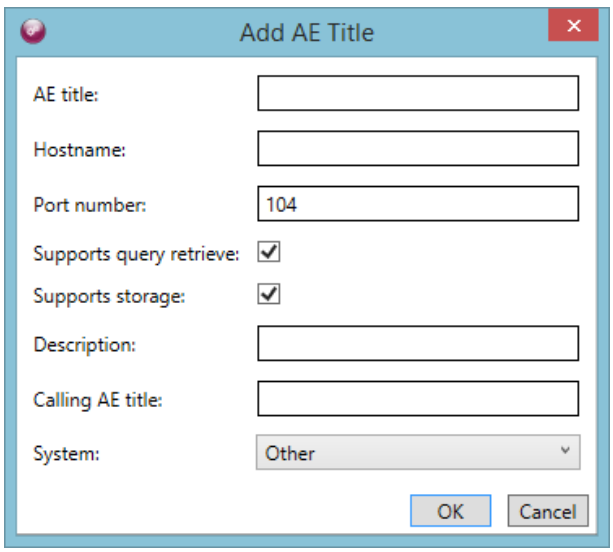


Figure 497. The **Add AE Title** dialog.

3. Enter **AE title** of peer (PACS or Storage SCP).
4. Enter **Hostname**.
5. Enter **Port number**.
6. Select if the application **Supports query retrieve**.
7. Select if the application **Supports storage**.

8. Enter a **Description**.
9. Enter **Calling AE title**. This is automatically set to hostname if left blank.
10. Select **System** (Other or ExacTrac). ExacTrac should only be selected for ExacTrac.

RayGateway Connections

In order to communicate with other systems, such as iDMS, a RayGateway connection is required. By specifying such a connection, RayStation will be able to import and export data through the selected RayGateway and to the target systems. How the actual RayGateway is set up and how it communicates with the target systems is specified during installation. In the Clinic Settings application the only thing that needs to be specified is the address and port of the RayGateway, and which target system the connection is meant for. The title acts like an identifier and needs to be unique. The title is what will be displayed in the RayStation application.

To add a RayGateway connection:

1. Click the **DICOM** tab in Clinic Settings application.
2. Click **Add** in the **RayGateway Connections** section. This opens the **Add RayGateway Connection** dialog.

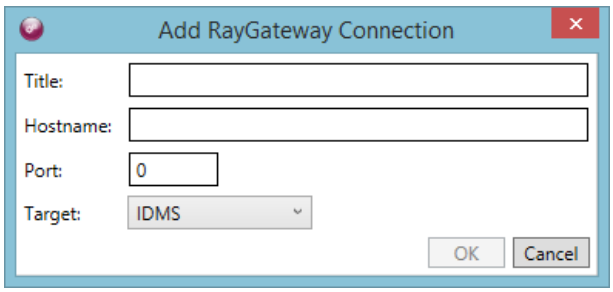


Figure 498. The **Add RayGateway Connection** dialog.

3. Enter a **Title**. This is what will be shown in the RayStation application.
4. Enter a **Hostname**. This is the hostname or the IP address of the RayGateway.
5. Enter the **Port** for the RayGateway.
6. Select the **Target** system. This is the target system that the RayGateway should communicate with when using the connection.
7. Click **OK**.

DICOM Settings

To enter DICOM settings:

1. Enter **DICOM Storage SCP location**.

2. Enter **Query/Retrieve port**: Set the local port for the SCP server that is used in query retrieve. The default port is 104 but it can be set to any unused port.

   Note: *The firewall must allow connection to the RayStation system for the specified port.*

3. Enter **QA Plan Identity**. Select one of the following options:

   - **Patient**: RT Plan and RT Dose exported from the QA Preparation module will use the patient name and ID. Only QA Plans and dose can be exported.
   - **Phantom**: All data exported from the QA Preparation module will use the QA phantom name and ID.

4. Enter **Default import mode**: Specify the import mode that will be used by default in the DICOM import dialog; **File Based**, **Query/Retrieve** or **Storage SCP**.
5. Enter **DICOM transfer syntax**. Select one of the following options:

   - **Implicit**: Export using Implicit VR Endian (1.2.840.10008.1.2) as DICOM Transfer Syntax.
   - **Explicit**: Export using Explicit VR Little Endian (1.2.840.10008.1.2.1) as DICOM Transfer Syntax.

6. Select to **Show crosshair in DRR** to show a crosshair in the exported DRR images. Uncheck to show a crosshair with the center removed, in order to obscure the image center less.
7. Select to **Close export dialog after export** by checking the corresponding checkbox.
8. Enter **Default export path**. Enter a valid directory path.
9. Enter **DRR Label and Name Mode**. Select one of the following options when writing RT Image Label (3002,0002) and RT Image Name (3002,0003) when exporting RT Image:

   - **Beam Number**: Use Beam Number.
   - **Beam Name**: Use Beam Name.

10. Enter an **Institution Name** (0008,0080) for export in the General Equipment module of RT Plans and RT Ion Plans.

D.2.5 Report Templates

Report templates can be designed using RayStation Report Designer. See *Appendix F RayStation Report Designer* for more information.

To add a template to the clinical database:

1. Click the **Report Templates** tab in the Clinic Settings application.

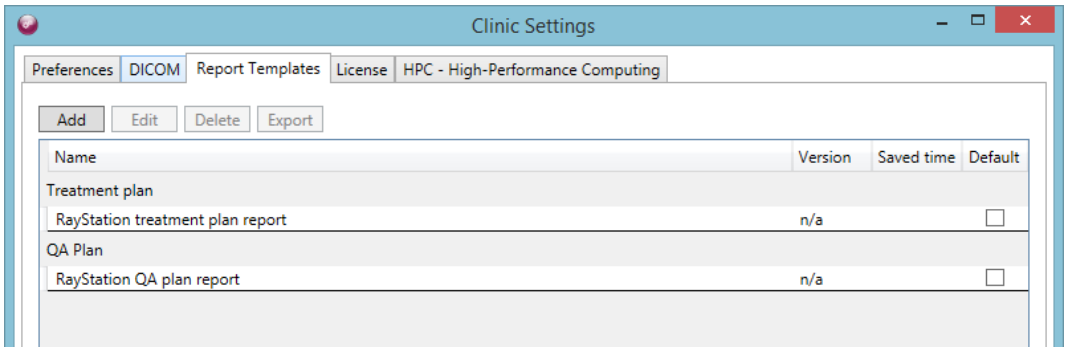
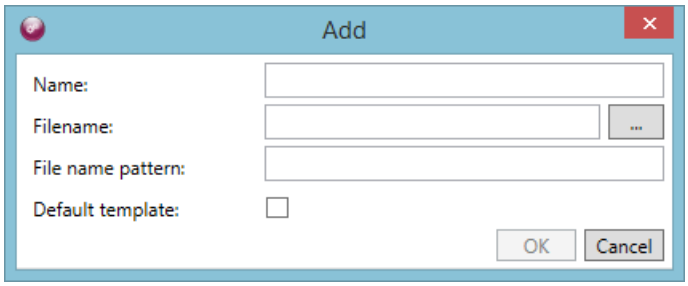


Figure 499. The **Report Templates** tab in the Clinic Settings application.

2. Click the **Add** button. This opens the Add dialog.



3. Enter a **Name** for the template.
4. Enter the **Filename** or search the file clicking the **...** button.
5. Specify the **File name pattern**, or leave the checkbox empty to use the default pattern.
6. Select to use the template as a **Default template** by checking the corresponding checkbox.
7. Click **OK**.
8. Click **Save**.

   The template is saved to the database and can be used in all RayStation clients.

File name pattern

The file name for a report generated by RayStation can be altered by specifying a file name pattern. This is specified in the **File name pattern** field in the Add dialog.

The following switches can be used to alter the generated file name:

- %ReportType% - Report type
- %PatientName% - Patient name
- %PlanName% - Treatment plan name
- %BeamSetName% - Beam set name
- %LastSaveTime% - Last save time
- %ReportCreationTime% - Report creation time
- %Approval% - "Approved" if the plan has been approved

If no pattern is specified, the default pattern will be used: "%ReportType%, %PatientName%, %PlanName%, %ReportCreationTime%".

D.2.6 License

To edit the license configuration and license profile:

1. Click the **License** tab in the Clinic Settings application.

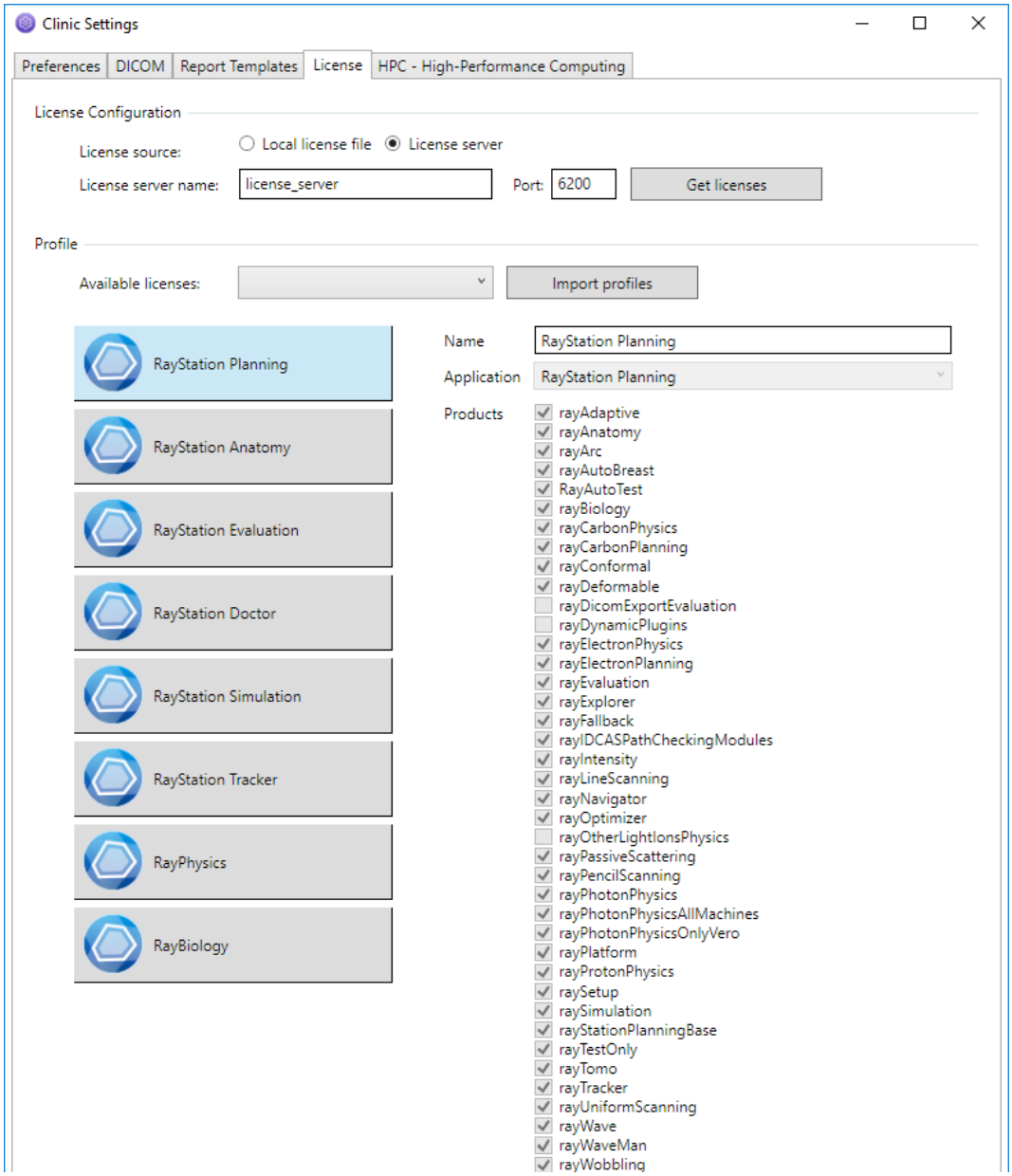


Figure 500. The **License** tab in the Clinic Settings application.

2. Select **License source**:

   - **Local license file**: Place the license (lic) file in a folder, called LicenseFile , above the RayStation installation folder. Only one license (lic) file should be present in the license file directory.
   - **License server**: Where a central license server is in place the setting in the diagram should be selected after the license file has been uploaded to the license server machine and the license service started.

     More than one license server can be specified but only the first responding server will be used. The other ones will act as fallback servers. To enter several license servers, separate the names by semicolon. If more than one server is used, they must use the same port.

3. If a **License server** has been selected, click **Get licenses**.
4. For both local and central licenses, the types of license should appear in the **Available licenses** drop-down list. Select the correct option in the drop-down list and click **Import profiles**.

Adding new licenses

If one or more new licenses are issued and installed locally or at the server, the profiles in the database must be updated. To update the profiles, repeat the edit the license configuration and license profile procedure above.

D.2.7 HPC

To edit the High Performance Computing (HPC) configuration:

1. Click the **HPC - High-Performance-Computing** tab in the Clinic Settings application.

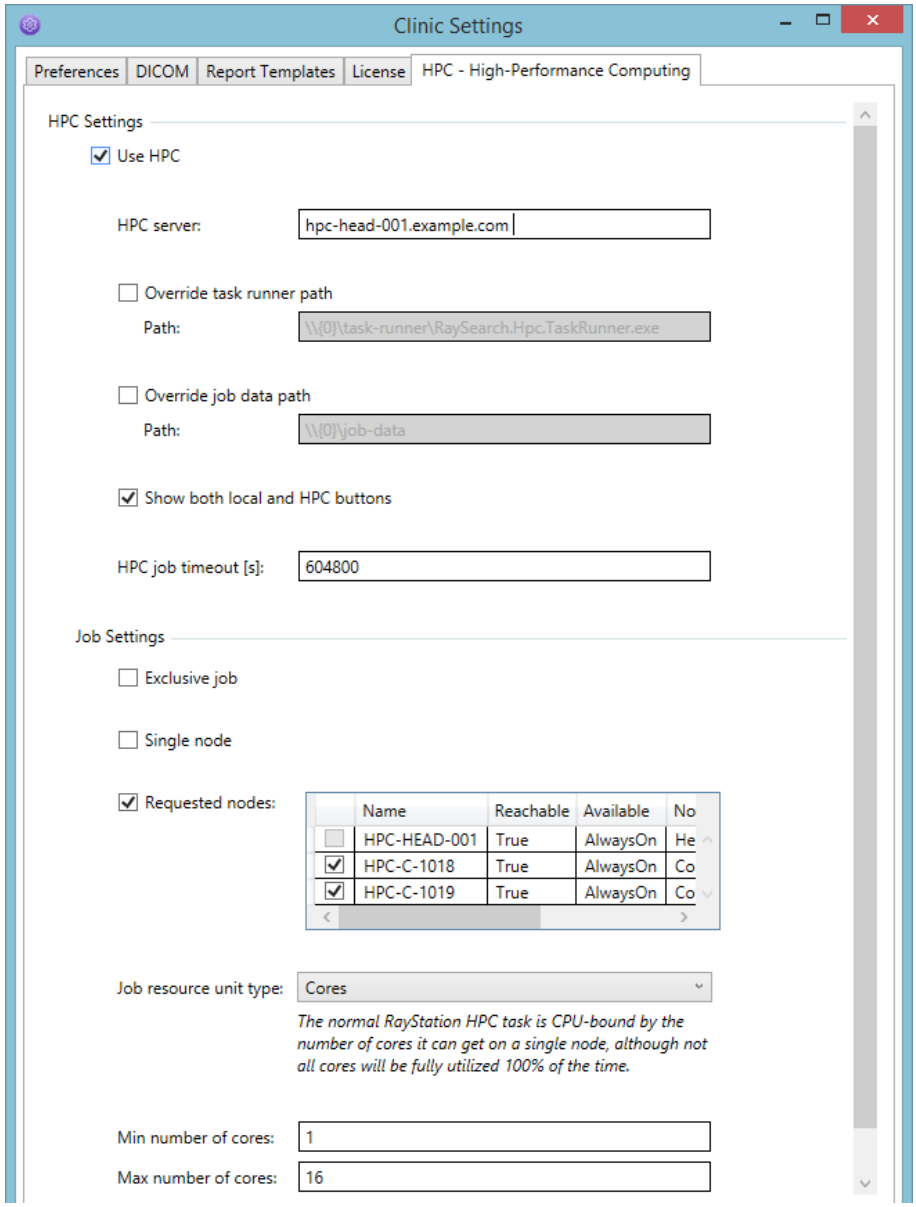


Figure 501. The **HPC - High Performance Computing** tab in the Clinic Settings application.

2. Enter **HPC settings**. For the standard case, only the **Use HPC** and **HPC server** settings need to be used.

    - **Use HPC**: Check the **Use HPC** checkbox to enable HPC support in RayStation. This requires that a HPC cluster is available.
    - **HPC server**: Enter the A-pointer name of the **HPC server**. This should be the DNS name or IP address of the HPC head node used in the HPC cluster.
    - **Override task runner path**: Check the **Override task runner path** checkbox in order to override the task runner path. This may be useful for example if the storage is segregated from the binaries under different A-pointers. A C# string format placeholder, '{0}' can be included in the string, which will be replaced with the HpcServer setting.

        Note: *The task runner path needs to be readable by the users for whom the cluster scheduler works.*

    - **Override job data path**: Check the **Override job data path** checkbox in order to override the location where the HPC cluster stores its job data. This is useful if the HPC Head node does not have enough space available or if a custom data storage node should be implemented. The job data path needs to be available from all the RayStation workstation nodes; the HPC Head node and each of the HPC computer nodes.

        Note: *The job data path needs to be in read-write mode for the users for whom the cluster scheduler works.*

    - **Show both local and HPC buttons**: This option refers to the **Start** buttons in the Plan Explorer module for starting plan explorations. Check the **Show both local and HPC buttons** checkbox in order to display both a button for optimizing exploration plans locally, and another button for optimizing exploration plans on the HPC cluster. If this is unchecked, the default **Start** button will schedule work on the HPC cluster if it is correctly configured and available, but otherwise schedule work on the local node.
    - **HPC job timeout**: This specifies the maximum allowed time interval for a HPC job given in seconds. The default value is 7 days.

3. Enter **Job settings**: The HPC job settings can be used to adjust the running of tasks depending on the hardware configuration. It is recommended to try different variations in order to find the optimal performance.

    - **Exclusive Job**: Ensures that no other job runs on the same nodes as this job while this job runs. This is checked by default because a single node can easily be saturated with work for a single plan exploration run with multiple plans.
    - **Single Node**: All resources for a job will be allocated to a single node. If the HPC cluster cannot fit all jobs at once, it will queue them and run as many as possible at the same time.
    - **Requested nodes**: Specific nodes in the cluster that are candidates for the job to run on, but not all of the nodes will necessarily run the job.

- **Job resource unit type**: Select the mode that the HPC manager is using when scheduling jobs; Cores, Nodes or Sockets.
  - **Cores**: This means that the HPC manager will prioritize scheduling tasks on nodes that have many cores.
  - **Nodes**: This means that the HPC manager will try to spawn a single task across many nodes.
  - **Sockets**: When scheduling using GPUs, it is possible to specify the Sockets resource type. Hence, if there are GPU-enabled nodes in the cluster, it is possible to schedule based on Sockets instead of Cores. No single task can make use of more than one GPU.
- **Min number of cores** and **Max number of cores**: This should be left unchanged at min 1 and max 16.

4. Click **Save**.

D.3 THE RAYSTATION STORAGE TOOL APPLICATION

In the RayStation Storage Tool application it is possible to configure and upgrade the RayStation databases. Database administration privileges are required to use this application, see *section D.1 Database administration on page 918*.

Note: *Modifying the databases will affect all RayStation clients.*

In this section

This section contains the following sub-sections:

D.3.1	Database system	p. 941
D.3.2	System overview	p. 942
D.3.3	Edit database system	p. 944
D.3.4	Database details	p. 946
D.3.5	Upgrading databases	p. 947
D.3.6	Move patients between databases	p. 948
D.3.7	Batch upgrade of several patients	p. 949
D.3.8	Add secondary patient database	p. 950
D.3.9	Create new primary patient database	p. 951
D.3.10	HIPAA	p. 953
D.3.11	Index services	p. 956
D.3.12	New system	p. 957
D.3.13	Settings	p. 959
D.3.14	Refresh	p. 960

D.3.1 Database system

A database system consists of three databases:

- one machine database (RayStationMachineDB)
- one clinic database (RayStationClinicDB)
- one primary patient database (RayStationPatientDB)

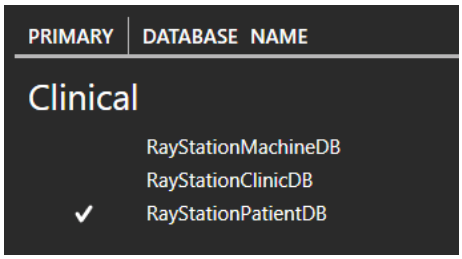


Figure 502. Database system example in the RayStation Storage Tool.

Secondary databases

The database system can also include secondary databases of three types:

- patient databases of old RayStation versions
- patient databases of version RayStation 7
- patient databases of version RayStation 7 that are read-only

A secondary database can be made read-only, a primary database cannot. Secondary databases of the current RayStation version can be used to move patient data out of the primary database. The patients moved to the secondary database can still be seen when the RayStation indexing service is active.

Note: *If the indexing service is active, there might be problems with changing a secondary database to read-only. To prevent this, set the database to "Offline mode" in advance, or temporarily turn off the indexing service.*

D.3.2 System overview

The System overview shows all registered database systems and connects to the databases to get their status.

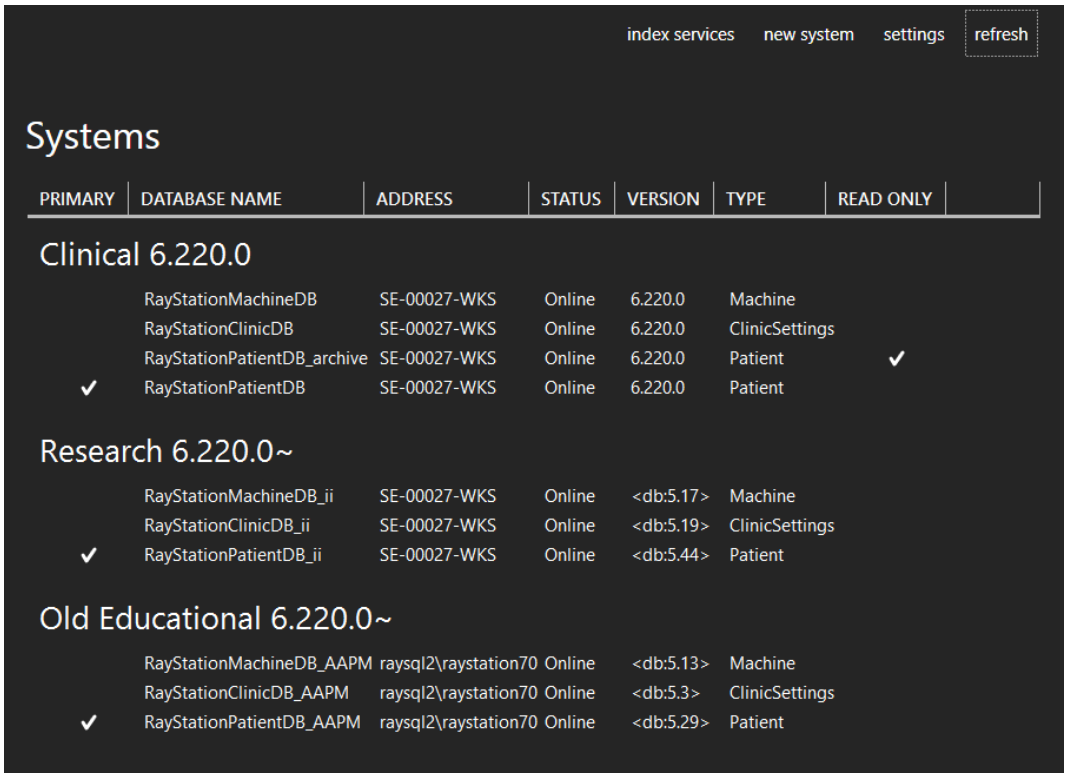


Figure 503. The System overview in the RayStation Storage Tool.

The following table describes the displayed data in the System overview and in the System details:

Column name	Description
PRIMARY	The primary patient database of the system.
DATABASE NAME	The name of the database.
ADDRESS	The name/address of the SQL Server including instance name and port.

Column name	Description
STATUS	All databases within a system shall have the same clinical status. There are three statuses: • **Online** - open for multi-user access • **Restricted** - open only for database administrators • **Offline** - connection failed • **Unavailable** - database cannot be reached
VERSION	RayStation database version.
TYPE	The model type of the database.
READ ONLY	Database is read-only. Note that only a secondary database can be made read-only, a primary database cannot.

Actions in the System overview

In the System overview it is possible to perform the following actions:

- Register index services by clicking the **index services** button.
- Create or register a new system (a set of databases) by clicking the **new** button.
- Configure advanced RayStation and RayStation Launcher settings by clicking the **settings** button.
- Refresh the content by clicking the **refresh** button.

D.3.3 Edit database system

1. Start the application using the program start menu: RayStation 7\RayStation Storage Tool.
2. Open the System details view by clicking on the system.

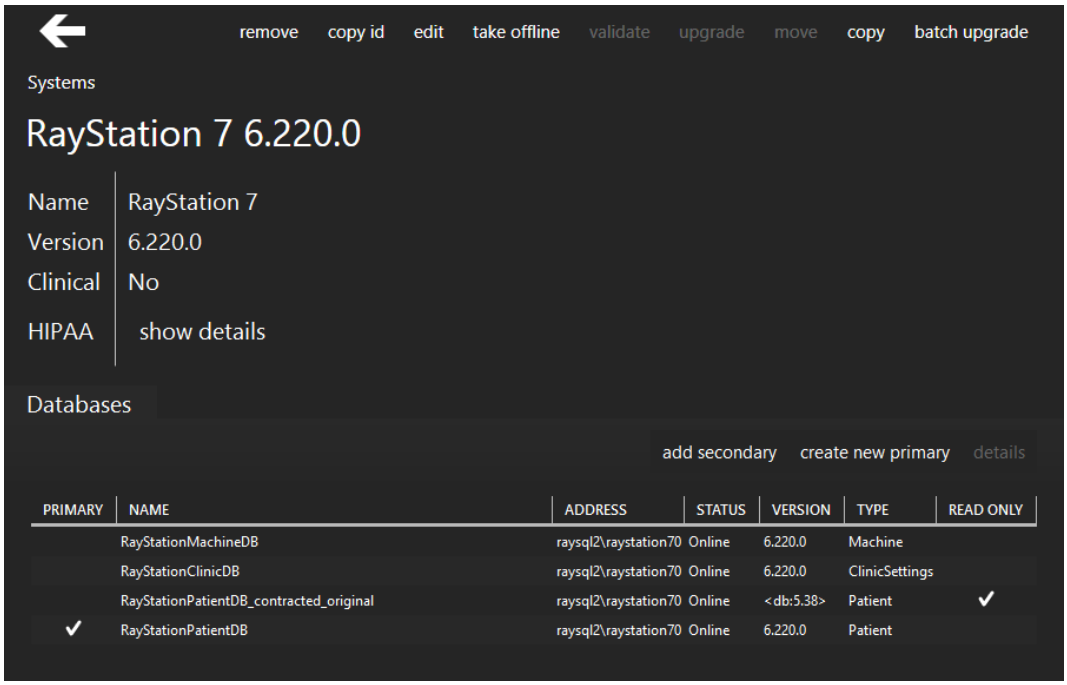


Figure 504. The System details view in the RayStation Storage Tool. For more information about the displayed data in the System details view, see *section D.3.2 System overview on page 942*.

3. In the System details view it is possible to perform the following actions:

Actions	Description
Remove	Click the **remove** button to delete the system configuration. Note that deleting the system will not delete the databases on the database server. Delete of the physical databases should be done using SQL Server Management Studio.
Copy id	Click the **copy id** button to copy the unique id of the system to the clipboard. The system id should be used in the configuration file for RayStation Launcher to disable/enable systems.
Edit	Click the **edit** button to edit the name of the system. Click **save** to commit the changes, or click the **back** button to cancel.

Actions	Description
Take offline/Bring online	The **take offline/bring online** buttons are used when upgrading the databases. For instructions, see *section D.3.5 Upgrading databases on page 947*. When the databases are offline, the access to the databases are restricted and ordinary RayStation users will not be able to access them.
Validate	Before a system is upgraded, it is sound to validate rules and checksums in the database. This must be done with a RayStation 7\RayStation Storage Tool of the same version as the databases. Databases must be offline before validation can take place.
Upgrade	It is possible to upgrade the databases in a system. For instructions, see *section D.3.5 Upgrading databases on page 947*. The system must be offline before the upgrade can be run.
Move	It is possible to move selected patients between databases within a system. For instructions, see *section D.3.6 Move patients between databases on page 948*.
Copy	The copy functionality copies patients from one database to another. Use this functionality to set up education and evaluation systems. Non-clinical data cannot be copied into clinical systems. It is possible to copy patients from older versions to RayStation 7.
Batch upgrade	It is possible to batch upgrade the selected patients to the RayStation 7 format. For instructions, see *section D.3.7 Batch upgrade of several patients on page 949*.
Add secondary	It is possible to add a secondary patient database. For instructions, see *section D.3.8 Add secondary patient database on page 950*.
Create new primary	Click the **create new primary** button to set up an empty primary database and set the current primary database as secondary. When a new primary database is created, all common data (e.g., templates) will be copied from the primary database. The system must be offline before a new primary database can be created.
Details	Select a database and click the **details** button to show details of the database configuration. For more information, see *section D.3.4 Database details on page 946*.

D.3.4 Database details

It is possible to view the details of a specific database by selecting it and clicking **details** in the System details view.

Figure 505. The Database details view in the RayStation Storage Tool.

In the Database details view it is possible to perform the following actions:

Actions	Description
Make writable	Click the **make writable** button to be able to edit patients within the database.
Make read only	Click the **make read only** button to change the database to read-only.
Remove	Click the **remove** button to delete the database from the system configuration. Note that deleting the database will not delete the database on the database server. Delete of the physical databases should be done using SQL Server Management Studio.

D.3.5 Upgrading databases

Upgrading the databases in a system will convert the patient, machine and clinic settings databases from the current versions to the RayStation 7 format. Note that converting the databases will make them incompatible with the currently supported RayStation version. Upgrading an entire system is not recommended, instead a new system should be created based on the existing one. Upgrade will not include secondary patient databases.

Recommended workflow

The recommended workflow when upgrading the databases is:

1. Run a full backup of the databases or make sure that recent full backups are available.
2. Close all RayStation clients connected to the databases that should be upgraded.
3. In the System details screen, click the **take offline** button to take the database system offline.
4. Make differential backups of the effected databases.
5. Run the Consistency Analyzer Tool included in the same RayStation version as the databases to be upgraded.
6. Click the **start** button in the upper right corner to start the upgrade.

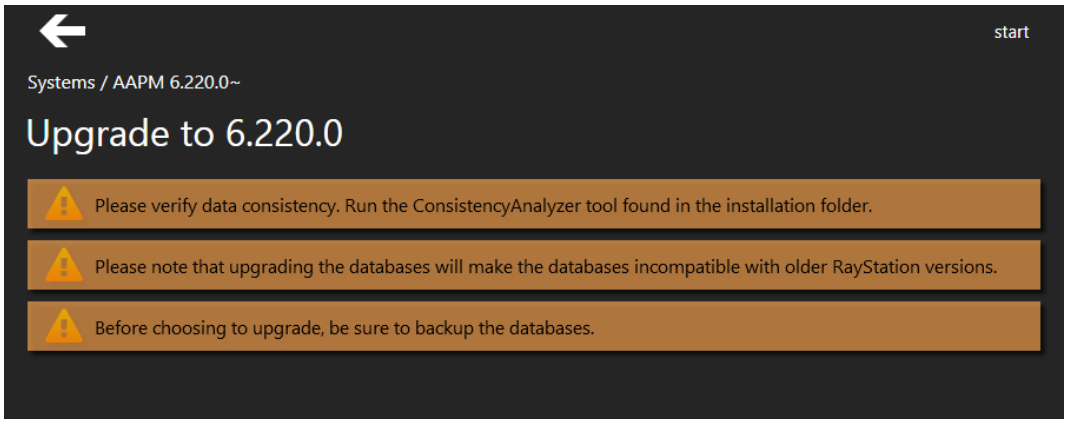

start
Systems / AAPM 6.220.0~
Upgrade to 6.220.0
Please verify data consistency. Run the ConsistencyAnalyzer tool found in the installation folder.
Please note that upgrading the databases will make the databases incompatible with older RayStation versions.
Before choosing to upgrade, be sure to backup the databases.

Figure 506. The RayStation Storage Tool Upgrade view.

7. Verify that the upgrade has completed without errors.

   Contact Support if errors are found. Logging is done in the RayStation_Storage_Tool_log file in folder "%ProgramData%\RaySearch\".

8. In the System details screen, click the **bring online** button to bring the database system online.

D.3.6 Move patients between databases

It is possible to move patients between databases within a system. The primary purpose of this function is to move patients that has completed their treatment out of the primary database. The move functionality moves patients within the same system and requires a least one secondary patient database with RayStation version matching the primary database to work.

To move patients between databases:

1. Open the System details by clicking on the system.
2. Click the **move** button.
3. Select the source database in the **From** drop-down list.
4. Select the destination database in the **To** drop-down list.
5. Use the **Filter** field to search for patients to move to the destination.
6. Select one or multiple patients using a combination of left mouse click, shift and the control key.
7. Click **start** in the upper right corner to move the patients.

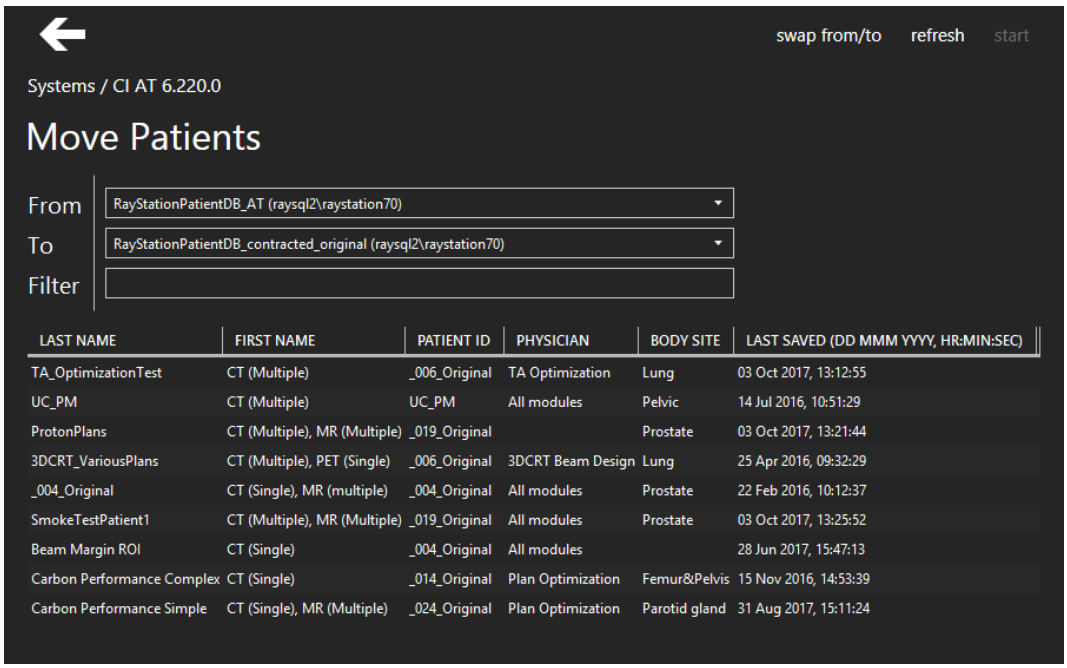


Figure 507. The RayStation Storage Tool Move Patients view.

D.3.7 Batch upgrade of several patients

Batch upgrade will upgrade the selected patients to the RayStation 7 format. The purpose of the functionality is to avoid the upgrade step in RayStation and to speed up the first load for patients that shall be treated with RayStation 7. Batch upgrade will copy the patient data from the source to the primary patient database. Data in the source database will not be changed.

To batch upgrade selected patients to the RayStation 7 format:

1. Open the System details by clicking on the system.
2. Click the **Batch upgrade** button.
3. Select the source database in the **From** drop-down list.

   Only databases with RayStation version older than the primary database will be available in the list.
4. Select the destination database in the **To** drop-down list.
5. Use the **Filter** field to search for patients to upgrade and copy to the destination.
6. Select one or multiple patients using a combination of left mouse click, shift and control key.
7. Click **start** in the upper right corner to upgrade the patients.

   Upgraded patients will still be present in their old RayStation version in the source system and can be reviewed using the matching RayStation version.

D.3.8 Add secondary patient database

A secondary patient database can be added as a new patient source. The database can be of version RayStation 4.0 or later. The clinical status of the secondary database must match the clinical status of the system. Patients from the secondary source will be available in RayStation (requires installation of the RayStation 7 index service) and will be upgraded to the RayStation 7 format when they are accessed. Edited patients will be stored in the primary database. Secondary databases of the RayStation 7 version can be used as archives to reduce the load/number of patients on the primary database.

1. Open the System details by clicking on the system.
2. Click the **Add secondary** button.
3. Enter the following information in the Register patient database view: **Host**, **Instance**, **Port** and **Suffix**.
4. Click **next**.

   If the address and name matches an existing database, the database will be added as a secondary database.

   Run Consistency Analyzer on the secondary database to verify rules and checksum consistency. If the secondary database acts as primary database in another system, please run Consistency Analyzer regularly to avoid inconsistency.

   Note that if the entered address and name do not match an existing database, a new database will will be created with the RayStation 7 version.

D.3.9 Create new primary patient database

A new primary database can be created with templates from the current primary database and will be used as the database where edited patients are stored. Use this function when the primary database becomes too large to handle.

1. Take the system offline.
2. Click the **create new primary** button.
3. Enter the following information about the database server:
   - **Host**: Make sure to use a host name that the RayStation clients can use; avoid localhost.
   - **Instance**: Leave the field blank if no instance name is being used.
   - **Port**: Leave blank if default port (1433) is being used.
   - **Suffix**: Initial underscore will be added. Leave blank to use the default names.
   - **Connection Encryption**: Check this checkbox in order to use encrypted connection when communicating with the database server.
   - **Trust Server Certificate**: Check this to trust any server certificate without validation. Only enabled when also checking **Connection Encryption**.
   - **Custom Parameters**: Custom connection string parameters entered as a semicolon separated string of key value pairs.

   Connection String displays the final connecting string used for the database. This field is read-only.
4. Click **next** to register the database. If the database registration does not match an existing database, the paths to the data file, the log file, the filestream folder and the audit file can be specified. The paths will default to the database server default paths. Make sure that the entered values matches the paths on the database server. This is important when creating databases/systems on another machine.
5. Click **create** to accept the database paths. The following data from the current primary patient database will be copied:
   - Beam list templates
   - Biological models
   - Fallback protocols
   - Function list templates
   - Phantoms
   - Plan generation protocols
   - RBE models

- Structure Templates
- Template arc trajectories
- Template color maps
- Template MBS models
- Template plan explorations

6. Bring the system online.

D.3.10 HIPAA

HIPAA overview

The Health Insurance Portability and Accountability Act (HIPAA) was published in 1996 by the U.S. Department of Health & Human Services. Among other things, this act regulates secure storage and secure transmission of patient and personal information in electronic health care systems, specifically the HIPAA Security Rules outlines the required security controls that should or is recommended to be in place in order to keep patient privacy and protect patient information that is stored in a computer system.

HIPAA Security Rules

In the HIPAA Security Rules screen in the RayStation Storage Tool an administrator can get an overview of the current status of the HIPAA Security controls for a particular RayStation installation (system). For systems that are created with the HIPAA Security Rules option set, it is recommended to implement all the security controls outlined in the screen below, i.e., all options should be in "YES" status.

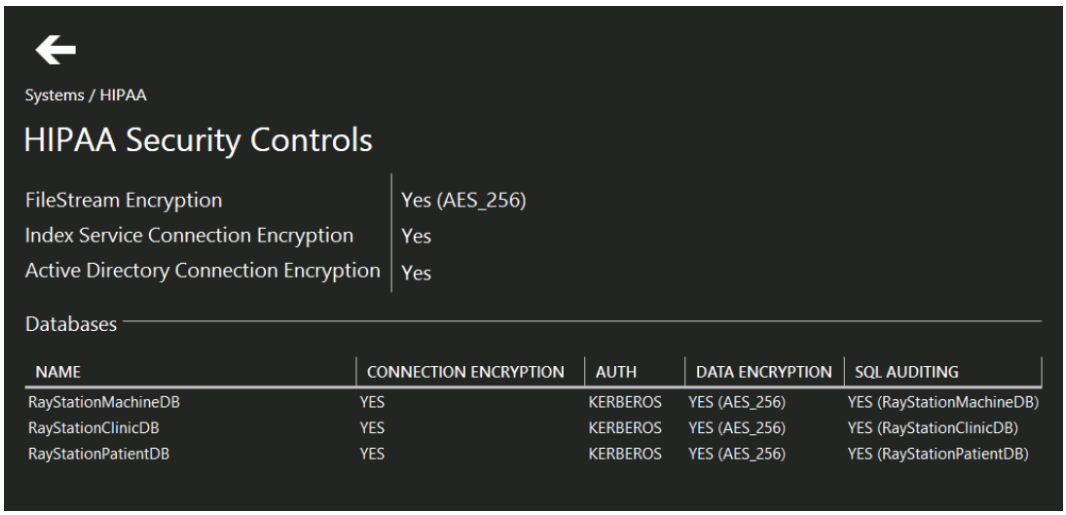


Figure 508. The HIPAA Security Rules in the RayStation Storage Tool.

FileStream Encryption

Specifies if FileStream data used by the SQL Server database is encrypted at rest and in motion over the Local Area Network.

- **NO** - File Stream Encryption is not enabled. FileStream data is sent in the clear over the network.
- **YES** (<Encryption algorithm>) – FileStream data is encrypted at rest and in motion using the <Encryption algorithm>.

The <Encryption algorithm> should be any of the following values (AES_128, AES_256, TRIPLE_DES_3KEY_192). FileStream encryption cannot be turned off and is enabled when the system is created. By default the system will use the AES_256 encryption algorithm.

Index Service Connection Encryption

Specifies if the RayStation client will connect to the RayStation index service using TLS connection encryption.

- **N/A** – Not available, i.e., the RayStation Storage Tool was unable to detect the current connection encryption used *).
- **NO** – One or more registered RayStation index services is not using connection encryption.
- **YES** – All registered RayStation index services are configured to use connection encryption.

* This is often caused by insufficient permissions on the SQL server.

HIPAA status overview and HIPAA details

The following table describes the displayed data in the HIPAA status overview and in the HIPAA details:

Column name	Description
NAME	The name of the database.
CONNECTION ENCRYPTION	Specifies if SQL server connection encryption is enabled and in use for the specified database. This corresponds to the Encrypt=True parameter in the SQL connection string used by the RayStation Client.
AUTH	Specifies the currently detected authentication method for to the specified database. The following values are possible: • N/A - Not available, i.e., the RayStation Storage Tool was unable to detect the current connection encryption used [i]) • KERBEROS – Connection is authenticated with Kerberos authentication. (Best security) • NTLM – Connection is authenticated with NTLM authentication.

Column name	Description
DATA ENCRYPTION	Specified the current encryption algorithm that is in use for data at rest in the database. The following values are possible: • N/A – Not available, i.e., the RayStation Storage Tool was unable to connect to the specified database and collection information about the current database encryption used [i]) • NO - Data at rest (in the database) is not encrypted. • YES (<Encryption algorithm>). Data at rest is encrypted [ii] in the database with the <Encryption algorithm>. The <Encryption algorithm> should be any of the following values (AES_128, AES_192, AES_256, TRIPLE_DES_3KEY_192).
SQL AUDITING	Specifies the SQL Server Audit specification setup for the specified database. The following values are possible: • N/A - Not available, i.e., the RayStation Storage Tool was unable to connect to the specified database and enumerate the existing SQL server Audit specifications [i]) • NO – No SQL server audit specification was found for this database. • YES (<Database name>). An SQL Server Audit specification is present for this database.

i This is often caused by insufficient permissions on the SQL server.
ii This feature requires Microsoft SQL Server Enterprise Edition and Transparent Data Encryption (TDE).

D.3.11 Index services

Register index services by clicking the **index services** button in the main screen. One or more index services are required to enable secondary patient databases. Register multiple index services to setup a redundant system. RayStation Indexing Service should be setup at installation. To add a new index service:

1. Click the **add service url** button.
2. Enter a valid address ([http|https]://host:port). Use the https scheme to register a secure index service.
3. Click **ok**.
4. Click **save** in order to save the settings.

D.3.12 New system

Select **New system** to register or create a new set of databases (system).

Create a new system

Use this function to create a new system based on factory settings data or to register an existing set of databases.

1. Select a system **Name** that identifies the set of databases.
2. Select **<New>** as base on option.
3. Check **HIPAA Security Rule** to create a system that fulfills the HIPAA requirements regarding transport and data encryption.
4. Check the **Clinical** checkbox in order to create a new clinical set of databases using a clinical build.
5. Click **next**.
6. Register the patient, machine and clinic settings databases either by pointing to existing RayStation databases, by pointing to databases created using SQL Server Management Studio or by letting the storage tool create the physical databases.

   Enter the following information about the database server for the patient database:

   - **Host**: Make sure to use a host name that the RayStation clients can use; avoid localhost.
   - **Instance**: Leave the field blank if no instance name is being used.
   - **Port**: Leave blank if default port (1433) is being used.
   - **Suffix**: Initial underscore will be added. Leave blank to use the default names.
   - **Connection Encryption**: Check this checkbox in order to use encrypted connection when communicating with the database server.
   - **Trust Server Certificate**: Check this to trust any server certificate without validation. Only enabled when also checking **Connection Encryption**.
   - **Custom Parameters**: Custom connection string parameters entered as a semicolon separated string of key value pairs.

   Connection String displays the final connecting string used for the database. This field is read-only.
7. Click **next** to register the database. If the database registration does not match an existing database, the paths to the data file, the log file, the filestream folder and the audit file can be specified. The paths will default to the database server default paths. Make sure that the entered values matches the paths on the database server.
8. Click **create** to accept the database paths.
9. Repeat the steps 6-8 for the machine and clinic settings databases.

10. After the three RayStation databases have been registered, the application will create the physical databases if not present, create database schemes if not present and import factory settings data for new databases.

Create a new system based on an existing system

Use this function to setup a system with machines, clinic settings and patient templates from an existing system.

1. Select a system **Name** that identifies the set of databases.
2. Select system to base the new system on. Machines and clinic settings data will be copied from the source system to new system. The following data from the source patient database will be copied:
    - Beam list templates
    - Biological models
    - Fallback protocols
    - Function list templates
    - Phantoms
    - Plan generation protocols
    - RBE models
    - Structure Templates
    - Template arc trajectories
    - Template color maps
    - Template MBS models
    - Template plan explorations
3. Check the **HIPAA Security Rule** checkbox to create a system that fulfills the HIPAA requirements regarding transport and data encryption.
4. Check the **Clinical** checkbox in order to create a new clinical set of databases using a clinical build.
5. Register the patient, machine and clinic settings databasesby letting the storage tool create the physical databases. See *Create a new system on page 957*, steps 6-8, for more information.

D.3.13 Settings

Use the settings screen to configure advanced RayStation Launcher and RayStation settings.

1. Enter the primary domain controller in the **Active Directory DC Override** field in cases where the domain controller cannot be resolved from the current Windows user account.
2. Enter the path to the RayStation Launcher configuration file in the **Launcher Configurations File** field. Overrides of this field can be made in local RayStationLaucher.exe.config files using the ConfigurationsPath:s attribute. The config file selected can be edited using the edit icon button. In the editor, systems in RayStation Launcher can be added, sorted, deleted and changed.
3. Check the **Secure LDAP** in order to use secure ldap communication in the RayStation system.

D.3.14 Refresh

The **refresh** button refreshes the list of systems and connects to the databases to verify status.

D.4 GPU SETTINGS

RayStation 7 can compute Collapsed Cone photon dose, compute Carbon ion Pencil Beam dose and perform deformable registration using GPU (graphics processing unit) in addition to CPU (central processing unit). Settings for GPU calculations are reached from the RayStation or RayPhysics menu in the **Settings** sub menu. The command displays the **GPU Settings** dialog with two parts, general settings and **Verify treatment machines**.

Note: *Dose can only be calculated using GPU for dose grids with less than 512^3 voxels (134217728 voxels).*

Computations on the GPU are sensitive to the Windows Timeout Detection and Recovery (TDR) mechanism. If a sub-computation on the GPU runs longer than about 2 seconds this mechanism may, by design, result in a program crash. The carbon dose optimization and computation has been verified to pass the TDR mechanism for complex cases with, e.g., 200 000 spots, 4 beams, target volume 5 dm^3 and voxels size of 0.2 x 0.2 x 0.2 cm^3 on validated GPUs.

When the **GPU Settings** dialog is opened, RayStation/RayPhysics will scan the graphics boards of the computer (some computers may have more than one graphics board) and determine if the graphics board can be considered for GPU computations. If a potential graphics board is found, the dialog looks like:

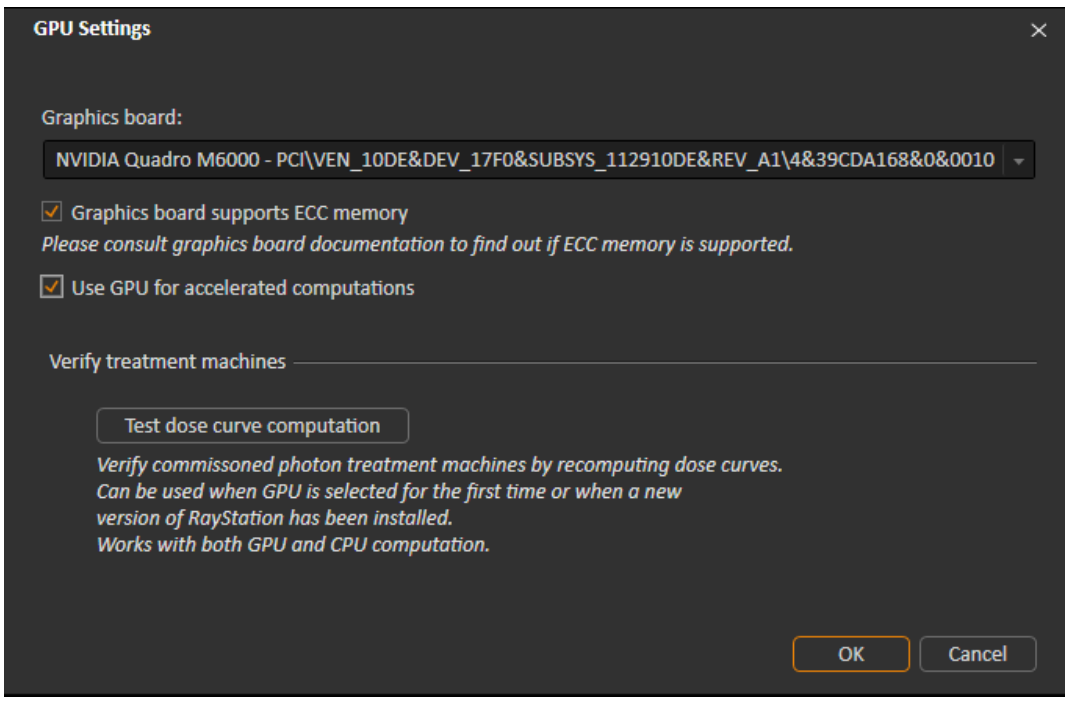

GPU Settings
Graphics board:
NVIDIA Quadro M6000 - PCI\VEN_10DE&DEV_17F0&SUBSYS_112910DE&REV_A1\4&39CDA168&0&0010
Graphics board supports ECC memory
Please consult graphics board documentation to find out if ECC memory is supported.
Use GPU for accelerated computations
Verify treatment machines
Test dose curve computation
Verify commissoned photon treatment machines by recomputing dose curves.
Can be used when GPU is selected for the first time or when a new
version of RayStation has been installed.
Works with both GPU and CPU computation.
OK
Cancel

Figure 509. The **GPU Settings** dialog.

If no graphics board is found the dialog looks like:

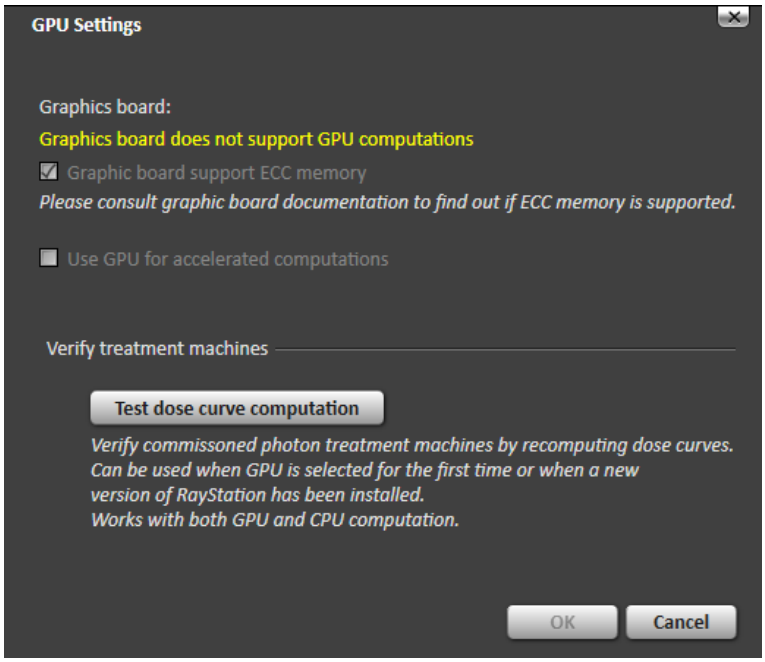

GPU Settings
Graphics board:
Graphics board does not support GPU computations
Graphic board support ECC memory
Please consult graphic board documentation to find out if ECC memory is supported.
Use GPU for accelerated computations
Verify treatment machines
Test dose curve computation
Verify commissoned photon treatment machines by recomputing dose curves.
Can be used when GPU is selected for the first time or when a new
version of RayStation has been installed.
Works with both GPU and CPU computation.
OK
Cancel

Figure 510. The GPU Settings dialog - no graphics board.

The graphics board name and device instance path (the graphics board location on the PCI-bus) is displayed. If several graphics boards are found, the available graphics boards will be listed in a drop-down list and the user can select which graphics board to use.

D.4.1 Graphics board supports ECC memory

The **Graphics board supports ECC memory** checkbox shall only be checked if the graphics board supports ECC memory.

WARNING!

Use of non-ECC GPU memory for dose calculation on GPU. ECC availability must only be set to true if:

1. The GPU supports ECC memory.
2. ECC memory is enabled in the GPU driver settings.

Otherwise, ECC availability must be set to false.

If ECC availability is erroneously set to true, checks mitigating non-ECC memory errors will be disabled and the clinical CC dose may be incorrect. (115893)

Note: *For Carbon ion dose computation on GPU, ECC memory is required.*

D.4.2 Use GPU for accelerated computations

The **Use GPU for accelerated computations** checkbox is used to select/deselect use of GPU computations.

When selecting/deselecting the **Use GPU for accelerated computations** checkbox, a runtime computation test of the GPU or CPU will be performed to verify that it is suitable for computations. If the runtime test yields a pass, an authentication dialog is displayed when the **OK** button is clicked, where the user has to acknowledge the new setting by giving a user name and correct password (with membership of RayStation-Administration or equivalent group). Only after this the new configuration will be saved. If the runtime test yields a fail, it is not possible to change the GPU setting. One reason for this happening may be outdated graphics board driver versions. Confirm that the host GPU driver version is consistent with the Deployment package GPU drivers.

The runtime computation test will also be run when launching RayStation or RayPhysics. If the runtime test fails when GPU is selected, the user may select to use CPU instead.

WARNING!

Dose calculation on GPU may be affected by computer/driver updates. If accelerator GPU is used, the dose calculation on GPU must be revalidated after any hardware or software platform changes, including operating system Service Packs. This can be done by comparing dose computed on GPU with dose computed on CPU (*RSL-D-RS-7.0-SEAT, RayStation 7 System Environment Acceptance Test Protocol*). For photon dose computation, additional validation should be performed by recalculating dose curves for all commissioned treatment machines in the database. (116588)

D.4.3 Verify treatment machines

It is also possible to re-compute photon dose curves for all commissioned machines in the database with the latest major dose engine version and verify that the re-computed dose curves are equal to the dose curves stored in the machine. The re-computation is started by clicking the **Test dose curve computation** button. If the re-computed curves are equal to the saved dose curves, the test will yield a pass. Otherwise, the machines for which the validation failed are listed and the differences can be inspected by the user by creating a copy of the machine in Beam Commissioning and compute new curves manually.

When comparing the stored dose curve to the re-computed dose curve, a relative difference of 5×10^{-3} is used as pass/fail criteria. For each data point in a dose curve, the relative difference is evaluated according to

$$Abs\left(\frac{d_{recomp} - d_{stored}}{d_{max}}\right) < 5 \cdot 10^{-3}, \qquad \text{[Eq. 2]}$$

where d_{recomp} is the re-computed dose value, d_{stored} is the stored dose value and d_{max} is the maximum dose value in the stored dose curve.

If any data point in the dose curve fails the relative difference criteria, the treatment machine fails the test.

Observe that it is still possible to select **Test dose curve computation** even if no suitable GPU is selected. Then the computation will be done on the CPU.

Note: *In RayStation 7, centering of wedged dose curves is no longer performed. (Refer to section Centering of dose curves in RSL-D-RS-7.0-RPHY, RayStation 7 RayPhysics Manual for more information about dose curve centering.) This means that wedged dose curves are computed in slightly different coordinates in RayStation 7 compared to previous versions. Therefore, wedged dose curves are not used in the test dose curves computation in RayStation 7. Wedged dose curves can be compared manually be making a copy of the machine, computing dose curves and comparing these to the previous curves. Note that there may be small deviations between previous curves and new curves for wedged curves due to the difference in dose curve centering.*

D.5 GRAPHICS CARD UPDATE

With the introduction of GPU computations, a graphics can have 2 functions - rendering and/or computations. For RayStation host computers with no GPU computations, we recommend that the latest drivers are applied:

To update the drivers:

1. Click the Windows **Start** button and navigate to System information\Components\Display. Check which graphics card is installed.
2. Go to http://www.nvidia.co.uk/Download/index.aspx?lang=en-uk and follow the instructions.

For RayStation host computers, where GPU computations occur, please refer to the Instructions for Use for guidance on the drivers.

E RAYBIOLOGY

The RayBiology application is launched from the RayStation Launcher application. For more information about RayStation Launcher, see *section 4.1 Starting RayStation 7 on page 108*.

The RayBiology application contains the Biological Model Administration module and the RBE Model Administration module.

In this chapter

This chapter contains the following sections:

E.1	Biological Model Administration module	p. 968
E.2	RBE Model Administration module	p. 973

Precautions

WARNING!

Factory default biological models. The database of factory default biological model parameters comes from published clinical and pre-clinical studies. Still, this is an evolving field of science and more recent studies may provide evidence for other biological model parameters that are more suitable for clinical use.

The user shall always review the literature and base their usage of biological model parameters on the current state of knowledge in the field and clinic-specific treatment techniques. (96234)

E.1 BIOLOGICAL MODEL ADMINISTRATION MODULE

The Biological Model Administration module can be used to manage the parameters of the biological models that the RayStation 7 system provides as factory defaults. It is also possible to add new parameter sets, however restricted to Lyman Kutcher Burman (LKB) or Poisson-LQ models.

In this section

This section contains the following sub-sections:

E.1.1	Biological Model Administration workspace	p. 969
E.1.2	Adding, editing or deleting a biological model	p. 970

E.1.1 Biological Model Administration workspace

The Biological Model Administration workspace consists of a list of the available biological models and functionality for filtering the list to get a better overview, or to find a specific model easily. Below the list is a set of buttons for adding, copying, editing and removing biological models.

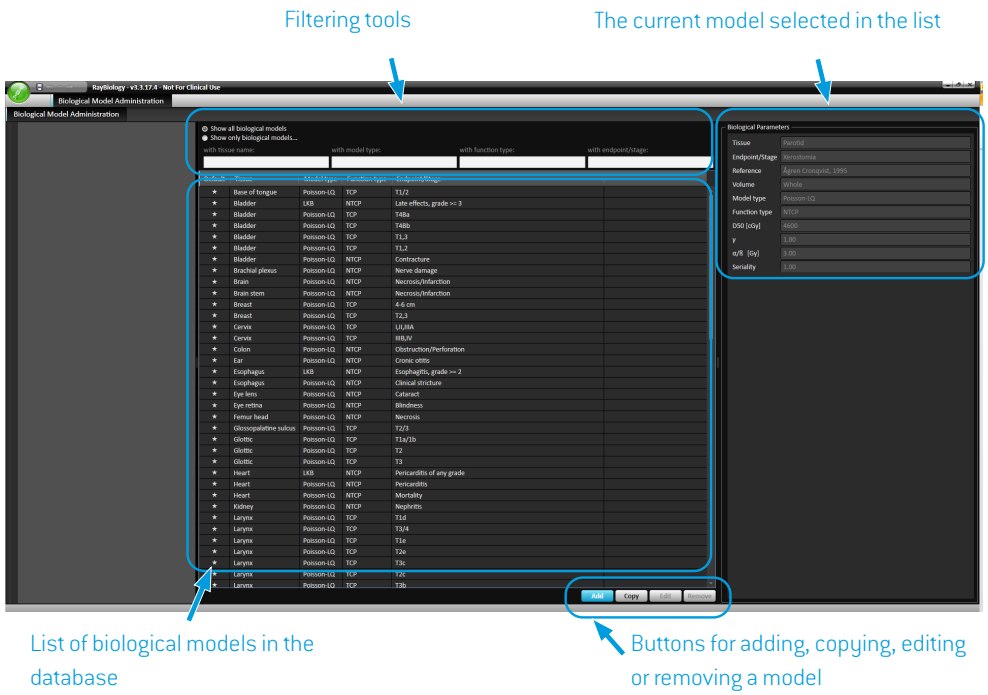

Filtering tools
The current model selected in the list
List of biological models in the database
Buttons for adding, copying, editing or removing a model

Figure 511. The Biological Model Administration workspace.

Viewing the entire library

Click the option button **Show all biological models**.

Filtering the library

In order to display only a certain set of biological models, click the option button **Show only biological models...** and type in a combination of search criteria in the search fields **with tissue name:**, **with model type**, **with function type**, **with endpoint/stage**.

E.1.2 Adding, editing or deleting a biological model

The RayStation 7 system comes with a set of factory default biological models. These are marked with a star and cannot be edited. User-defined biological models can be added, edited or deleted.

Note: *When adding a biological model, the user has the freedom to define models that makes no sense, such as a model for nasopharynx tissue with xerostomia as endpoint. It is the user's sole responsibility to make sure that the biological model added makes sense.*

Adding a biological model

To add a biological model to the database:

1. Click the **Add** button.

   This opens the **Add Function** dialog.

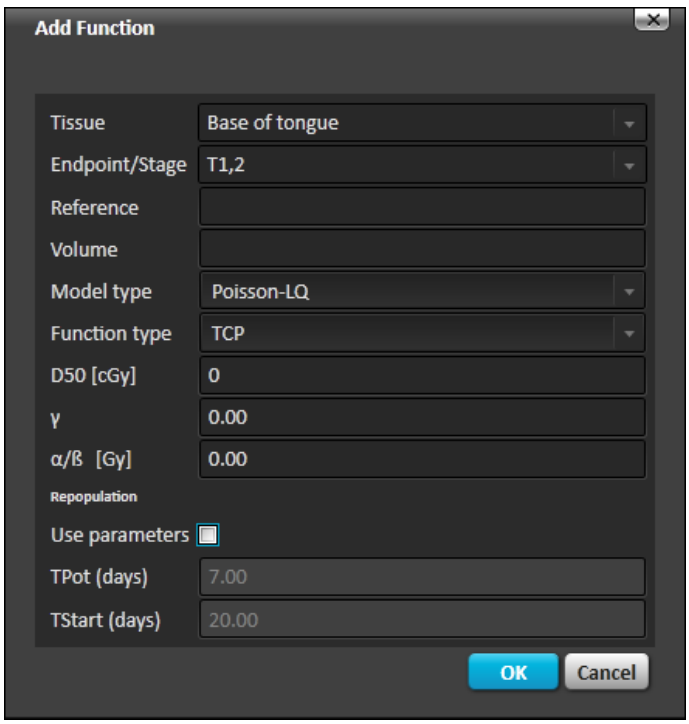


Figure 512. The **Add Function** dialog.

2. Select **Tissue** type and **Endpoint/stage** from a predefined set of choices.
3. Select **Model type** (Poisson LQ or LKB).
4. Select **Function type** (NTCP or TCP).
5. Carefully enter new model parameter values.

6. Enter a new **Reference** value. When a parameter is modified, the **Reference** field will be updated with **User defined**. It is strongly recommended to change the reference value.

   Note: *If changing the model parameters when adding a biological function for optimization the reference is changed to User defined to notify the user that parameters deviate from the parameters in the database. It is therefore recommended to enter a new name in the reference field.*

7. Click **OK**.

Copying an existing biological model

To add a model to the database by copying the parameters of an existing model:

1. Select an existing model in the list. The model can be either a factory default model or a user-defined model.
2. Click the **Copy** button.

   This opens the **Add Function** dialog.

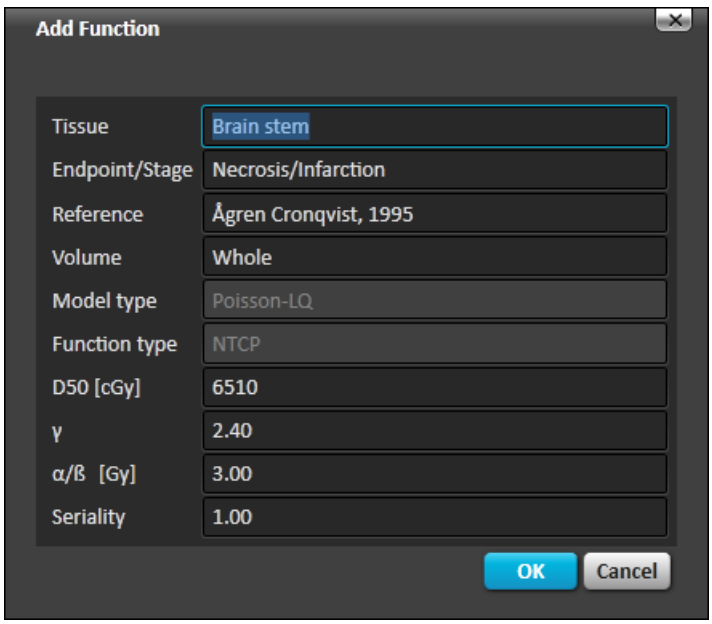


Figure 513. The **Add Function** dialog.

3. Modify the parameters as desired.
4. Click **OK**.

   The new model is added to the list.

Editing the parameters of a biological model

User-defined biological models can be edited in RayBiology. Click the **Edit** button and edit the parameters as desired.

Removing a user-defined biological model

To remove a biological model from the list:

1. Select the desired model in the list.
2. Click the **Remove** button.

Note: *Factory default models cannot be deleted.*

Save edits

Click the **Save** button in the top left corner of the view or type Ctrl + S to save all edits performed into the library.

E.2 RBE MODEL ADMINISTRATION MODULE

The RBE Model Administration module can be used to manage RBE (Relative Biological Effectiveness) models that are used for computing RBE dose for carbon ions.

In this section

This section contains the following sub-sections:

E.2.1	The RBE Model Administration workspace	p. 975
E.2.2	The RBE model tree view	p. 976
E.2.3	RBE model information	p. 977
E.2.4	Model-specific parameters for LEM	p. 979
E.2.5	Operations on RBE models	p. 982
E.2.6	Create a new LEM-I RBE model	p. 983
E.2.7	Create a new user-defined LEM model	p. 985
E.2.8	Save to and read from database	p. 986
E.2.9	Backup and restore RBE models	p. 987

Precautions

WARNING!

Limitations in the LEM model for high doses. Due to the limited availability of experimental data for high fraction doses, the Local Effect Model (LEM) has not been comprehensively evaluated and the user should be aware that the model may be unreliable at high fraction doses. (261598)

WARNING!

Variations in RBE for different LET values using LEM-I. It has been observed that LEM-I tends to overestimate the RBE at low Linear Energy Transfer (LET) values, and underestimate the RBE at high LET. From a clinical point of view, these trends go in the "right" direction in the sense that the actual effect in normal tissue located in the entrance channel should be lower than predicted by the model, whereas the effect in the tumor region should be higher than predicted. The user should still be aware of these effects. (261600)

WARNING!

Track dose parameter limitations for RBE using LEM-I. The RBE-weighted dose according to LEM-I has only been validated using the following track dose parameters:

- Track core radius = 0.01 µm
- Prefactor (γ) = 0.05 µm/(MeV/u) $^{\delta}$
- Exponent (δ) = 1.7
- No Kiefer low energy approximation

Although it is possible to choose different parameters as input to RayStation, this should be handled with extra care as it lies outside the bounds of the Local Effect Model. (261599)

WARNING!

Cell type parameter limitations for RBE using LEM-I. The RBE-weighted dose according to LEM-I has been validated for a range of cell types with varying radio sensitivity. However, the user should acknowledge that the following cell type parameters (Chordoma) are predominantly used in clinical practice:

- $\alpha_x = 0.10\ Gy^{-1}$
- $\beta_x = 0.050\ Gy^{-2}$
- $D_t = 30\ Gy$
- $r_n = 5.0\ \mu m$

Although other cell type parameters can be chosen as input to the model in RayStation, users should not apply this for clinical purposes until an extensive evaluation of the safety and the clinical efficacy has been carried out. (261601)

E.2.1 The RBE Model Administration workspace

The RBE Model Administration workspace consists of the RBE model tree view and the RBE model parameters.

For uncommissioned RBE models it is possible to edit the RBE model parameters by clicking the **Enter edit mode** button. To return to normal mode, click the **Exit edit mode** button (visible in edit mode).

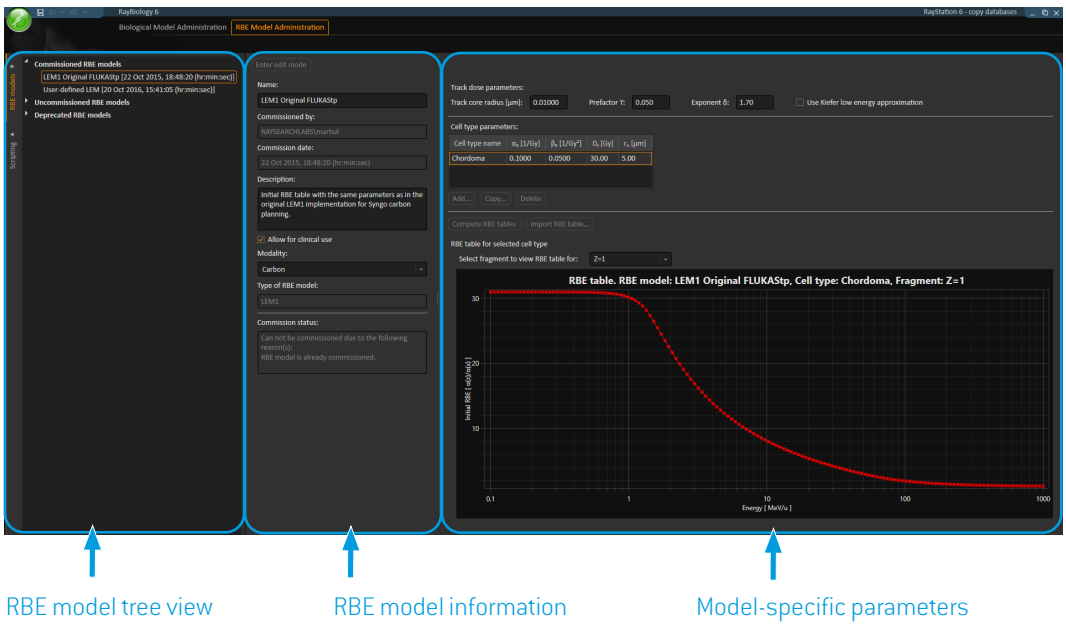


Figure 514. The RBE Model Administration workspace.

E.2.2 The RBE model tree view

The RBE model tree view shows the available RBE models in the patient database. The RBE models can be changed locally by the user. To view an RBE model, click on the RBE model name in the tree view.

There are three types of RBE models:

- **Commissioned RBE models** - RBE models at the user clinic that are ready for treatment. Commissioned RBE models cannot be edited.
- **Uncommissioned RBE models** – RBE models at the user clinic where the editing has not yet been completed. Uncommissioned RBE models can be edited.
- **Deprecated RBE models** – previously commissioned RBE models that are no longer eligible for plan generation. It is not possible to re-compute RBE doses calculated with a deprecated RBE model. Deprecated RBE models cannot be edited.

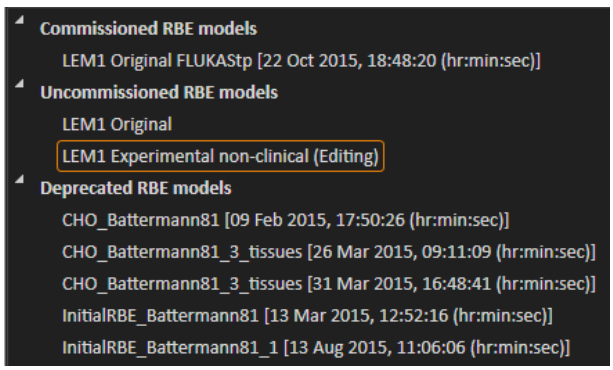

Commissioned RBE models
LEM1 Original FLUKAStp [22 Oct 2015, 18:48:20 (hr:min:sec)]
Uncommissioned RBE models
LEM1 Original
LEM1 Experimental non-clinical (Editing)
Deprecated RBE models
CHO_Battermann81 [09 Feb 2015, 17:50:26 (hr:min:sec)]
CHO_Battermann81_3_tissues [26 Mar 2015, 09:11:09 (hr:min:sec)]
CHO_Battermann81_3_tissues [31 Mar 2015, 16:48:41 (hr:min:sec)]
InitialRBE_Battermann81 [13 Mar 2015, 12:52:16 (hr:min:sec)]
InitialRBE_Battermann81_1 [13 Aug 2015, 11:06:06 (hr:min:sec)]

Figure 515. The RBE model tree view.

E.2.3 RBE model information

RBE model name and description

The RBE model name must be unique for all commissioned and uncommissioned RBE models. Deprecated RBE models will keep the commissioned RBE model name. It is also possible to add an optional description of the RBE model.

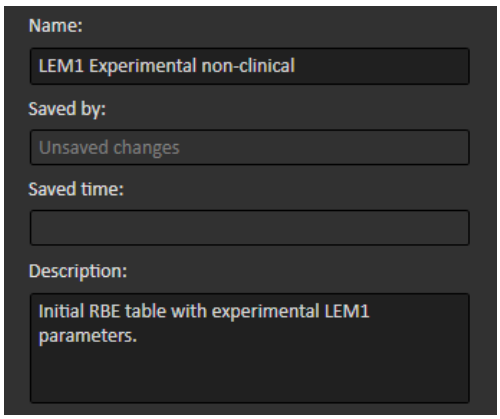


Figure 516. The **Name** and **Description** fields for an uncommissioned RBE model. The figure also shows who the RBE model was saved by (**Saved by** field) and at what time (**Saved time** field).

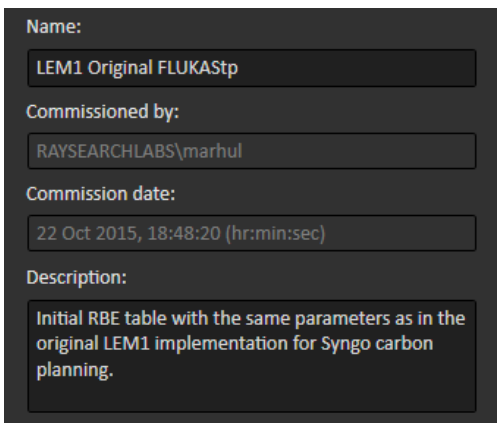
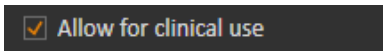

Name:
LEM1 Original FLUKAStp
Commissioned by:
RAYSEARCHLABS\marhul
Commission date:
22 Oct 2015, 18:48:20 (hr:min:sec)
Description:
Initial RBE table with the same parameters as in the original LEM1 implementation for Syngo carbon planning.

Figure 517. The **Name** and **Description** fields for a commissioned RBE model. The figure also shows who the RBE model was commissioned by (**Commissioned by** field) and at what date (**Commission date** field).

Allow for clinical use of the RBE model

The **Allow for clinical use** checkbox has to be checked in order to allow the RBE model to be used clinically.



It is also possible to commission an RBE model without allowing it to be used clinically. The RBE model can then be used for evaluation purposes in dose calculations, but will never be able to yield a clinical dose.

Modality and type of RBE model

The available RBE model types are LEM-I (Local Effect Model version 1) and user-defined LEM (imported data). Both types can be used to compute RBE weighted dose for carbon ions.

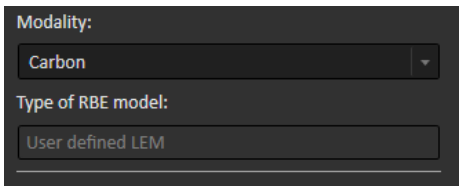


Figure 518. Modality and type of RBE model is shown.

Commission status

The **Commission status** field lists the reasons why an RBE model cannot be commissioned.

Note: *The Commission status field only lists the formal requirements of an RBE model in RayStation. Just because an RBE model can be commissioned does not mean that it is suitable for treatment planning.*

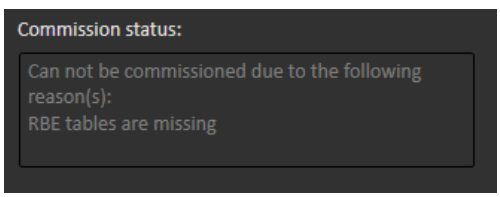


Figure 519. The **Commission status** field.

E.2.4 Model-specific parameters for LEM

Track dose parameters for LEM-I

The **Track dose parameters** for calculation of initial RBE tables with LEM-I are described in the table below:

Parameter name	Unit	Description
Track core radius, r_c	µm	Radius of the core of the ion track (minimum radius).
Prefactor, γ	$\mu\mathrm{m} \cdot \left(\frac{\mathrm{MeV}}{\mathrm{u}}\right)^{-\delta}$	A constant (prefactor) that is used to obtain the maximum radius of the track.
Exponent, δ	-	A constant (exponent) that is used to obtain the maximum radius of the track.

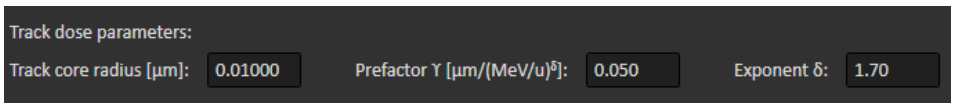
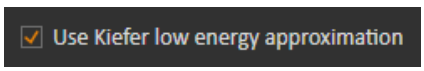


Figure 520. The **Track dose parameters** for LEM-I.

Check the **Use Kiefer low energy approximation** checkbox to use a different track dose model for energies below 2 MeV/u. For more information, refer to the *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual*.



Cell type parameters

It has to be specified which cell types the Local Effect Model should be applied to. For the original LEM, only one cell type (with its specific parameter values) is used. To be able to compute RBE dose for the entire patient, the external ROI must have a cell type that is defined in the RBE model used for dose computation.

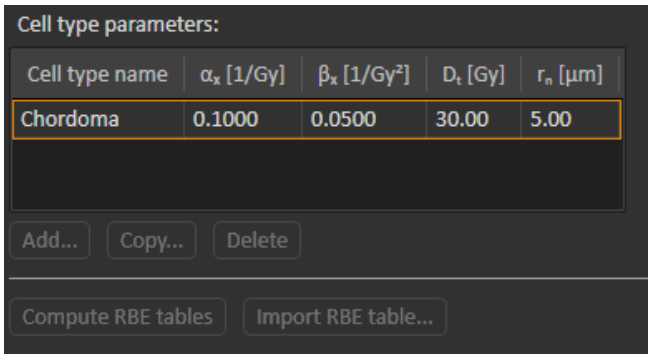


Figure 521. The **Cell type parameters** list for LEM-I/user-defined LEM.

Use the **Add...**, **Copy...** and **Delete** buttons to add, copy or delete cell types in the **Cell type parameters** list. The cell type names have to be unique within the RBE model. When adding a cell type, the user has the option to select an existing cell type from any biological model or RBE model. Cell types already added to the model will not be available for selection. It is also possible to add a completely new cell type by writing a new name in the **Name** field. When copying a cell type, all LEM parameters will be copied to a new cell type, and a new cell type name needs to be entered.

The cell type specific parameters in the **Cell type parameters** list are described in the table below:

Parameter name	Unit	Description
α_x	Gy^{-1}	Alpha value for photons.
β_x	Gy^{-2}	Beta value for photons.
D_t	Gy	Dose transition, the dose where the survival curve becomes exponential.
r_n	µm	Radius of the cell nucleus.

Initial RBE table

When computing RBE dose, a table mapping energy to initial RBE will be used (RBE table). To speed up dose computation, this table is stored in the commissioned RBE model. For LEM-I, the RBE tables are computed based on the LEM parameters. For user-defined LEM, the tables are imported from a text file together with the corresponding parameters. The RBE tables for each fragment can be viewed in a graph.

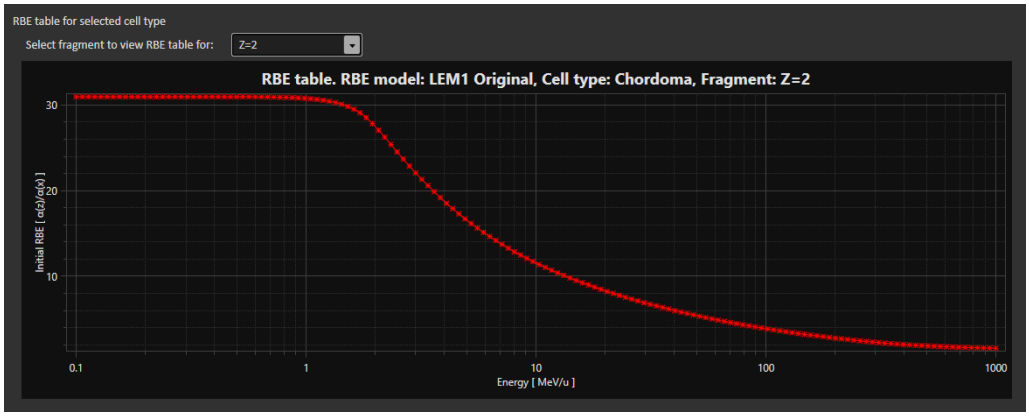


Figure 522. The RBE table for the selected cell type.

E.2.5 Operations on RBE models

Right-clicking on an RBE model name will give access to a few alternatives.

Alternatives for a commissioned RBE model:

- **Copy RBE model** – copies the RBE model to the uncommissioned RBE models, allowing the user to edit the RBE model properties.
- **Deprecate RBE model** – moves the RBE model to the deprecated RBE models. This step is password protected.

Alternatives for an uncommissioned RBE model:

- **Commission RBE model** – moves the uncommissioned RBE model to the commissioned RBE models, making it impossible to edit the RBE model and making the RBE model eligible for clinical planning and dose computation. It is important that the user responsible for commissioning an RBE model has good knowledge of how the model works and carefully reviews the model parameters before commissioning. The RBE model parameters will be displayed for the user in a wizard when the commissioning process is started. The commissioning step is password protected.
- **Copy RBE model** – copies the RBE model to the uncommissioned RBE models, allowing the user to edit the RBE model properties.
- **Delete RBE model** – deletes the RBE model from the patient database.

Alternative for a deprecated RBE model:

- **Copy RBE model** – copies the RBE model to the uncommissioned RBE models, allowing the user to edit the RBE model properties.

Additional alternative by right-clicking on the **Uncommissioned RBE models** node:

- **Create new LEM-I model** – creates a new empty LEM-I model under uncommissioned RBE models.
- **Create new user defined LEM model** – creates a new empty user defined LEM model under uncommissioned RBE models.

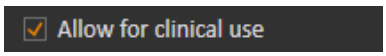
When creating a new version of an RBE model, that is deprecating a commissioned RBE model and creating a new commissioned RBE model with the same name, the deprecated RBE model will no longer be available in RayStation. When opening a patient mapped to the deprecated RBE model, the user will be notified that it exists a newer version of the RBE model. It will be possible to review old doses that have been calculated using the deprecated RBE model, however it will not be possible to calculate new dose without updating to the new RBE model version. Updating to the new version will invalidate calculated RBE doses.

E.2.6 Create a new LEM-I RBE model

To create a new LEM-I RBE model:

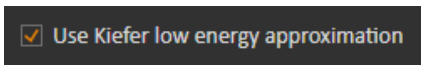
1. In the RBE model tree view, right-click on **Uncommissioned RBE models** and select **Create new LEM-I model**.

2. Enter a model name in the **Name** field.
3. Enter a description in the **Description** field (optional).
4. Check the **Allow for clinical use** checkbox if the RBE model should be used clinically.



Note: *The Allow for clinical use checkbox has to be checked in order to yield a clinical dose.*

5. Check the **Use Kiefer low energy approximation** checkbox to use a different track dose model for energies below 2 MeV/u (optional).



6. Use the **Add...**, **Copy...** and **Delete** buttons to add, copy or delete cell types in the **Cell type parameters** list.

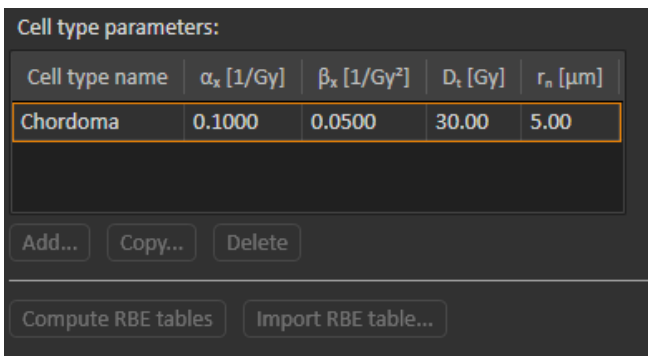


Figure 523. The **Cell type parameters** list for LEM-I.

7. Edit the cell type specific parameters in the **Cell type parameters** list. For more information, see *Cell type parameters on page 979*.
8. Click the **Compute RBE tables** button to compute the RBE tables.

9. Check that the RBE tables in the RBE table visualization look as expected based on the entered values for the cell type specific parameters.

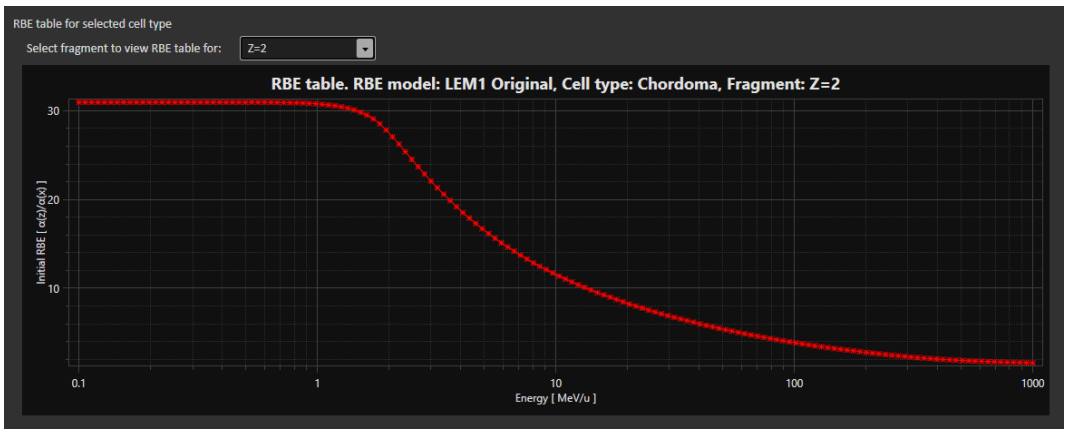


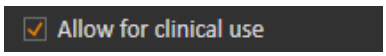
Figure 524. The RBE table visualization.

10. Click **Save**.

E.2.7 Create a new user-defined LEM model

1. In the RBE model tree view, right-click on **Uncommissioned RBE models** and select **Create new user defined LEM model**.

2. Enter a model name in the **Name** field.
3. Enter a description in the **Description** field (optional).
4. Check the **Allow for clinical use** checkbox if the RBE model should be used clinically.



5. Use the **Add...**, **Copy...** and **Delete** buttons to add, copy or delete cell types in the **Cell type parameters** list.

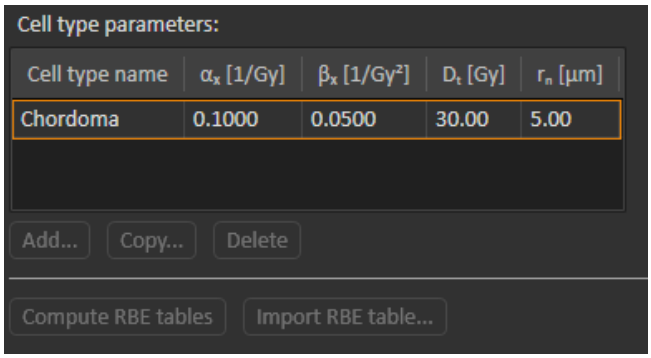


Figure 525. The **Cell type parameters** list for the user-defined LEM model.

6. Select a cell type in the list and click the **Import RBE tables** button to import cell type parameters and precomputed RBE tables from an external data file. For a description of the required data format, refer to the *RSL-D-RS-7.0-REF, RayStation 7 Reference Manual*.
7. Check that the RBE cell type parameters are correct and that the tables in the RBE table visualization look as expected based on the input.
8. Click **Save**.

E.2.8 Save to and read from database

RBE models are saved to the machine database at **Save**, **Commission**, **Deprecate** or **Delete** and optionally when clicking the **Exit edit mode** button. Saving RBE models requires synchronization with the patient database, that may have been changed by another user. The synchronization can also be forced by clicking the **Refresh RBE model list** button at the bottom of the tree view.

Opening an RBE model in edit mode also triggers an automatic synchronization with the database.

Note: *Once saved, changes cannot be undone. The user should be aware of that commissioning, depricating and deleting actions trigger autosave.*

E.2.9 Backup and restore RBE models

The backup and restore functionality is primarily designed for communicating data between the clinic and RaySearch, e.g., if there are problems related to a specific data set. It will not be possible to restore an RBE model backed up in one RayStation version using an earlier version of RayStation. The backup and restore functionality should not be used for long-term storage of RBE model data. However, it can be useful for backups in the current RayStation version.

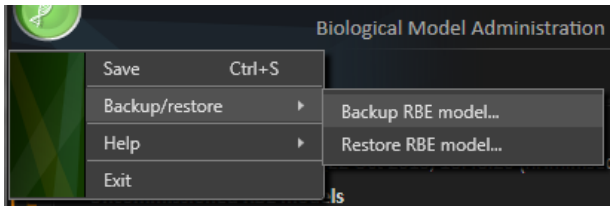


Figure 526. **Backup RBE model** and **Restore RBE model** are both found in the RayBiology menu.

Backup RBE models

An RBE model backup can be exported as an .rsbak file. This file is checksum protected and therefore it cannot be imported if it has been edited.

To backup an RBE model:

1. Select **Backup/Restore** from the RayBiology menu and **Backup RBE model...**.

   This opens the **Backup RBE model** dialog.

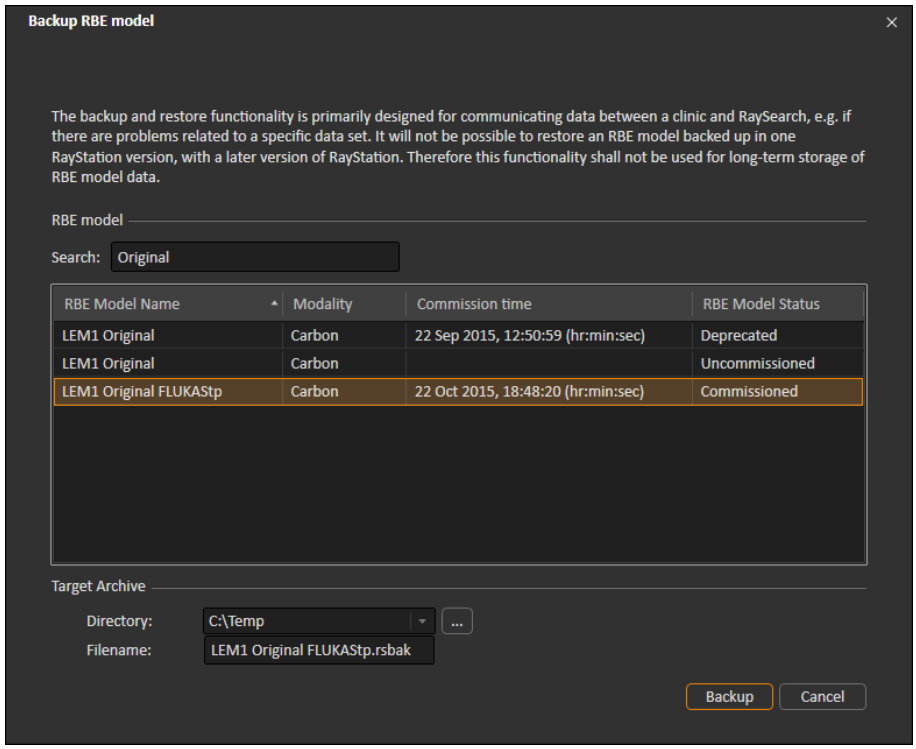

Backup RBE model
The backup and restore functionality is primarily designed for communicating data between a clinic and RaySearch, e.g. if there are problems related to a specific data set. It will not be possible to restore an RBE model backed up in one RayStation version, with a later version of RayStation. Therefore this functionality shall not be used for long-term storage of RBE model data.
RBE model
Search: Original
RBE Model Name
Modality
Commission time
RBE Model Status
LEM1 Original
Carbon
22 Sep 2015, 12:50:59 (hr:min:sec)
Deprecated
LEM1 Original
Carbon
Uncommissioned
LEM1 Original FLUKAStp
Carbon
22 Oct 2015, 18:48:20 (hr:min:sec)
Commissioned
Target Archive
Directory: C:\Temp
Filename: LEM1 Original FLUKAStp.rsbak
Backup
Cancel

Figure 527. The **Backup RBE model** dialog.

2. Select an **RBE model** in the list by clicking on it.
3. Select a **Directory** for the RBE model.
4. Click **Backup**.

Restore RBE models

All .rsbak files with RBE models can be restored only if they have been created with the same version or earlier versions of RayStation, and have not been changed manually between backup and restore.

If a commissioned or uncommissioned RBE model with the same name and modality is present, the RBE model cannot be restored without changing the name at import. This is done automatically by RayBiology and a suffix will be added at the end of the RBE model name, e.g., "_1". If name, modality and commissioning time are identical for a commissioned RBE model, restore will not be allowed.

Note: *The commissioning status of the RBE models are kept at .rsbak restore. Restoring a commissioned RBE model will make the RBE model available for plan generation in RayStation.*

To restore an RBE model:

1. Select **Backup/Restore** from the RayBiology menu and **Restore RBE model...**.

   This opens the **Restore RBE model** dialog.

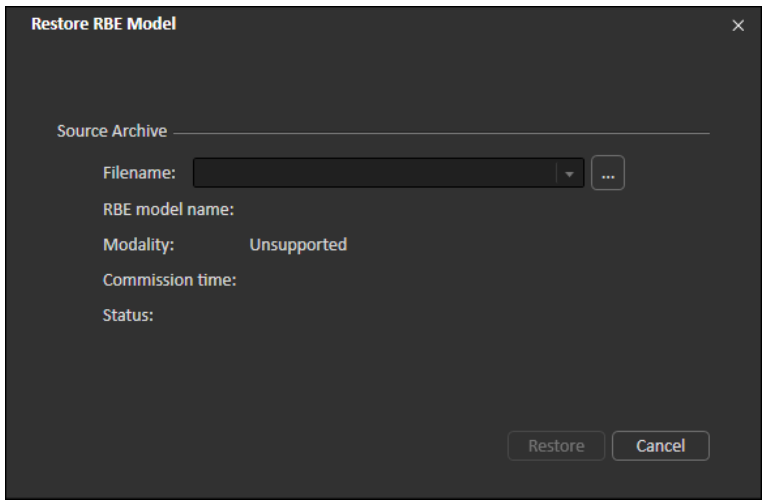


Figure 528. The **Restore RBE model** dialog.

2. Select an RBE model in the **Filename** drop-down list.
3. Click **Restore**.

   When a commissioned RBE model is restored, the model parameters will be displayed for the user to verify that it is the intended RBE model that is restored. The correct user password in the authentication dialog must be entered after the wizard has completed.

F RAYSTATION REPORT DESIGNER

RayStation enables configuration of printable treatment plan reports and QA plan reports. The report templates are created using the RayStation Report Designer that contains features such as:

- report content design by drag and drop
- default templates for a treatment plan and a QA plan
- report customization using conditions (e.g., creating templates that will display information for a certain beam type)
- report preview
- tools for basic layout design (inserting page breaks, designing tables etc.)

Launching RayStation Report Designer

To launch the RayStation Report Designer application, go to the folder **Program files: RaySearch Laboratories: RayStation 7** and launch the file ReportDesigner.exe.

In this chapter

This chapter contains the following sections:

F.1	The RayStation Report Designer workspace	p. 992
F.2	Data modules	p. 993
F.3	Iterators	p. 995
F.4	Conditions	p. 996
F.5	Layout modules	p. 997
F.6	Report content area	p. 998
F.7	Change the report logotype	p. 1000
F.8	Create a new report template	p. 1001
F.9	Create a report template based on a default template	p. 1002

F.1 THE RAYSTATION REPORT DESIGNER WORKSPACE

The RayStation Report Designer workspace is divided into three main areas: the modules area to the left, the report content area in the middle and the preview area to the right.

The modules area contains all modules that can be included in a report, such as data modules, iterators, conditions and layout modules. A module can contain other modules or module elements such as iterators and conditions.

The desired modules are added to the report content area by drag and drop. To edit the properties of a specific element, select the element and click **Edit** in the **Selected item** area in the middle of the RayStation Report Designer workspace.

When using the report preview, make sure that the correct **Beam set** and **Beam** have been selected in the bottom part of the RayStation Report Designer workspace.

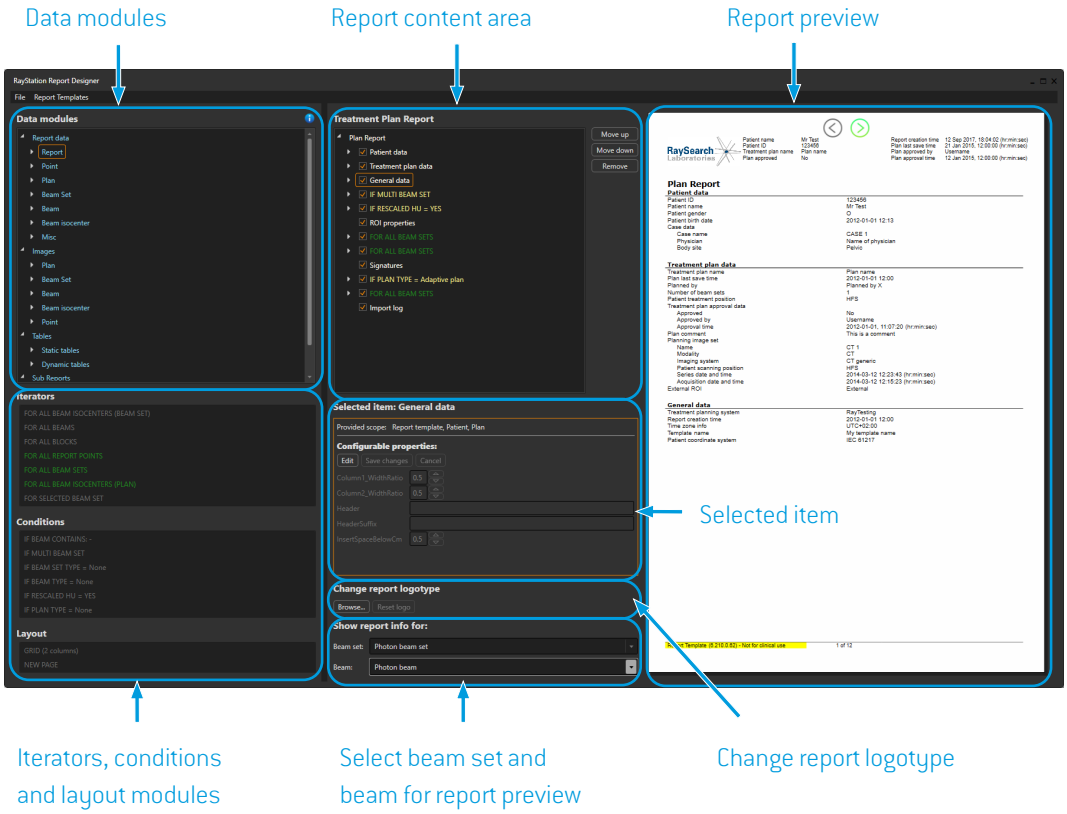


Figure 529. The RayStation Report Designer workspace.

F.2 DATA MODULES

Data modules generate output in the report. The data modules are divided into the following sub-categories:

- **Report data**
- **Images**
- **Tables**
- **Sub Reports**

Only the white data modules within each blue sub-category can be added to the report content area. Click the arrow next to a sub-category to expand it and see its data modules.

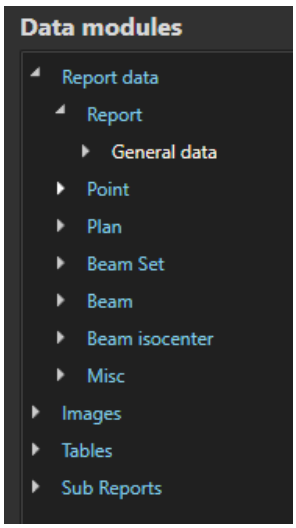


Figure 530. The Data modules are located to the upper left in the RayStation Report Designer workspace.

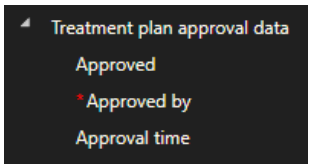
Report data

The Report data modules display different categories of patient data in the report:

- **Report** - general report data, for example, treatment planning system and patient coordinate system
- **Point** - POI coordinates
- **Plan** - general plan data, for example, Patient ID and Patient name
- **Beam Set** - for example, Beam Set overview and Patient setup
- **Beam** - for example, DMLC Beam data and Beam dose specification point
- **Beam isocenter** - for example, isocenter name for the plan or a beam set

- **Misc** - contains the **Free text node**. Any chosen text can be typed in the **Free text node** settings, for example the name of the clinic. The **Free text node** module element can be added to the report content area as many times as desired.

Some module elements are indicated by a red star. These are required in the template in order to make the report IEC 62083 compliant.



Note: *If the report template does not contain all parameters required by ISO 62083, a message will be displayed at the bottom of the report. Below the report there will also be a field called "IEC Compliance: Missing data modules" that can be expanded in order to locate the missing data modules.*

Images

Image modules display different image categories in the report:

- **Plan** - for example, the DVH for the plan dose
- **Beam Set** - for example, DVH for the beam set dose
- **Beam** - for example, block and compensator images for a specific beam
- **Beam isocenter** - for example, plan or beam set dose for a beam isocenter
- **Point** - for example, plan or beam set dose for a report point

Tables

Table modules display static and dynamic tables in the in the report. Static tables can for example be tables such as patient import log, beam set warnings or ROI properties.

Sub Reports

There are two types of sub report modules that can be added if applicable: beam set report and adaptation information.

F.3 ITERATORS

Iterators are used for iteration of collections within a patient. Typical collections in a patient are beam sets and beams. For example, in a beam set there will be one or multiple beams defined. To generate content about each beam, a **FOR ALL BEAMS** iterator will iterate through the collection of beams and generate the content defined by the sub-modules to the iterator module.

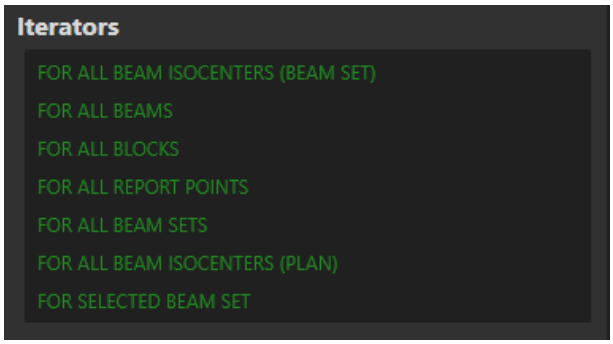


Figure 531. The iterators are located to the middle left in the RayStation Report Designer workspace.

Iterator modules can be added to the report content area in order to modify the scope. For example, the iterator **FOR ALL BEAM SETS** that has the provided scope **Beam Set** can be added to the report content area in order to allow insertion of a module element that has a required scope **Beam Set**.

F.4 CONDITIONS

Conditions can be used to control when certain information will be displayed in the report. For example, when using the condition **IF BEAM TYPE = SMLC beam**, the information will only be displayed for a SMLC beam.

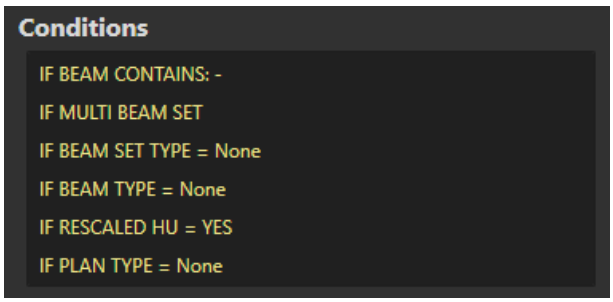


Figure 532. The conditions are located to the lower left in the RayStation Report Designer workspace.

F.5 LAYOUT MODULES

Layout modules such as page break (**NEW PAGE**) and table grid (**GRID (2 columns)**) can be added to the report template. The table grid element can contain data modules and image modules. If a data module is added to a grid, the size of the content should be modified in the settings dialog in order to fit the grid.

Figure 533. The layout modules are located to the lower left in the RayStation Report Designer workspace.

F.6 REPORT CONTENT AREA

The report content area is where the treatment plan report or the QA plan report is designed by drag and drop of different content modules.

The information structure is hierarchic and it is possible to change the level of the individual content modules either by drag and drop or by using the **Move up** and **Move down** buttons. It is also possible to add a content module to another content module.

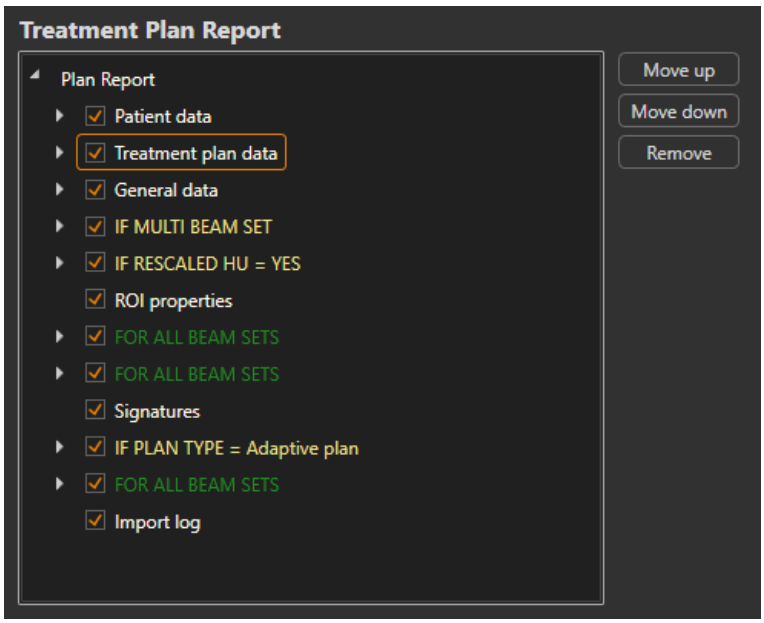


Figure 534. The report content area is located in the middle of the RayStation Report Designer workspace.

Edit the properties of a selected item

To edit the properties of a selected item in the **Treatment Plan Report** list:

1. Click the item in the list.
2. Click **Edit** in the **Selected item** area.

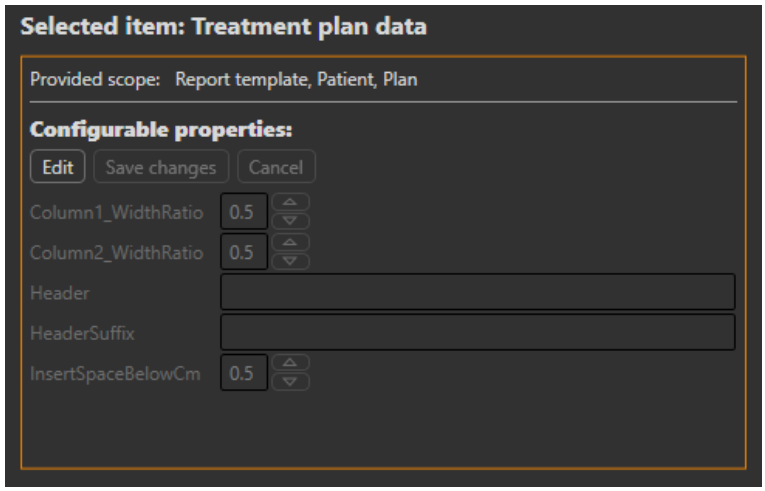


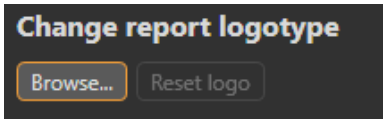
Figure 535. The Selected item area is located in the middle of the RayStation Report Designer workspace.

3. Edit the desired properties and click **Save changes**.

F.7 CHANGE THE REPORT LOGOTYPE

To change the report logotype to a logotype of your choice:

1. Click **Browse** in the **Change report logotype** area.



2. Select the new report logotype and click **Open**.

To change back to the RaySearch logotype, click **Reset logo**.

F.8 CREATE A NEW REPORT TEMPLATE

To create a new report template for a treatment plan or a QA plan:

1. Select **Report Templates: Empty Templates** and select either **Treatment Plan Report** or **QA Plan Report**.

   Result: The plan specific modules are enabled and the report content area is empty from start.

2. Add data modules from the **Data modules** area to the template by dragging and dropping them into the **Report content** area.

   Note: *The required scope for the module being added must be fulfilled. If the required scope is not fulfilled, the data module will be grey and cannot be added. Hovering over a grey data module will show information on the missing elements.*

   - Iterators can be added to the report content area in order to modify the scope. For example, the iterator **FOR ALL BEAM SETS** that has the provided scope **Beam Set** can be added to the report content area in order to allow insertion of a module element that has a required scope **Beam Set**.
   - Data modules can be moved up or down in the report content area using the arrow buttons.
   - To remove a data module from the template, select it and click **Remove** or uncheck the corresponding checkbox.

3. Add iterators and conditions by drag and drop. Double-click on the added item to specify settings.

4. Preview the created template. If iterators and/or conditions have been added to the template, these can be tested by changing **Beam set** and **Beam** in the lower part of the workspace.

   Note: *If the report template does not contain all parameters required by ISO 62083, a message will be displayed at the bottom of the report. Below the report there will also be a field called "IEC Compliance: Missing data modules" that can be expanded in order to locate the missing data modules.*

5. When the template is ready, click **File: Save as...** and enter a name for the template.

   Note: *User created report templates does not necessarily need to include all information about patient, plan, beam sets, etc. For example, a report template may only include the currently selected beam set. Use a clear naming convention when creating report templates.*

6. Save the template as a .rst file.

7. In order to use the template as a clinical template it must be added to the ClinicalDB database. For more information, see *section D.2 The Clinic Settings application on page 920*.

   When the template has been added to the database it can be used from within RayStation.

F.9 CREATE A REPORT TEMPLATE BASED ON A DEFAULT TEMPLATE

To create a new report template for a treatment plan or a QA plan based on a default template:

1. Select **File: Open: Default: Treatment plan report**.

   Result: The plan specific modules are enabled and the report content area is filled with the default modules.

2. Add data modules from the **Data modules** area to the template by dragging and dropping them into the **Report content** area.

   Note: *The required scope for the module being added must be fulfilled. If the required scope is not fulfilled, the data module will be grey and cannot be added. Hovering over a grey data module will show information on the missing elements.*

   - Iterators can be added to the report content area in order to modify the scope. For example, the iterator **FOR ALL BEAM SETS** that has the provided scope **Beam Set** can be added to the report content area in order to allow insertion of a module element that has a required scope **Beam Set**.
   - Data modules can be moved up or down in the report content area using the arrow buttons.
   - To remove a data module from the template, select it and click **Remove** or uncheck the corresponding checkbox.

3. Add iterators and conditions by drag and drop. Double-click on the added item to specify settings.

4. Preview the created template. If iterator modules and/or condition modules have been added to the template, these can be tested by changing **Beam set** and **Beam** in the lower part of the workspace.

   Note: *If the report template does not contain all parameters required by ISO 62083, a message will be displayed at the bottom of the report. Below the report there will also be a field called "IEC Compliance: Missing data modules" that can be expanded in order to locate the missing data modules.*

5. When the template is ready, click **File: Save as...** and enter a name for the template.

   Note: *User created report templates does not necessarily need to include all information about patient, plan, beam sets, etc. For example, a report template may only include the currently selected beam set. Use a clear naming convention when creating report templates.*

6. Save the template as a .rst file.

7. In order to use the template as a clinical template it must be added to the ClinicalDB database. For more information, see *section D.2 The Clinic Settings application on page 920*.

   When the template has been added to the database it can be used from within RayStation.

G LINE DOSE EXPORT

The exported line dose file may contain one or several line doses.

The file starts with a general header with the following information:

- **RayStationVersion** – Version of the RayStation/RayPhysics application that the file was exported from.
- **PatientName** – RayStation name of the patient.
- **PatientId** - RayStation Patient ID.
- **PhantomName** – RayStation name of the phantom. Only applicable when exporting from the QA Preparation module.
- **CoordinateSystem** – The coordinate system for the line dose points. This is always the IEC patient coordinate system, which is the same coordinate system visualized in the RayStation/RayPhysics GUI.

The following information is also included for each exported line dose:

- **LineName** – The name of the dose line as visualized in the line dose histogram.
- **DoseName** – Information about the exported dose, for example plan dose or fraction dose information.
- **DoseEngine** – Information about the dose engine that calculated the dose, the dose engine version and if the dose is clinical.
- **TreatmentMachine** – Name and commissioning time of the machine that calculated the dose, if the information is available. If the machine is uncommissioned, this is noted instead of commissioning time.

The dose line is written as X, Y, Z coordinates followed by the dose value (shown in the following example).

Example

```
############################################################
#RayStationVersion: 5.0
#PatientName: PHYSICS
#PatientId: 123456
#PhantomName: WaterPhantom
```

```
#CoordinateSystem: IEC patient coordinate system
############################################################
#LineName: 1
#DoseName: Fraction dose: 3D-CRT
#DoseEngine: Clinical: Collapsed Cone v3.2
#TreatmentMachine: TRUEBEAM Commission time: 01/30/2015 13:51:20

#X [cm] Y [cm] Z [cm] Dose [cGy]
10.645 -45.150 42.314 44.197
10.635 -45.150 42.315 44.214
10.625 -45.150 42.315 44.230
10.615 -45.150 42.316 44.247
10.605 -45.150 42.317 44.263
10.595 -45.150 42.318 44.280
10.585 -45.150 42.319 44.297
10.575 -45.150 42.320 44.313
10.565 -45.150 42.321 44.330
```

G.1 CARBON IONS

For carbon ions, the RBE model name and algorithm will also be written to the file.

RBE dose example

```
RBE dose example
############################################################
#RayStationVersion: 5.0.0.34
#PatientName: PHYSICS
#PatientId: WaterPhantom2
#CoordinateSystem: IEC patient coordinate system
############################################################
#LineName: 1
#DoseName: Plan dose (RBE): 10GyRBE_Classic (CT 1)
#DoseEngine: Clinical: Pencil Beam v1.0
#RBEModel: LEM1 Original, Classic, 1000 repetitions
#TreatmentMachine: CarbonMachine Commission time: 11/09/2015 11:00:00
#X [cm];Y [cm];Z [cm];Dose [cGy (RBE)]
20.147; 0.050; 0.040; 0.000
...
```

H IMPORTING TOMOTHERAPY HI-ART DOSE INTO RAYSTATION

It is possible to import TomoTherapy Hi-Art dose into RayStation and to create fallback plans for the Tomo dose. A filter designed for this import is required in order to enable import of Tomo into RayStation. Ask your RaySearch support representative how to receive this filter and for instructions to install it.

This import workflow can also be applied for other imported plans from other types of LINACs. In these cases, the Tomo Hi-Art Helical Plan conversion filter does not need to be applied during import (step 1 in the workflow) .

Workflow

1. Import the DICOM images, structure set, plan and dose files from the specified storage location. Select to apply the Tomo Hi-Art Helical Plan conversion filter upon import.

   For information and instructions on how to import patient data and using filters, see *section 4.3.1 Import new patient data on page 112*.

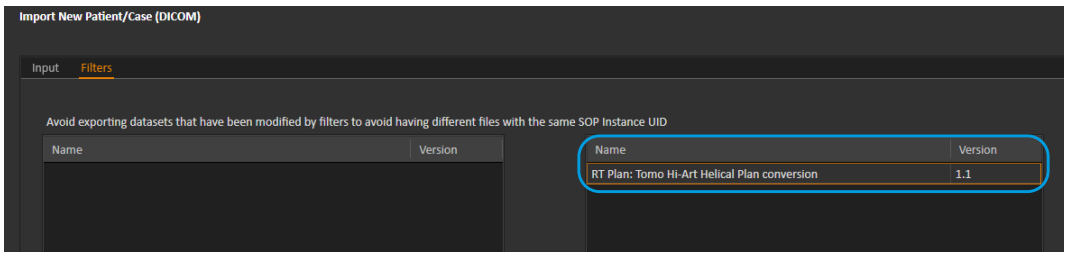


Figure 536. The **Import New Patient/Case (DICOM)** dialog with Tomo Hi-Art Helical Plan conversion filter selected.

The Tomo Hi-Art Helical Plan conversion filter will collapse the Tomo treatment to a single isocenter. The prescription will not be imported.

The treatment machine will be highlighted in yellow since it does not exist in the system database and it is considered to be a 3D-CRT technique upon import.

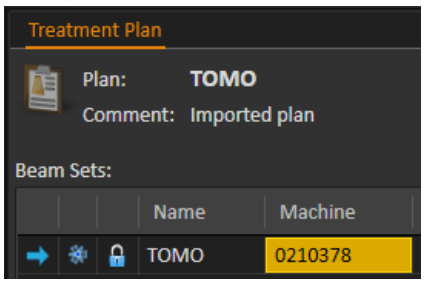
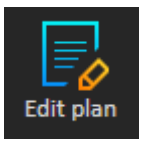
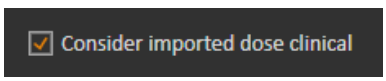


Figure 537. An imported Tomo plan with the treatment machine highlighted in yellow.

2. Click the **Edit plan** button to open the **Edit plan** dialog. In the dialog, edit the plan name if desired.



3. In the **Edit plan** dialog, check the **Consider the imported dose clinical** checkbox. This must be done in order to use the plan for fallback planning and protocol creation.



By considering the dose clinical, the dose will appear as "Clinical: Imported dose" in the patient views and the beam set referring to that dose will be set as read-only. This is shown by a blue padlock next to the beam set in the beam set list.

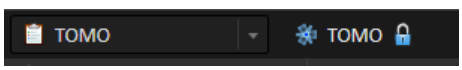


Figure 538. A blue padlock next to the beam set in the beam set list represents a clinical dose.

4. Approve the plan in the Plan Evaluation module. For information about plan approval, see *section 8.1.15 Plan approval on page 748*.
5. Once the plan has been approved, it is available to use as the nominal plan for fallback planning.

   Continue the process of Fallback Protocol creation and Fallback Plan generation as described in the fallback planning workflow, see *section 10.3 The Fallback Planning workflow on page 843*.

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RSL-D-RS-7.0-USM-EN-1.0-2017-12-08
RayStation 7 User Manual

RaySearch Laboratories